

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1387.8	99.8	1391	6	AR321600	AR321600 Sequence
2	1387.8	99.8	1391	9	HUWRAGE	M91211 Human recep
3	1373	98.7	1436	9	BC020669	BC020669 Homo sapi
4	1242	89.3	1268	9	AB036432	AB036432 Homo sapi
5	1193.6	85.8	1451	9	AB061669	AB061669 Homo sapi
6	1172.8	84.3	1218	6	CQ730900	CQ730900 Sequence
7	1062	76.3	1233	6	BD176670	BD176670 Soluble R
8	1062	76.3	1233	9	AB061668	AB061668 Homo sapi
9	1029.4	74.0	1250	9	HSAL13822	AJ113822 Homo sapi
10	944.6	67.9	1426	4	BOVRAGE	M91212 Cow recepto
11	944.8	67.9	1426	6	AR321599	AR321599 Sequence
12	826.4	59.4	1348	6	AR321601	AR321601 Sequence
13	826.4	59.4	1348	10	MUSRECEP	L33412 Mouse recept
14	822.6	59.1	1420	10	RATRECEP	L33413 Rat recept
15	821.6	59.1	1399	10	BC061182	BC061182 Mus muscu
16	610.4	43.9	990	4	AY330943	AY330943 Canis fam
17	476.6	34.3	610	6	AX333424	AX333424 Sequence
18	476.6	34.3	610	6	AX410951	AX410951 Sequence
19	467.2	33.6	598	6	AX795283	AX795283 Sequence

;

Db 121 GCCCCAAGAAACACCCAGCGGCTGGAAATGGAACCTGAAACAGACGGCCGACAGAGCT 180
Qy 181 TGAAGGTCTCTGCTCCCAAGGAGGAGGCCCTCGGACAGTGTGCTGCTGCTTCCC 240
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Qy 241 AACGGCTCCCTCTCTCTCCGCTGTGCGGATCCAGATCAGGAGATTTTCGGTCCAG 300
Db 241 AACGGCTCCCTCTCTCTCCGCTGTGCGGATCCAGATCAGGAGATTTTCGGTCCAG 300
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Db 1141 GAAGAGGAGGAGGCTCAGAACTGAATCAGTCCGAGGAACTTAGGAGCAGGCGAGTAGT 1200
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Qy 1261 CCTTGAACCTGTTCTGGCCTCAGACCAACTCTCTCTGTATAATCTCTCTCTCTATAACC 1320
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RESULT 3
BC020669
LOCUS
DEFINITION
Homo sapiens advanced glycosylation end product-specific receptor,
transcript variant 1, mRNA (CDNA clone MGC:22357 IMAGE:4718076),
complete cds.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BC020669.1 GI:18088362
MGC.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1436)
AUTHORS
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shennen, C.W., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Sánchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1436)
AUTHORS
Straussberg, R.
DIRECT SUBMISSION
Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
TITLE
human and mouse cDNA sequences
JOURNAL
PUBMED
REFERENCE
2 (bases 1 to 1436)
AUTHORS
Straussberg, R.
DIRECT SUBMISSION
Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 37 Row: e Column: 17

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 26787960.

FEATURES
source

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FEATURES             Location/Qualifiers
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     /note="Vector: pDNR-LIB"
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```

ORIGIN

Query Match	98.7%	Score 1373	DB 9	Length 1436
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1384	Conservative 0	Mismatches 0	Indels 1	Gaps 1
Qy	3	GGCAGCCGGAAACAGCAGTTCGGAGCCTGGGTGCTGTCCTCAGTCTGTGGGGGCGCAGTAGT	62	
Db	22	GGCAGCCGGAAACAGCAGTTCGGAGCCTGGGTGCTGCTCAGTCTGTGGGGGCGCAGTAGT	81	
Qy	63	AGGTGCTCAAAAACATCAGAGCCCGGATTTGGCGGCCACTGGTGCTGAAGTGTAAAGGGGGC	122	
Db	82	AGGTGCTCAAAAACATCAGAGCCCGGATTTGGCGGCCACTGGTGCTGAAGTGTAAAGGGGGC	141	
Qy	123	CCCCAAGAAACACCCACAGCGGCTTGGAAATGGAAACTGAACACAGCCCGGACAGAAAGCTTG	182	
Db	142	CCCCAAGAAACACCCACAGCGGCTTGGAAATGGAAACTGAACACAGCCCGGACAGAAAGCTTG	201	
Qy	183	GAAGGTCTGTCTCCACAGGAGAGAGCCCTCTGGACAGTGTGACTCGTGTCCTTCCCAA	242	
Db	202	GAAGGTCTGTCTCTCCACAGGAGAGAGCCCTCTGGACAGTGTGACTCGTGTCCTTCCCAA	261	
Qy	243	CGGCTCCCTCTTCTCCCTTCGGGCTGTCCGGATCCAGGATGAGGGGATTTTCGGTGCAGGC	302	
Db	262	CGGCTCCCTCTTCTCCCTTCGGGCTGTCCGGATCCAGGATGAGGGGATTTTCGGTGCAGGC	321	
Qy	303	AATGAACAGGAAATGGAAGGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATCC	362	
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Qy	363	TGGGAAGCCAGAAATTTGTAGATTTCTGCCCTCTGAACCTCACGGCTGGTGTTCCTCAATAAGGT	422	
Db	382	TGGGAAGCCAGAAATTTGTAGATTTCTGCCCTCTGAACCTCACGGCTGGTGTTCCTCAATAAGGT	441	
Qy	423	GGGACATGTGTCTCAGAGGAGAGTACCCCTGCAGGGACTCTTACCTGGCACTTCGATGG	482	
Db	442	GGGACATGTGTGTCTCAGAGGAGAGTACCCCTGCAGGGACTCTTACCTGGCACTTCGATGG	501	
Qy	483	GAAGCCCTTGGTGCCTTAATGAGAGGGAGTATCTCTGTGAAGGAACAGACAGAGAGACACC	542	

RESULT 4	AB036432	1268 bp	linear	PRI 13-JAN-2000
LOCUS	AB036432			
DEFINITION	Homo sapiens RAGE mRNA for advanced glycation endproducts receptor, complete cds.			
ACCESSION	AB036432			
VERSION	AB036432.1			
KEYWORDS	advanced glycation endproducts receptor.			
SOURCE	Homo sapiens (human)			

D _b	502	GAAGCCCTTGGTGCCCTAATGAAAGGGAGTAGTCCTGTGAAGGAAACAGACCAGGAGACAACCC	561
Q _y	543	TGAGACAGGGCTTTCAACACTGCAGTCCGAGCTAAATGGTGAACCCACGACCCCGGGGAGAGA	602
D _b	562	TGAGACAGGGCTTTCAACACTGCAGTCCGAGCTAAATGGTGAACCCACGACCCCGGGGAGAGA	621
Q _y	603	TCCCCTGCCACCTTCTCCTGTAGATTAGCCACAGGCCCTTCCCAGAACCCGGGCGCTTGGC	662
D _b	622	TCCCCTGCCACCTTCTCCTGTAGATTAGCCACAGGCCCTTCCCAGAACCCGGGCGCTTGGC	681
Q _y	663	CACAGCCCCCATCAGACCCCGTGTCTGGAGCCTGTGTCTCTGGAGGAGGTCCAATTGGT	722
D _b	682	CACAGCCCCCATCAGACCCCGTGTCTGGAGCCTGTGTCTCTGGAGGAGGTCCAATTGGT	741
Q _y	723	GFTGGAGCCAGAAGGTGGACAGTAGTAGCTCTCTGGTGGAAACCGTAAACCCTTGACCTGTGAAGT	782
D _b	742	GFTGGAGCCAGAAGGTGGAGCAGTAGTAGCTCTCTGGTGGAAACCGTAAACCCTTGGAAGT	801
Q _y	783	CCCTGCCACGCCCTCTCTCAAATCCACTGGAATGAAGGATGGTGTGCGCTTGGCCCTTCC	842
D _b	802	CCCTGCCACGCCCTCTCTCAAATCCACTGGAATGAAGGATGGTGTGCGCTTGGCCCTTCC	861
Q _y	843	CCCCAGCCCTGTCTGATCCTCCCTGAGATAGGGCTCAGGACCAAGGAAACCTACAGCTG	902
D _b	862	CCCCAGCCCTGTCTGATCCTCCCTGAGATAGGGCTCAGGACCAAGGAAACCTACAGCTG	921
Q _y	903	TGTGGCCACCAATTCACAGCCACGGGCCCCAGAAAAGCCGTGTGTCAAGCATCAGCATCAT	962
D _b	922	TGTGGCCACCAATTCACAGCCACGGGCCCCAGAAAAGCCGTGTGTCAAGCATCAGCATCAT	981
Q _y	963	CGAACCMAGCGAGGAGGGGCCCAACTGCAGGCTCTGTGGGAGGATCAGGGCTGGGAACCTCT	1022
D _b	982	CGAACCMAGCGAGGAGGGGCCCAACTGCAGGCTCTGTGGGAGGATCAGGGCTGGGAACCTCT	1041
Q _y	1023	AGCCCTGGCCCTGGGGATCTCTGGAGGCCCTGGGGACAGCCGCCTGTCTCATTTGGGGTCAT	1082
D _b	1042	AGCCCTGGCCCTGGGGATCTCTGGAGGCCCTGGGGACAGCCGCCTGTCTCATTTGGGGTCAT	1101
Q _y	1083	CTTGTGCAAGGCGGCAACGCCGAGGAGGAGGAGGAGGCCCCAGAAAAACAGGAGGA	1142
D _b	1102	CTTGTGCAAGGCGGCAACGCCGAGGAGGAGGAGGAGGCCCCAGAAAAACAGGAGGA	1161
Q _y	1143	AGAGGAGGCGTGCAGAACTGAATCAGTCGAGGAAACCTGAGGCAAGGCGGAGAGTAGTAGTAC	1202
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Q _y	1323	ACCTTGCCAAGCTTTCTTCTACACCAAGAGCCCCCAATGATGATTAACACCTTGACA	1382
D _b	1342	ACCTTGCCAAGCTTTCTTCTACACCAAGAGCCCCCAATGATGATTAACACCTTGACA	1400
Q _y	1383	CATCT 1387	
D _b	1401	CATCT 1405	

RESULT 4	ACCESSION
AB036432	VERSION
LOCUS	KEYWORDS
DEFINITION	SOURCE

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (sites) Abedin,M.J., Yonekura,H., Migita,H., Karasawa,J., Yamamoto,Y. and Yamamoto,H.
TITLE	Molecular heterogeneity of the receptor for advanced glycation endproducts
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1268)
AUTHORS	Abedin,M.J., Yonekura,H. and Yamamoto,H.
TITLE	Direct Submission
JOURNAL	Submitted (05-JAN-2000) Hideto Yonekura, Kanazawa University School of Medicine, Department of Biochemistry; 13-1 Takara-machi, Kanazawa, Ishikawa 920-8640, Japan (E-mail:hyone@med.kanazawa-u.ac.jp, Tel:+81-76-265-2181, Fax:+81-76-234-4226)
FEATURES	Location/Qualifiers 1..1268 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /cell_type="microvascular endothelial" 1..1268 /gene="RAGE" 25..1239 /gene="RAGE" /codon_start=1 /product="advanced glycation endproducts receptor" /protein_id="BAA89369.1" /db_xref="GI:6691626" /translation="\"MAAGTAVGAWLVLSLWGVVGAQNITARIGELVLKCKGAPKK NRQLEWKLNTSRVAVLSPQGGPMDVSLVPLNGSLFLPAVGQDEGIFRCQAM PNQKETSINRYRVYQIPGKPEIVDSASLTAGVPNKVGTCTVSEGSYPAGTILSWILD GXPLVNEKGVSKQSTRHBTGLFTLOSELMTVPARGGDPRTFSCSPGLPRHR ALRTAPIQRWEPVPLEVQLVVEPEGGAADPGTVTLTCEVPAQSPSPQIHWKQGV PIPLPSPVLIILPEIGPODQYTSVTHSHSGPOESRAVSISIIIEPGBEGPTAGSVG GSGLGTLALALGILAGLGTALLIGVILWQRQRGRERKAPENQEEEBEERELNQSE EPEAGESSTGGP\" 25..90 /gene="RAGE" 322..323 /gene="RAGE" /note="polymorphism sequence differs from that reported in Acc# M91211" /replace="ag"
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variation	322..323
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REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 16934 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES Location/Qualifiers
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ORIGIN
Query Match 84.3%; Score 1172.8; DB 6; Length 1218;
Best Local Similarity 98.4%; Pred. No. 9e-291;
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QY 63 AGGTGCTCAAAACATCACAGCCCGGATTGCGAGCCCACTGGTCTGAAGTGTAAAGGGGC 122
DB 63 AGGTGCTCAAAACATCACAGCCCGGATTGCGAGCCCACTGGTCTGAAGTGTAAAGGGGC 122
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QY 243 CGGCTCCCTCTCTCCCGGCTGCGGATCAGGATGAGGGATTTCCGGTCCGAGC 302
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LOCUS Soluble RAGE protein.
DEFINITION Soluble RAGE protein.
ACCESSION BD176670.1 GI:29122380
VERSION WO 02074805-A/1.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1223)
AUTHORS Yamamoto,H., Yonekura,H., Yamamoto,Y., Sakurai,S. and Watanabe,T.
TITLE Soluble RAGE protein
JOURNAL Patent: WO 02074805-A 1 26-SEP-2002;
JAPAN AS REPRESENTED BY PRESIDENT OF KANAZAWA UNIVERSITY, HIROSHI
YAMAMOTO, HIDETO YONEKURA, YASUHIKO YAMAMOTO, SHIGERU SAKURAI, TAKUO
WATANABE
COMMENT OS Homo sapiens (human)
PN WO 02074805-A/1
PD 26-SEP-2002
PF 19-MAR-2002 WO 2002JP002623
PR 19-MAR-2001 JP 01P 078409, 10-AUG-2001 JP 01P 243114 PR
25-FEB-2002 JP 02P 048182
PI HIROSHI YAMAMOTO, HIDETO YONEKURA, YASUHIKO YAMAMOTO, SHIGERU SAKURAI,
TAKUO WATANABE
PC C07K14/47, C12N1/12, C12N1/21, C12N5/10, C12N1/19, A61K39/395, PC
A61K45/00,
PC A61P3/06, A61P3/10, A61P9/10, A61P25/28, A61P29/00, A61P35/00, PC
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CC Soluble RAGE protein
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LOCUS HSA133822 1250 bp mRNA linear PRI 17-NOV-1999
DEFINITION Homo sapiens mRNA for receptor for Advanced Glycation End Product,
secreted isoform (RAGEsec gene).
ACCESSION AJ133822
VERSION AJ133822.1 GI:4877290
KEYWORDS RAGEsec gene; receptor for Advanced Glycation End Products;
secreted isoform.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Malherbe,P., Richards,J.G., Gaillard,H., Thompson,A., Diener,C.,
Schuler,A. and Huber,G.
CDNA cloning of a novel secreted isoform of the human receptor for
advanced glycation end products and characterization of cells
co-expressing cell-surface scavenger receptors and Swedish mutant
amyloid precursor protein
Brain Res. Mol. Brain Res. 71 (2), 159-170 (1999)
99453317
MEDLINE 10521570
PUBMED 2 (bases 1 to 1250)
REFERENCE 2
AUTHORS Malherbe,P.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-1999) Malherbe P., Pharma Division PRPN, F.
Hoffmann-La Roche Ltd., Bldg. 69/333, CH-4070 Basel, SWITZERLAND
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LOCUS
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Cow receptor for advanced glycosylation end products (RAGE) mRNA,
complete cds.
ACCESSION
M91212
VERSION
M91212.1 GI:163650
KEYWORDS
RAGE; cell surface receptor.
SOURCE
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ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
1 (bases 1 to 1426)
Neeper,M., Schmidt,A.M., Brett,J., Yan,S.D., Wang,F., Pan,Y.C.,
Elliston,K., Stern,D. and Shaw,A.
Cloning and expression of a cell surface receptor for advanced
glycosylation end products of proteins
J. Biol. Chem. 267 (21), 14998-15004 (1992)
J. Biol. Chem. 267 (21), 14998-15004 (1992)
92340547
1378843
PUBMED
REFERENCE
2 (bases 1 to 1426)
Shaw,A.
Direct Submission
Submitted (15-APR-1992) A. Shaw, Department of Cellular and
Molecular Biology, Merck Sharp and Dohme Research Laboratories,
West Point, PA 19486 USA
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GenCore version 5.1.6
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SUMMARIES

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10	239	71.1	1347	4	US-09-638-648-6
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C 41	31.4	9.3	4418	4	US-09-064-193-13	Sequence 13, Appli
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ALIGNMENTS

RESULT 1
US-08-633-148-1
; Sequence 1, Application US/08633148
; Patent No. 5864018
; GENERAL INFORMATION:
; APPLICANT: MORSE, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; APPLICANT: HOLLANDER, DORIS A.
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,148
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 014618-00560005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1023 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-633-148-1

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; Sequence 5154, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5154
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5154
Query Match 100.0%; Score 336; DB 4; Length 1215;
Best Local Similarity 100.0%; Pred. No. 1.1e-93;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 67 GCTCAAAACATCACAGCCGAGTGGCGACCACTGGTGAAGTGAAGGGGCCCC 126
QY 61 AAGAACACACCCAGCGCTGGAATGGAACCTGAACACAGCGCGGACAGAAAGCTTGGAAAG 120
DB 127 AAGAACACACCCAGCGCTGGAATGGAACCTGAACACAGCGCGGACAGAAAGCTTGGAAAG 186
QY 121 GTCTCTGTCTCCCGAGGAGAGCGCCCTGGGACAGTGTGGCTGTCTCTTCCCAACGCG 180
DB 187 GTCTCTGTCTCCCGAGGAGAGCGCCCTGGGACAGTGTGGCTGTCTCTTCCCAACGCG 246
QY 181 TCCCTCTCTCTCCCGAGGAGAGCGCGCTGGAATGGAACCTGAACACAGCGCGGACAGAAAGCTTGGAAAG 240
DB 247 TCCCTCTCTCTCCCGAGGAGAGCGCGCTGGAATGGAACCTGAACACAGCGCGGACAGAAAGCTTGGAAAG 306
QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGATTCCTGGG 300
DB 307 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGATTCCTGGG 366
QY 301 AAGCCAGAAATTTAGATTCTGCCTCTGAATCTCAG 336
DB 367 AAGCCAGAAATTTAGATTCTGCCTCTGAATCTCAG 402

DB 367 AAGCCAGAAATTTAGATTCTGCCTCTGAATCTCAG 402

RESULT 3

US-08-633-148-3
; Sequence 3, Application US/08633148
; Patent No. 5864018
; GENERAL INFORMATION:
; APPLICANT: MORSE, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; APPLICANT: HOLLANDER, DORIS A.
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,148
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 014618-005600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2422
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 957 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-633-148-3
Query Match 99.0%; Score 332.8; DB 2; Length 957;
Best Local Similarity 99.4%; Pred. No. 9.5e-93;
Matches 334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCTCAAAACATCACAGCCGAGTGGCGACCACTGGTGAAGTGAAGGGGCCCC 60
DB 1 GCTCAAAACATCACAGCCGAGTGGCGACCACTGGTGAAGTGAAGGGGCCCC 60
QY 61 AAGAACACACCCAGCGCTGGAATGGAACCTGAACACAGCGCGGACAGAAAGCTTGGAAAG 120
DB 61 AAGAACACACCCAGCGCTGGAATGGAACCTGAACACAGCGCGGACAGAAAGCTTGGAAAG 120
QY 121 GTCTCTGTCTCCCGAGGAGAGCGCCCTGGGACAGTGTGGCTGTCTCTTCCCAACGCG 180
DB 121 GTCTCTGTCTCCCGAGGAGAGCGCCCTGGGACAGTGTGGCTGTCTCTTCCCAACGCG 180
QY 181 TCCCTCTCTCTCCCGAGGAGAGCGCGCTGGAATGGAACCTGAACACAGCGCGGACAGAAAGCTTGGAAAG 240
DB 181 TCCCTCTCTCTCCCGAGGAGAGCGCGCTGGAATGGAACCTGAACACAGCGCGGACAGAAAGCTTGGAAAG 240
QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGATTCCTGGG 300
DB 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGATTCCTGGG 300
QY 301 AAGCCAGAAATTTAGATTCTGCCTCTGAATCTCAG 336
DB 301 AAGCCAGAAATTTAGATTCTGCCTCTGAATCTCAG 336

RESULT 4
US-09-638-649-4
; Sequence 4, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1391
; TYPE: DNA
; ORGANISM: Human
US-09-638-649-4

Query Match 99.0%; Score 332.8; DB 4; Length 1391;
Best Local Similarity 99.4%; Pred. No. 1.1e-92;
Matches 334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 60
DB 67 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 126

QY 61 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAAAG 120
DB 127 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAAAG 186

QY 121 GTCCTGTCTCCCGAGGAGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCCAACGGC 180
DB 187 GTCCTGTCTCCCGAGGAGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCCAACGGC 246

QY 181 TCCCTCTTCCCGAGGAGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCCGTCCAGGCAATG 240
DB 247 TCCCTCTTCCCGAGGAGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCCGTCCAGGCAATG 306

QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCCTGAACTCAAG 336
DB 367 AAGCCAGAAATGTAGATTCTGCCTCTGAATCAAG 402

RESULT 5
US-09-638-648-4
; Sequence 4, Application US/09638648
; Patent No. 6825164
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; APPLICANT: Zlokovic, Berislav
; TITLE OF INVENTION: A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID
; TITLE OF INVENTION: ANGIOPATHY
; FILE REFERENCE: 0575/62097
; CURRENT APPLICATION NUMBER: US/09/638,648
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1391
; TYPE: DNA
; ORGANISM: Human

US-09-638-648-4

Query Match 99.0%; Score 332.8; DB 4; Length 1391;
Best Local Similarity 99.4%; Pred. No. 1.1e-92;
Matches 334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 60
DB 67 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 126

QY 61 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAAAG 120
DB 127 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAAAG 186

QY 121 GTCCTGTCTCCCGAGGAGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCCAACGGC 180
DB 187 GTCCTGTCTCCCGAGGAGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCCAACGGC 246

QY 181 TCCCTCTTCCCGAGGAGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCCGTCCAGGCAATG 240
DB 247 TCCCTCTTCCCGAGGAGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCCGTCCAGGCAATG 306

QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCCTGAACTCAAG 336
DB 367 AAGCCAGAAATGTAGATTCTGCCTCTGAATCAAG 402

RESULT 6
US-08-755-235-3
; Sequence 3, Application US/08755235
; Patent No. 6790443
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1405
; TYPE: DNA
; ORGANISM: Human
US-08-755-235-3

Query Match 99.0%; Score 332.8; DB 4; Length 1405;
Best Local Similarity 99.4%; Pred. No. 1.1e-92;
Matches 334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 60
DB 67 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 126

QY 61 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAAAG 120
DB 127 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAAAG 186

QY 121 GTCCTGTCTCCCGAGGAGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCCAACGGC 180
DB 187 GTCCTGTCTCCCGAGGAGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCCAACGGC 246

QY 181 TCCCTCTTCCCGAGGAGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCCGTCCAGGCAATG 240
DB 247 TCCCTCTTCCCGAGGAGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCCGTCCAGGCAATG 306

QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTCCTGAACTCAAG 336
DB 367 AAGCCAGAAATGTAGATTCTGCCTCTGAATCAAG 402

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Db 307 AACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCGGTGTCTACAGATTCTCTGGG 366
QY 301 AAGCCAGAAATGTAGATTCTCCCTCTGAATCAGC 336
Db 367 AAGCCAGAAATGTAGATTCTCCCTCTGAATCAGC 402

RESULT 7
US-09-638-649-2
; Sequence 2, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1426
; TYPE: DNA
; ORGANISM: Bos Taurus
US-09-638-649-2

Query Match 80.5%; Score 270.6; DB 4; Length 1426;
Best Local Similarity 90.4%; Pred. No. 1.7e-73;
Matches 301; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

QY 4 CAAAACATCACAGCCCGGATTCGGAGCCACTGTGCTGAAGTGTAAAGGGGCCCCCAAG 63
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QY 64 AAACACCCCGGCTGGATGAACTGAACACAGCCGACAGAGCTTGAAGGTC 123
Db 139 AAACACCCCGGCTGGATGAACTGAACACAGCCGACAGAGCTTGAAGGTC 198
QY 124 CTGTCTCCCGGAGGAGGCCCTCGGACAGTGTGGCTCGTCTTCCCAACGGCTCC 183
Db 199 CTGTCTCCCGGAGGAGGCCCTCGGACAGTGTGGCTCGTCTTCCCAACGGCTCC 255
QY 184 CTGTCTCCCGGAGGAGGCCCTCGGACAGTGTGGCTCGTCTTCCCAACGGCTCC 243
Db 256 CTGTCTCCCGGAGGAGGCCCTCGGACAGTGTGGCTCGTCTTCCCAACGGCTCC 315
QY 244 AGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGTCTCTGGGAAG 303
Db 316 CGGAGCGGAAGGAGACCAAGTCTAACTACCGAGTCCGTGTCTACCAAGTCTCTGGGAAG 375
QY 304 CCAGAAATGTAGATTCTGCTCTGAATCAGC 336
Db 376 CCAGAAATGTAGATTCTGCTCTGAATCAGC 408

RESULT 9
US-08-755-235-1
; Sequence 1, Application US/08755235
; Patent No. 6790443
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1438
; TYPE: DNA
; ORGANISM: Bovine
US-08-755-235-1

Query Match 80.5%; Score 270.6; DB 4; Length 1438;
Best Local Similarity 90.4%; Pred. No. 1.7e-73;
Matches 301; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

QY 4 CAAAACATCACAGCCCGGATTCGGAGCCACTGTGCTGAAGTGTAAAGGGGCCCCCAAG 63
Db 79 CAAAACATCACAGCCCGGATTCGGAGCCACTGTGCTGAAGTGTAAAGGGGCCCCCAAG 138
QY 64 AAACACCCCGGCTGGATGAACTGAACACAGCCGACAGAGCTTGAAGGTC 123
Db 139 AAACACCCCGGCTGGATGAACTGAACACAGCCGACAGAGCTTGAAGGTC 198
QY 124 CTGTCTCCCGGAGGAGGCCCTCGGACAGTGTGGCTCGTCTTCCCAACGGCTCC 183
Db 199 CTGTCTCCCGGAGGAGGCCCTCGGACAGTGTGGCTCGTCTTCCCAACGGCTCC 255
QY 184 CTGTCTCCCGGAGGAGGCCCTCGGACAGTGTGGCTCGTCTTCCCAACGGCTCC 243
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Db 307 AACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCGGTGTCTACAGATTCTCTGGG 366
QY 301 AAGCCAGAAATGTAGATTCTCCCTCTGAATCAGC 336
Db 367 AAGCCAGAAATGTAGATTCTCCCTCTGAATCAGC 402

RESULT 7
US-09-638-649-2
; Sequence 2, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1426
; TYPE: DNA
; ORGANISM: Bos Taurus
US-09-638-649-2

Query Match 80.5%; Score 270.6; DB 4; Length 1426;
Best Local Similarity 90.4%; Pred. No. 1.7e-73;
Matches 301; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

QY 4 CAAAACATCACAGCCCGGATTCGGAGCCACTGTGCTGAAGTGTAAAGGGGCCCCCAAG 63
Db 79 CAAAACATCACAGCCCGGATTCGGAGCCACTGTGCTGAAGTGTAAAGGGGCCCCCAAG 138
QY 64 AAACACCCCGGCTGGATGAACTGAACACAGCCGACAGAGCTTGAAGGTC 123
Db 139 AAACACCCCGGCTGGATGAACTGAACACAGCCGACAGAGCTTGAAGGTC 198
QY 124 CTGTCTCCCGGAGGAGGCCCTCGGACAGTGTGGCTCGTCTTCCCAACGGCTCC 183
Db 199 CTGTCTCCCGGAGGAGGCCCTCGGACAGTGTGGCTCGTCTTCCCAACGGCTCC 255
QY 184 CTGTCTCCCGGAGGAGGCCCTCGGACAGTGTGGCTCGTCTTCCCAACGGCTCC 243
Db 256 CTGTCTCCCGGAGGAGGCCCTCGGACAGTGTGGCTCGTCTTCCCAACGGCTCC 315
QY 244 AGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGTCTCTGGGAAG 303
Db 316 CGGAGCGGAAGGAGACCAAGTCTAACTACCGAGTCCGTGTCTACCAAGTCTCTGGGAAG 375
QY 304 CCAGAAATGTAGATTCTGCTCTGAATCAGC 336
Db 376 CCAGAAATGTAGATTCTGCTCTGAATCAGC 408

RESULT 8
US-09-638-648-2
; Sequence 2, Application US/09638648
; Patent No. 6825164
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; APPLICANT: Zlokovic, Berislav
; TITLE OF INVENTION: A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID
; TITLE OF INVENTION: ANGIOPATHY
; FILE REFERENCE: 0575/62097
; CURRENT APPLICATION NUMBER: US/09/638,648
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 6
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 17:21:07 ; Search time 197.91 Seconds
(without alignments)
8433.118 Million cell updates/sec

Title: US-10-091-019-2
Perfect score: 1020
Sequence: 1 atggcagccggaacagcagt.....gaggatcagggctgtgtctag 1020

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/prodata1/ina/6A COMB.seq.*
4: /cgn2_6/prodata1/ina/6B COMB.seq.*
5: /cgn2_6/prodata1/ina/PCTUS COMB.seq.*
6: /cgn2_6/prodata1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1015	99.5	1023	2	US-08-633-148-1
2	1015	99.5	1215	4	US-09-949-016-5154
3	1009.8	99.0	1391	4	US-09-638-649-4
4	1009.8	99.0	1391	4	US-09-638-648-4
5	986.8	96.7	1405	4	US-08-755-235-3
6	945.8	92.7	957	2	US-08-633-148-3
7	746.4	73.2	1426	4	US-09-638-649-2
8	746.4	73.2	1426	4	US-09-638-648-2
9	717.6	70.4	1438	4	US-08-755-235-1
10	696.6	68.3	1347	4	US-09-638-648-6
11	696.6	68.3	1348	4	US-09-638-649-6
12	197	19.3	7080	4	US-09-949-016-16896
13	108.6	10.6	601	4	US-09-949-016-178939
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16	72.6	7.1	601	4	US-09-949-016-178938
17	40	3.9	601	4	US-09-949-016-178941
18	39.6	3.9	561	4	US-09-702-705-72
19	39.6	3.9	561	4	US-09-736-457-2
20	39.6	3.9	561	4	US-09-614-124B-72
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22	39.6	3.9	561	4	US-09-589-184-72
23	39.6	3.9	561	4	US-09-658-824-72
24	39.6	3.9	2539	2	US-08-432-016-1
25	39.6	3.9	2539	2	US-08-684-594-1
26	39.6	3.9	2539	4	US-09-023-655-1496
27	39.6	3.9	2539	4	US-09-949-016-3677

28	39.6	3.9	4235	4	US-09-702-705-317	Sequence 317, App
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31	39.6	3.9	4235	4	US-09-671-325-317	Sequence 317, App
32	39.6	3.9	4235	4	US-09-589-184-317	Sequence 317, App
33	39.6	3.9	4235	4	US-09-658-824-317	Sequence 317, App
34	39.6	3.9	23796	4	US-09-949-016-17581	Sequence 17581, A
35	39.2	3.8	6108	4	US-09-949-016-12213	Sequence 12213, A
36	38.8	3.8	7218	1	US-08-232-463-14	Sequence 14, Appl
37	38.4	3.8	22218	4	US-09-949-016-14240	Sequence 14240, A
38	38	3.7	1416	4	US-09-902-540-4687	Sequence 4687, Ap
39	38	3.7	3991	3	US-08-506-296B-3	Sequence 3, Appli
40	38	3.7	28558	4	US-09-902-540-1231	Sequence 1231, Ap
41	37.6	3.7	510	4	US-09-252-991A-5973	Sequence 5973, Ap
42	37.6	3.7	1596	4	US-09-252-991A-5938	Sequence 5938, Ap
43	37.6	3.7	1674	4	US-09-252-991A-5894	Sequence 5894, Ap
44	37.4	3.7	1707	1	US-08-790-309-1	Sequence 1, Appli
45	37.4	3.7	1707	3	US-09-250-585A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-633-148-1
; Sequence 1, Application US/08633148
; Patent No. 5864018
; GENERAL INFORMATION:
; APPLICANT: MORSE, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,148
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 014618-0056000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1023 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-633-148-1

Query Match 99.5%; Score 1015; DB 2; Length 1023;
Best Local Similarity 100.0%; Pred. No. 6e-271;
Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCAGCCGGAACAGCAGTTCGAGCCTGGGTCTGTCTCAGTCTGTGGGGGGCAGTA 60
DB 1 ATGGCAGCCGGAACAGCAGTTCGAGCCTGGGTCTGTCTCAGTCTGTGGGGGGCAGTA 60

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001307

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949.016

; CURRENT AFFILIATION NUMBER: 05/05/2017, 010
 ; CURRENT FILING DATE: 2000-04-14

; CURRENT FILING DATE: 2000-04-14
 ;
 ; SECTION IDENTIFICATION NUMBER: 50/241 755

; PRIOR APPLICATION NUMBER: 60/241,755

;
; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

;
PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

EXPIRATION DATE: 2000-03-03
NUMBER OF SEQ TO NOS: 207012

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; NUMBER OF SEQ ID NOS: 207012
;
; COMMENT: BlastSeq for Windows Version 4.0

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; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
; CPO ID NO 5154

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; SEQ ID NO 5154

; LENGTH: 1215

; TYPE: DNA

Query Match	99.5%	Score 1015;	DB 4;	Length 1215;
Best Local Similarity	100.0%;	Pred. No. 6.5e-271;		
Matches 1015;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

RESULT 2

RESULT 2
US-09-949-016-5154

US-09-949-016-5154
: Sequence 5154: Application US/09949016

; Sequence 5154, App.
: Patent No. 6812339

Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

QY 902 GTGTGGCCACCCATTCCAGCCACGGGCCCCAGGAAAGCCCTGTCTCAGCATCAGCATCA 961
Db 902 GTGTGGCCACCCATTCCAGCCACGGGCCCCAGGAAAGCCCTGTCTCAGCATCAGCATCA 961
QY 962 TCGAACACGAGGAGGGGCGCAACTCAGGCTCTGTGGGAGGATCAGGGCTGG 1015
Db 962 TCGAACACGAGGAGGGGCGCAACTCAGGCTCTGTGGGAGGATCAGGGCTGG 1015
RESULT 6
US-08-633-148-3
; Sequence 3, Application US/08633148
; Patent No. 5864018
; GENERAL INFORMATION:
; APPLICANT: MORSE, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; APPLICANT: HOLLANDER, DORIS A.
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/633,148
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 014618-005600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 957 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-633-148-3
Query Match 92.7%; Score 945.8; DB 2; Length 957;
Best Local Similarity 99.8%; Pred. No. 8.4e-252;
Matches 947; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 67 GCTCAAAACATCAGACCCCGGATTGGCGAGCCACTGGTGTGAAGTGAAGGGGCCCC 126
Db 1 GCTCAAAACATCAGACCCCGGATTGGCGAGCCACTGGTGTGAAGTGAAGGGGCCCC 60
QY 127 AAGAAACACCCAGCGGCTGGAAATGGAATGGAACACAGCCGCGGACAGAGCTTGAAG 186
Db 61 AAGAAACACCCAGCGGCTGGAAATGGAATGGAACACAGCCGCGGACAGAGCTTGAAG 120
QY 187 GTCTGTCTCCAGGAGGAGGCCCCCTGGACAGTGTGGCTGTCTTCCCAAGGC 246
Db 121 GTCTGTCTCCAGGAGGAGGCCCCCTGGACAGTGTGGCTGTCTTCCCAAGGC 180
QY 247 TCCTCTTCTCTCCGCTGTCCGGATCCAGGATGAGGGGATTTTCGGTCCAGGCAATG 306
Db 181 TCCTCTTCTCTCCGCTGTCCGGATCCAGGATGAGGGGATTTTCGGTCCAGGCAATG 240
QY 307 AACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTTACCAAGATTCCTGGG 366

Db 241 AACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTTACCAAGATTCCTGGG 300
QY 367 AACCCAGAAATTTAGATTCTGCTCTGAATCAGGCTCAGGCTGTGTCTCCCAATAAGAGTGGG 426
Db 301 AAGCCAGAAATTTAGATTCTGCTCTGAATCAGGCTCAGGCTGTGTCTCCCAATAAGTGGG 360
QY 427 ACATGTGTGTAGAGGAGGAGTACCTCTGAGGAGTCTTGTAGCTGGCACTTGGATGGGAAG 486
Db 361 ACATGTGTGTAGAGGAGGAGTACCTCTGAGGAGTCTTGTAGCTGGCACTTGGATGGGAAG 420
QY 487 CCCCTGGTGCCTTAATCAGAGGAGGATCTGTGAAGGAAACAGACAGGAGACACCCCTGAG 546
Db 421 CCCCTGGTGCCTTAATCAGAGGAGGATCTTGTGAAGGAAACAGACAGGAGACACCCCTGAG 480
QY 547 ACAGGGCTCTTTCACACTGCAGTCCGAGCTAAATGGTGAACCCAGCCCGGGGAGGAGATCCC 606
Db 481 ACAGGGCTCTTTCACACTGCAGTCCGAGCTAAATGGTGAACCCAGCCCGGGGAGGAGATCCC 540
QY 607 CGTCCACACTTCTCTGTAGTTCAGCCAGGCTTCCCGCAACACCGGGCTTTGCGGCACA 666
Db 541 CGTCCACACTTCTCTGTAGTTCAGCCAGGCTTCCCGCAACACCGGGCTTTGCGGCACA 600
QY 667 GCGCCCATCCAGCCCCGCTGTCTGGGAGCCTGTGCTCTGGAGAGGTCCCAATTTGGTGGTG 726
Db 601 GCGCCCATCCAGCCCCGCTGTCTGGGAGCCTGTGCTCTGGAGAGGTCCCAATTTGGTGGTG 660
QY 727 GAGCCAGAAAGGTGAGCAGTAGCTCTGTGTGGAACCGTAACCTGACCTGTGTAAGTCCCT 786
Db 661 GAGCCAGAAAGGTGAGCAGTAGCTCTGTGTGGAACCGTAACCTGACCTGTGTAAGTCCCT 720
QY 787 GCGCAGCCCTCTCTCAATTCACCTGATGAAGATGGTGTGCTTGCCTTGCCTTCCCTCC 846
Db 721 GCGCAGCCCTCTCTCAATTCACCTGATGAAGATGGTGTGCTTGCCTTGCCTTCCCTCC 780
QY 847 AGCCCTGTCTGATCTCTCTGATAGTAGGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGG 906
Db 781 AGCCCTGTCTGATCTCTCTGATAGTAGGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
QY 907 GCGCAGCCATTCAGCCACCGGCCCCAGGAAAGCGCTGTCTCAGCATCAGCATCATCGAA 966
Db 841 GCGCAGCCATTCAGCCACCGGCCCCAGGAAAGCGCTGTCTCAGCATCAGCATCATCGAA 900
QY 967 CCAGGCGAGGAGGGGCGCAACTGCACTGTGGGAGGATCAGGGCTGG 1015
Db 901 CCAGGCGAGGAGGGGCGCAACTGCACTGTGGGAGGATCAGGGCTGG 949

RESULT 7

US-09-638-649-2
; Sequence 2, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du

; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1426
; TYPE: DNA
; ORGANISM: Bos Taurus
US-09-638-649-2

Query Match 73.2%; Score 746.4; DB 4; Length 1426;
Best Local Similarity 84.1%; Pred. No. 1.5e-196;
Matches 881; Conservative 0; Mismatches 131; Indels 36; Gaps 2;

QY 1 ATGGCAGCGGAAACAGCAGTTGGAGCTTGGGTCTGCTCCTCAGTCTGTGGGGGCGAGTA 60
Db |||||
QY 10 ATGGCAGCAGGGCAGTGTGGAGCTGGATGCTAGTCTCAGTCTGGGGGGGACAGTC 59
Db |||||
QY 61 GTAGTGTCTAAACATCAACGCCGGATTTGGCGACCACTGGTCTGAAGTGTAAAGGG 120
Db |||||
QY 70 ACGGGGACCAAAACATCAACGCCGGATTTGGCGACCACTGGTCTGAAGTGTAAAGGG 129
QY 121 GCGCCCAAGAACACCCAGCGGTGGATGGAACTGAAACACACAGCCGGGACAGAGCT 180
Db |||||
QY 130 GCGCCCAAGAACACCCAGCGGTGGATGGAACTGAAACACACAGCCGGGACAGAGCT 189
QY 181 TGAAGGTCTGTCTCCCGAGGAGAGCGCCCTGGGACAGTGTGGTCTGCTCTCTTCCC 240
Db |||||
QY 190 TGAAGGTCTGTCTCCCGAGGAGAGCGCCCTGGGACAGTGTGGTCTGCTCTCTTCCC 246
QY 241 AAGCGTCTCTCTCTCCCGAGGAGAGCGCCCTGGGACAGTGTGGTCTGCTCTCTTCCC 300
Db |||||
QY 247 AAGCGTCTCTCTCTCCCGAGGAGAGCGCCCTGGGACAGTGTGGTCTGCTCTCTTCCC 306
QY 301 GCATGAAACAGGATGGAAGGAGAGCAAGTCCAACTACCGAGTCCGTCTTACAGATT 360
Db |||||
QY 307 GCATGAAACAGGATGGAAGGAGAGCAAGTCCAACTACCGAGTCCGTCTTATCAGATT 366
QY 361 CTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACTCACGGCTGGTCTTCCCAATAAG 420
Db |||||
QY 367 CTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACTCATGGCTGGTCTTCCCAATAAG 426
QY 421 GTGGGACATGTGTCTGGGATTCAGCGGACCTTCTAGCTGGGACCTTTAGCTGGGAC 480
Db |||||
QY 427 GTGGGACATGTGTCTGGGATTCAGCGGACCTTCTAGCTGGGACCTTTAACTGGCT 486
QY 481 GGGAAAGCCCTGTGTCTGAGAGGAGAGTCTGTGAGAGGAGAGTCTGAGAGGAGAGAC 540
Db |||||
QY 487 GGGAAAGCCCTGTGTCTGAGAGGAGAGTCTGTGAGAGGAGAGTCTGAGAGGAGAGAC 546
QY 541 CTGTAGACAGGAGTCTTCACTACCTGAGTGGAGTAACTGACCCAGCGGAGGAGGAG 600
Db |||||
QY 547 CCAAGAGCAGGGCTTTTCACTGCTTCCATTCGAGTGTGATGGTCTTCCCAATAAG 606
QY 601 GATTCCTGTCAGAGTCTTCTGAGTCTTCTGAGTCTTCTGAGTCTTCTGAGTCTTCTG 660
Db |||||
QY 607 GCTCTCCAGCCACCTTCTCTGAGTCTTCTGAGTCTTCTGAGTCTTCTGAGTCTTCTG 666
QY 661 CGCAGAGCCCGATCCAGCCCGGCTGTG----- 689
Db |||||
QY 667 CACAGCGCCCGATCCAGCTCAGGGTCTGAGTGAGCACCGAGGTGGGAGGGGCCCCAAC 726
QY 690 --GGAGCCTGTGCTCTGGAGGAGGTCCAAATTGGTGGAGCCAGAGGTGGAGCAGTA 747
Db |||||
QY 727 GTGACGCTGTGCCACTGAAGGAGTCCAGTTGGTGGAGCCAGAGGGGAGCAGTA 786
QY 748 GCTCTGGTGGAAACCGTAACCTGACCTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 807
Db |||||
QY 787 GCTCTGGTGGTACTGTGACTTGAACCTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 846
QY 808 CACTGGATGAAGATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 867
Db |||||
QY 847 CACTGGATGAAGATGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
QY 868 GAGATAGGGCTCTGAGGACAGGAACTTACAGTGTGTGGGACCACTTCCAGCCAGGG 927
Db |||||
QY 907 GAGTAGGGCTCTGAGGACAGGAACTTACAGTGTGTGGGACCACTTCCAGCCATGG 966
QY 928 CCGCAGAAAGCGGTGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 987
Db |||||
QY 967 CCGCAGGAGAGCGGTGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 1026
QY 988 GCAGGCTCTGTGGAGGATCAGGCTGG 1015
Db |||||
QY 1027 GCAGGCTCTGTGGAAGGCGGGGCTGG 1054

RESULT 8
US-09-638-648-2
; Sequence 2, Application US/09638648
; Patent No., 6825164
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; APPLICANT: Zlokovic, Berislav
; TITLE OF INVENTION: A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID
; FILE REFERENCE: 0575/62097
; CURRENT APPLICATION NUMBER: US/09/638,648
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1426
; TYPE: DNA
; ORGANISM: Bos Taurus
US-09-638-648-2

Query Match 73.2%; Score 746.4; DB 4; Length 1426;
Best Local Similarity 84.1%; Pred. No. 1.5e-196;
Matches 881; Conservative 0; Mismatches 131; Indels 36; Gaps 2;

QY 1 ATGGCAGCGGAAACAGCAGTTGGAGCTTGGGTCTGCTCCTCAGTCTGTGGGGGCGAGTA 60
Db |||||
QY 10 ATGGCAGCAGGGCAGTGTGGAGCTGGATGCTAGTCTCAGTCTGGGGGGGACAGTC 69
Db |||||
QY 61 GTAGTGTCTAAACATCAACGCCGGATTTGGCGACCACTGGTCTGAAGTGTAAAGGG 120
Db |||||
QY 70 ACGGGGACCAAAACATCAACGCCGGATTTGGCGACCACTGGTCTGAAGTGTAAAGGG 129
QY 121 GCGCCCAAGAACACCCAGCGGTGGATGGAACTGAAACACACAGCCGGGACAGAGCT 180
Db |||||
QY 130 GCGCCCAAGAACACCCAGCGGTGGATGGAACTGAAACACACAGCCGGGACAGAGCT 189
QY 181 TGAAGGTCTCTCTCTCCCGAGGAGAGCGCCCTGGGACAGTGTGGTCTGCTCTCTTCCC 240
Db |||||
QY 190 TGAAGGTCTCTCTCTCCCGAGGAGAGCGCCCTGGGACAGTGTGGTCTGCTCTCTTCCC 246
QY 241 AAGCGTCTCTCTCTCTCCCGAGGAGAGCGCCCTGGGACAGTGTGGTCTGCTCTCTTCCC 300
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QY 247 AAGCGTCTCTCTCTCTCCCGAGGAGAGCGCCCTGGGACAGTGTGGTCTGCTCTCTTCCC 306
QY 301 GCATGAAACAGGATGGAAGGAGAGCAAGTCCAACTACCGAGTCCGTCTTACAGATT 360
Db |||||
QY 307 GCATGAAACAGGATGGAAGGAGAGCAAGTCCAACTACCGAGTCCGTCTTATCAGATT 366
QY 361 CTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACTCACGGCTGGTCTTCCCAATAAG 420
Db |||||
QY 367 CTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACTCATGGCTGGTCTTCCCAATAAG 426
QY 421 GTGGGACATGTGTCTGGGATTCAGCGGACCTTCTAGCTGGGACCTTTAGCTGGGAC 480
Db |||||
QY 427 GTGGGACATGTGTCTGGGATTCAGCGGACCTTCTAGCTGGGACCTTTAACTGGCT 486
QY 481 GGGAAAGCCCTGTGTCTGAGAGGAGAGTCTGTGAGAGGAGAGTCTGAGAGGAGAGAC 540
Db |||||
QY 487 GGGAAAGCCCTGTGTCTGAGAGGAGAGTCTGTGAGAGGAGAGTCTGAGAGGAGAGAC 546
QY 541 CTGTAGACAGGAGTCTTCACTACCTGAGTGGAGTAACTGACCCAGCGGAGGAGGAG 600
Db |||||
QY 547 CCAAGAGCAGGGCTTTTCACTGCTTCCATTCGAGTGTGATGGTCTTCCCAATAAG 606
QY 601 GATTCCTGTCAGAGTCTTCTGAGTCTTCTGAGTCTTCTGAGTCTTCTGAGTCTTCTG 660
Db |||||
QY 607 GCTCTCCAGCCACCTTCTCTGAGTCTTCTGAGTCTTCTGAGTCTTCTGAGTCTTCTG 666
QY 661 CGCAGAGCCCGATCCAGCCCGGCTGTG----- 689
Db |||||

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 17:18:58 ; Search time 877.54 Seconds
(without alignments)
9383.456 Million cell updates/sec

Title: US-10-091-019-1
Perfect score: 1391
Sequence: 1 959gcagccggaacagcagt.....aacacctgacacattcttga 1391

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
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8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1389	99.9	1415	6	ABQ99597 Human cod
3	1387.8	99.8	1391	6	ABK10856 DNA encod
4	1387.8	99.8	1391	6	ABK84114 Human cdn
5	1387.8	99.8	1391	6	AAD36952 Human rec
6	1387.8	99.8	1391	10	AAD59952 Human RAG
7	1387.8	99.8	1391	10	ADG32021 Human DNA
8	1375.8	98.9	1582	4	AAS7444 Human lun
9	1373	98.7	1436	12	ADK00130 Human RAG
10	1331	95.7	1463	6	ABQ99598 Human cod
11	1303.8	93.7	1539	9	ACC59920 Human REM
12	1293.4	93.0	1678	9	ACC59907 Human REM
13	1265.6	91.0	1329	12	ADP19665 Human LP2
14	1250	89.9	1323	12	ADP19667 Human LP2
15	1242	89.3	1268	10	ADG33024 Human DNA
16	1233.8	88.7	1627	9	ACC59921 Human REM
17	1228	88.3	1384	12	ADP19659 Human LP2
18	1211.4	87.1	1217	10	ADP59563 Human NOV
19	1192	85.7	1294	12	ADP19669 Human LP2
20	1146.4	82.4	1226	10	ADP59565 Human NOV

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23	1106	79.5	1291	12	ADP19655 Human LP2
24	1062	76.3	1223	6	ABV73151 Human sol
25	1062	76.3	1223	10	ADG37043 Receptor
26	1048	75.3	1339	12	ADP19661 Human LP2
27	1025.2	73.7	1761	12	ADK00128 Human RAG
28	1018	73.2	1023	2	AAV12394 Human sol
29	1018	73.2	1023	2	AAV06517 Human RAG
30	1013	72.8	1020	6	ABQ79956 Human sol
31	992	71.3	1194	12	ADP19657 Human LP2
32	992	71.3	1239	12	ADP19663 Human LP2
33	954	68.6	957	2	AAV06518 Human RAG
34	950.8	68.4	957	2	AAV12395 Human mat
35	944.8	67.9	1426	6	ABK10855 DNA encod
36	944.8	67.9	1426	6	AAD36951 Cow recep
37	944.8	67.9	1426	10	AAD59951 Bovine RA
38	944.8	67.9	1426	10	ADG32020 DNA encod
39	826.4	59.4	1347	6	ABK10858 DNA encod
40	826.4	59.4	1348	6	ABK10857 DNA encod
41	826.4	59.4	1348	6	AAD36953 Mouse rec
42	826.4	59.4	1348	10	AAD59953 Murine RA
43	820	59.0	1090	12	ADM80824 Human CAD
44	708.4	50.9	2057	12	ADK00123 Murine so
45	476.6	34.3	610	6	ABL55596 Lung canc

ALIGNMENTS

RESULT 1
ABQ79955
ID ABQ79955 standard; DNA; 1391 BP.
XX
AC ABQ79955;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human RAGE nucleotide sequence.
XX
KW Receptor for Advanced Glycated end product; RAGE; recombinant; nootropic;
KW antiarteriosclerotic; antidiabetic; cytosatic; nephrotropic; vasotropic;
KW neuroprotective; antiinflammatory; gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WC200270667-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US006881.
XX
PR 05-MAR-2001; 2001US-0273418P.
XX
PA (TRAN-) TRANSTECH PHARMA INC.
XX
PI Harris R, Shen J, Shabbaz M;
XX
DR WPI; 2002-713443/77.
XX
PT High level expression of recombinant Receptors for Advanced Glycated end products (RAGE) proteins for treating increased levels of advanced glycosylation end products, comprises infecting cells with a high titer recombinant virus.
XX
PS Claim 12; Fig 2A; 5lpp; English.
XX
CC The invention relates to a method for high level expression of recombinant forms of the Receptor for Advanced Glycated end products (RAGE) or its fragments. The method involves (i) subcloning a nucleotide sequence encoding RAGE or its fragment into a virus; (ii) preparing a high titer stock of recombinant virus; and (iii) infecting host cells with the high titer recombinant virus under conditions such that

CC predetermined levels of RAGE or its fragment is produced, where the
CC predetermined levels of RAGE comprises at least 25 mg recombinant protein
CC per liter of culture. The method is useful for high level expression of
CC recombinant RAGE polypeptide or its fragment which may be useful in
CC preventing, treating or ameliorating diseases associated with increased
CC levels of advanced glycosylation end products, such as atherosclerosis,
CC diabetes and its symptoms, amyloidosis, kidney failure, Alzheimer's
CC disease, inflammation, systemic lupus nephritis, inflammatory lupus
CC nephritis, cancer or erectile dysfunction. The present sequence
CC represents the nucleotide sequence of human RAGE as reported in GenBank
CC /EMBL Accession no. XM004205
XX
SQ Sequence 1391 BP; 305 A; 408 C; 417 G; 261 T; 0 U; 0 Other;

Query Match 100.0%; Score 1391; DB 6; Length 1391;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACGCGGACACAGCAGTTGGAGCTGGGTGCTGGTCTCTCAGTCTGTGGGGGCGAGTA 60
DB 1 GGGGACGCGGACACAGCAGTTGGAGCTGGGTGCTGGTCTCTCAGTCTGTGGGGGCGAGTA 60

QY 61 GTAGTGTCTCAAAACATCAAGCCCGGATTGGGAGCCACTGGTCTGAAGTGTAAAGGG 120
DB 61 GTAGTGTCTCAAAACATCAAGCCCGGATTGGGAGCCACTGGTCTGAAGTGTAAAGGG 120

QY 121 GCGCCCAAGAAACACCCAGCGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCT 180
DB 121 GCGCCCAAGAAACACCCAGCGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCT 180

QY 181 TGAAGTCTCTGTCTCCCGAGGAGGAGCCCTCGGACAGTGTGGTCTGTCTTCTTCCC 240
DB 181 TGAAGTCTCTGTCTCCCGAGGAGGAGCCCTCGGACAGTGTGGTCTGTCTTCTTCCC 240

QY 241 AACGGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 300
DB 241 AACGGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 300

QY 301 GCATCAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTCTTACAGATT 360
DB 301 GCATCAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTCTTACAGATT 360

QY 361 CTGGGAAGCCAGAAATGTAGATTCTGCTCTGAACTCACGGCTGGTGTTCCTCAATAAG 420
DB 361 CTGGGAAGCCAGAAATGTAGATTCTGCTCTGAACTCACGGCTGGTGTTCCTCAATAAG 420

QY 421 GTGGGACATGTGTTCAGAGGAACTACCTTCAGGGAGCTCTTAGCTGGGACCTTGGAT 480
DB 421 GTGGGACATGTGTTCAGAGGAACTACCTTCAGGGAGCTCTTAGCTGGGACCTTGGAT 480

QY 481 GGGAGCCCTGTGCTTAATGAGAGGAGTATCTGTGAAGAAACAGACACAGGAGACAC 540
DB 481 GGGAGCCCTGTGCTTAATGAGAGGAGTATCTGTGAAGAAACAGACACAGGAGACAC 540

QY 541 CTTGAGACAGGGCTCTTCACTGCACTGCGAGCTAATGTGTACCCAGCCGCGGAGGA 600
DB 541 CTTGAGACAGGGCTCTTCACTGCACTGCGAGCTAATGTGTACCCAGCCGCGGAGGA 600

QY 601 GATCCCGTCCACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 660
DB 601 GATCCCGTCCACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 660

QY 661 CGCACAGCCCTTCCAGCCCTGCTGCTGGAGCCCTGCTGCTGGAGGAGTCCAAATTG 720
DB 661 CGCACAGCCCTTCCAGCCCTGCTGCTGGAGCCCTGCTGCTGGAGGAGTCCAAATTG 720

QY 721 GTGGTGGAGCCAGAGGTGGAGCAGTAGCTCTTGTGTGGAACCGTAACCTGACCTGTGAA 780
DB 721 GTGGTGGAGCCAGAGGTGGAGCAGTAGCTCTTGTGTGGAACCGTAACCTGACCTGTGAA 780

QY 781 GTCCCTGCCAGCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 840
DB 781 GTCCCTGCCAGCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 840

QY 841 CCCCCAGCCCTGTGTCTGATCTCTCTGATAGTAGGCTCTCAGGACCAGGAACTTACAGC 900
DB 841 CCCCCAGCCCTGTGTCTGATCTCTCTGATAGTAGGCTCTCAGGACCAGGAACTTACAGC 900

QY 901 TGTGTGGCCACCATTCAGCCACGGGCCCAAGAAAGCCGTGTGTAGCATCAGCATC 960
DB 901 TGTGTGGCCACCATTCAGCCACGGGCCCAAGAAAGCCGTGTGTAGCATCAGCATC 960

QY 961 ATCGAACACAGGAGGAGGCGGCTGAGCTCTGTGGAGGATCAGGGCTGGGAAT 1020
DB 961 ATCGAACACAGGAGGAGGCGGCTGAGCTCTGTGGAGGATCAGGGCTGGGAAT 1020

QY 1021 CTAGCCCTGGCCCTGGGATCTCTGGAGGCTCTGGGACAGCCGCTCTTCTTGGGGTC 1080
DB 1021 CTAGCCCTGGCCCTGGGATCTCTGGAGGCTCTGGGACAGCCGCTCTTCTTGGGGTC 1080

QY 1081 ATCTTGTGCAAAAGCGGCAACCGCAGAGAGAGAGAGAGGAGGAGGAGGAGGAG 1140
DB 1081 ATCTTGTGCAAAAGCGGCAACCGCAGAGAGAGAGAGAGGAGGAGGAGGAGGAG 1140

QY 1141 GAAGGAGGAGGCGTGCAGAACTGAATCAGTCGAGGAACTTCTTCTTCTTCTTCTTCTT 1200
DB 1141 GAAGGAGGAGGCGTGCAGAACTGAATCAGTCGAGGAACTTCTTCTTCTTCTTCTTCTT 1200

QY 1201 ACTGAGGAGGCTTGGGGGCCACACAGATCCCATCAGCTCCCTTCTTCTTCTTCTTCTT 1260
DB 1201 ACTGAGGAGGCTTGGGGGCCACACAGATCCCATCAGCTCCCTTCTTCTTCTTCTTCTT 1260

QY 1261 CTTGAACTGTGTCTGGCTCAGACCACTCTCTCTGTATATCTCTCTCTCTCTCTCTCTCT 1320
DB 1261 CTTGAACTGTGTCTGGCTCAGACCACTCTCTCTGTATATCTCTCTCTCTCTCTCTCTCT 1320

QY 1321 CCACCTTGCAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1380
DB 1321 CCACCTTGCAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1380

QY 1381 CACATCTTGCA 1391
DB 1381 CACATCTTGCA 1391

RESULT 2
ABQ99597
ID ABQ99597 standard; cdna; 1415 BP.
XX
AC ABQ99597;
XX
DT 25-FEB-2003 (first entry)
XX
Human coding sequence SEQ ID 330.
DE
XX
Human; expressed sequence tag; EST; chromosome 6p21.3;
KW haematopoietic disorder; central nervous system disease; viral infection;
KW peripheral nervous system disease; non-healing wound; infectious disease;
KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;
KW fungal infection; autoimmune disorder; coagulation disorder; neutropenic;
KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;
KW cytostatic; haemostatic; virucide; antibacterial; fungicide;
KW immunostimulant; cerebroprotective; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200259260-A2.
XX
PD 01-AUG-2002.
XX
PF 16-NOV-2001; 2001WO-US042950.
XX
PR 17-NOV-2000; 2000US-00714936.
XX
PA (HYSE-) HYSEQ INC.
XX

Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;
 Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
 WPI; 2002-590824/63.
 N-PSDB; ABP65011.
 New isolated polynucleotide, useful in research, diagnostic or
 therapeutic methods, e.g. preventing or treating disorders involving
 aberrant protein expression or biological activity.
 Claim 1; SEQ ID NO 330; 394pp; English.
 The present invention relates to novel human coding sequences (ABQ9268-
 ABQ93608) and proteins (ABP64682-ABP65022). The sequences are useful in
 therapeutic, diagnostic and research methods. The polynucleotides may be
 used in the field of molecular biology as hybridisation probes, primers
 for PCR, for chromosome and gene mapping, for the recombinant production
 of protein, or in generation of anti-sense DNA or RNA. The
 polynucleotides are useful in diagnostics as expressed sequence tags
 (ESTs) for identifying expressed genes or for physical mapping of the
 human genome. The proteins may be used as molecular weight markers, or as
 nutritional sources or supplements. The proteins may be used to maintain
 and expand cell population in a totipotent or pluripotential state
 useful for re-engineering damaged or diseased tissues, transplantation,
 manufacture of bio-pharmaceuticals or the development of bio-sensors. The
 polynucleotides and proteins are useful for preventing, treating or
 ameliorating disorders involving aberrant protein expression or
 biological activity, e.g. haematopoietic disorders, central/peripheral
 nervous system diseases, mechanical and traumatic disorders, non-healing
 wounds, immune deficiencies and disorders, infectious diseases caused by
 viral, bacterial or fungal infection, autoimmune disorders, allergic
 reactions and conditions, coagulation disorders, or cancer. The
 polynucleotide sequences of the invention were assembled from ESTs
 isolated mainly by sequencing by hybridisation, and in some cases,
 sequences obtained from one or more public databases. Note: The sequence
 data for this patent did not form part of the printed specification, but
 was obtained in electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences
 Sequence 1415 BP; 313 A; 414 C; 425 G; 263 T; 0 U; 0 Other

Query Match	99.9%;	Score 1389;	DB 6;	Length 1415;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1389;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	3	GGCAGCGGACACAGCTTGAGCGCTGGGTCTCGTCTCAGTCAGTCGTGGGGCGCAGTAGT	62	
Db	27	GGCAGCGGAAACAGAGCTTGAGCGCTGGGTCTCGTCTCAGTCGTGGGGCGCAGTAGT	86	
Qy	63	AGGTGCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTCTGAAGTGTGAAGGGGCG	122	
Db	87	AGGTGCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTCTGAAGTGTGAAGGGGCG	146	
Qy	123	CCCCAAGAAACACCCAGCGGCTGGAAATGAAACTGAACACAGCCCGGACAGAACTTG	182	
Db	147	CCCCAAGAAACACCCAGCGGCTGGAAATGAAACTGAACACAGCCCGGACAGAACTTG	206	
Qy	183	GAAGGTCTGTCTCCCAAGGAGGAGGCCCTTGGGACAGTGTGGCTCGTGTCTCTCCCA	242	
Db	207	GAAGGTCTGTCTCCCAAGGAGGAGGCCCTTGGGACAGTGTGGCTCGTGTCTCTCCCA	266	
Qy	243	CGGCTCCTCTTCTCTCCGCTGTCCGGATCCAGGATGAGGGGATTTTCCGGTGCAGGC	302	
Db	267	CGGCTCCTCTTCTCTCCGCTGTCCGGATCCAGGATGAGGGGATTTTCCGGTGCAGGC	326	
Qy	303	AATGAACAGGAATGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCGAGTTCC	362	
Db	327	AATGAACAGGAATGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCGAGTTCC	386	
Qy	363	TGGGAAGCCAGAAATTGTAGATTCTGCCTCTGAACTCAGCGCTGGTGTTCCTCAATAAGGT	422	
Db	387	TGGGAAGCCAGAAATTGTAGATTCTGCCTCTGAACTCAGCGCTGGTGTTCCTCAATAAGGT	446	

RESULT 3
ABK10856
ID ABK10856 standard; cDNA; 1391 BP.
XX

Db 1141 GAAGAGGAGCGCTGAGAACTGAATCACTCGAGGAACCTGAGGACGGGAGAGTAGT 1200

Qy 1201 ACTGAGGGCTTGGAGGGCCACAGACAGATCCATCCATCAGCTCCCTTTCTTTTC 1260

Db 1201 ACTGAGGGCTTGGAGGGCCACAGACAGATCCATCCATCAGCTCCCTTTCTTTTC 1260

Qy 1261 CCTGAACTGTTTGGCTCAGACCAACTCTCTCTGTATAATCTCTCTCTGTATAACC 1320

Db 1261 CCTGAACTGTTTGGCTCAGACCAACTCTCTCTGTATAATCTCTCTCTGTATAACC 1320

Qy 1321 CCACCTTGCAAGCTTCTTCTACACAGAGCCGCCCAATGATGATTAAACACTGA 1380

Db 1321 CCACCTTGCAAGCTTCTTCTACACAGAGCCGCCCAATGATGATTAAACACTGA 1380

Qy 1381 CACATCTTGA 1391

Db 1381 CACATCTTGA 1391

RESULT 4

ABK84114

ID ABK84114 standard; cDNA; 1391 BP.

XX

AC ABK84114;

XX

DT 14-AUG-2002 (first entry)

XX

DE Human cDNA differentially expressed in granulocytic cells #685.

XX

KW Human; ss; granulocytic cell; DNA chip; bacterial infection;

KW viral infection; parasitic infection; protozoal infection;

KW fungal infection; sterile inflammatory disease; psoriasis;

KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;

KW cardiac reperfusion injury; renal reperfusion injury; ARDS;

KW adult respiratory distress syndrome; inflammatory bowel disease;

KW Crohn's disease; ulcerative colitis; periodontal disease;

KW granulocyte activation; chronic inflammation; allergy.

XX

OS Homo sapiens.

PN WO200228999-A2.

XX

PD 11-APR-2002.

XX

PF 03-OCT-2001; 2001WO-US030821.

XX

PR 03-OCT-2000; 2000US-0237189P.

XX

PA (GENE-) GENE LOGIC INC.

XX

PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX

DR WPI; 2002-435328/46.

XX

PT Detecting granulocyte activation by detecting differential expression of

PT genes associated with granulocyte activation, which serves as diagnostic

PT markers that is useful for monitoring disease states and drug toxicity.

XX

PS Claim 1; SEQ ID NO 685; 114pp; English.

XX

CC The invention relates to detecting (M1) granulocyte (GC) activation

CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by

CC DNA chip analysis as given in the specification, and comparing the

CC expression level to an expression level in an unactivated GC, where

CC differential expression of Gs is indicative of GCA. Also included are

CC modulating (M2) GA by contacting GC with an agent that alters the

CC expression of at least one gene in Gs; (2) screening (M3) for an agent

CC capable of modulating GCA or an inflammation (especially chronic) in a

CC tissue, an allergic response in a subject, exposure of a subject to a

CC pathogen or sterile inflammatory disease using the gene expression

CC profile; (3) detecting (M4) an inflammation (especially chronic) in a

CC tissue, an allergic response in a subject, exposure of a subject to a

CC pathogen or sterile inflammatory disease, by detecting the level of

CC expression in a sample of the tissue of gene(s) from Gs, where the level

CC of expression of the gene is indicative of inflammation; (4) treating

CC (M5) an inflammation (especially chronic) or in a tissue, an allergic

CC response in a subject, exposure of a subject to a pathogen or sterile

CC inflammatory disease, by contacting a tissue having inflammation with an

CC agent that modulates the expression of gene(s) from Gs in the tissue. M1

CC is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful

CC for screening an agent capable of modulating GCA preferably in an

CC inflammation in a tissue; M4 is useful for detecting an inflammation

CC (especially chronic) in a tissue, an allergic response in a subject,

CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.

CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,

CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult

CC respiratory distress syndrome, inflammatory bowel disease, Crohn's

CC disease, ulcerative colitis, periodontal disease; also bacterial

CC infection, viral infection, parasitic infection, protozoal infection,

CC fungal infection and M5 is useful for treating one of the above

CC conditions. The present sequence represents a gene differentially

CC expressed in granulocytes. Note: the sequence data for this patent did

CC not form part of the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX

SEQ Sequence 1391 BP; 305 A; 407 C; 418 G; 261 T; 0 U; 0 Other;

Query Match 99.8%; Score 1387.8; DB 6; Length 1391;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1389; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGAGCCGGAAACAGACAGTTCAGGCTCGGTGCTGCTCAGTCTGTGGGGGAGTA 60

Db 1 GGGGAGCCGGAAACAGACAGTTCAGGCTCGGTGCTGCTCAGTCTGTGGGGGAGTA 60

Qy 61 GTAGGTGCTCAAAAATCATCAGCCCGATTTGGGAGCCACTGTGTCTGAAGTCTAAGGGG 120

Db 61 GTAGGTGCTCAAAAATCATCAGCCCGATTTGGGAGCCACTGTGTCTGAAGTCTAAGGGG 120

Qy 121 GCGCCCAAGAAACACCCAGCGGCTTGGAAATGGAATCTGAACAAGCT 180

Db 121 GCGCCCAAGAAACACCCAGCGGCTTGGAAATGGAATCTGAACAAGCT 180

Qy 181 TGAAGGTCTCTGTCTCCCGAGGAGAGCCCTTGGGACAGTGTGGCTGTCTTCCC 240

Db 181 TGAAGGTCTCTGTCTCCCGAGGAGAGCCCTTGGGACAGTGTGGCTGTCTTCCC 240

Qy 241 AACGGCTCCTCTCTCTCCCGCTGTGGGATCCAGGATGAGGGATTTTCGGTCCAG 300

Db 241 AACGGCTCCTCTCTCTCCCGCTGTGGGATCCAGGATGAGGGATTTTCGGTCCAG 300

Qy 301 GCAATGAACAGGAATGGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATT 360

Db 301 GCAATGAACAGGAATGGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATT 360

Qy 361 CTGGAAGCCAGAAATTTAGATTCTGCTCTGAATCTACCGCTGGTGTTCCTCAATAG 420

Db 361 CTGGAAGCCAGAAATTTAGATTCTGCTCTGAATCTACCGCTGGTGTTCCTCAATAG 420

Qy 421 GTGGGACATGTTGTTCAGAGGAGAGTACCTTCAGGAGTCTTTAGCTGGCACTTGGAT 480

Db 421 GTGGGACATGTTGTTCAGAGGAGAGTACCTTCAGGAGTCTTTAGCTGGCACTTGGAT 480

Qy 481 GGGAGAGCCCTCGTCTTAATGAGAGGAGGATATCTGTGAAGGAAACAGACAGGAGACAC 540

Db 481 GGGAGAGCCCTCGTCTTAATGAGAGGAGGATATCTGTGAAGGAAACAGACAGGAGACAC 540

Qy 541 CTGTGAGAGAGGCTCTTCACTGTGAGTCTGAGTCTAATGGTGAACCCAGCCGGGAGGA 600

Db 541 CTGTGAGAGAGGCTCTTCACTGTGAGTCTAATGGTGAACCCAGCCGGGAGGA 600

Qy 601 GATCCCGTCCCACTTCTCTCTGAGTCTACGCCAGGCTTCCCGACACACCGGCTTG 660

Db 601 GATCCCGTCCCACTTCTCTCTGAGTCTACGCCAGGCTTCCCGACACACCGGCTTG 660

Qy		661	CGCACGCCCCCATCCAGACCCCGTGTTCTGGGAGCCTGTGCCTCTGGAGGAGGTCCAATTG	720
Dd		661	CGCACAGCCCCCATCCAGACCCCGTGTTCTGGGAGCCTGTGCCTCTGGAGGAGGTCCAATTG	720
Qy		721	GTGGTGGAGCCAGAAAGTGGAGCAGTAGTCCTGGTGTGAACCGCTAACCCCTGACTGTGAA	780
Dd		721	GTGGTGGAGCCAGAAAGTGGAGCAGTAGTCCTGGTGTGAACCGCTAACCCCTGACTGTGAA	780
Qy		781	GTCCTCTGCCAGCCCTCTCTCAAATCCACTGGATGAAGGATGGTGTGCCCTTGCCCCTT	840
Dd		781	GTCCTCTGCCAGCCCTCTCTCAAATCCACTGGATGAAGGATGGTGTGCCCTTGCCCCTT	840
Qy		841	CCCCCAGCCCTGTGCTGATCTCTCCCTGAGATAGGCTCTCAGGACCAGGGAAACCTA CAGC	900
Dd		841	CCCCCAGCCCTGTGCTGATCTCTCCCTGAGATAGGCTCTCAGGACCAGGGAAACCTA CAGC	900
Qy		901	TGTTGTGCCACCAATTCACGCCACGGGCCCCAGGAAAGCGTGTGCAGCATCAGCATC	960
Dd		901	TGTTGTGCCACCAATTCACGCCACGGGCCCCAGGAAAGCGTGTGCAGCATCAGCATC	960
Qy		961	ATCGAAACAGCCAGGAGGGGCCAACTGCAAGCTCTCTGGGAGGATCAGGGCTGGGAACT	1020
Dd		961	ATCGAAACAGGCGAGGAGGGGCCAACTGCAAGCTCTCTGGGAGGATCAGGGCTGGGAACT	1020
Qy		1021	CTAGCCTTGGCCCTTGGGGATCTTGGGAGGCCCTGGGGA CAGCGCCCTGTCTATTGGGGTC	1080
Dd		1021	CTAGCCTTGGCCCTTGGGGATCTTGGGAGGCCCTGGGGA CAGCGCCCTGTCTATTGGGGTC	1080
Qy		1081	ATCTTTGTGGNAAGGCGCAACGCCGAGGAGAGAGAGGAGGCCCCAGAAAAC CAGGAG	1140
Dd		1081	ATCTTTGTGGCAAGAAGCGCGCAACGCCGAGGAGAGAGAGGAGGCCCCAGAAAAC CAGGAG	1140
Qy		1141	GAAGAGGAGGACGTGCAGAACTGAATCAGTCGGAGGAACTC GAGGCGAGCGAGTAGT	1200
Dd		1141	GAAGAGGAGGAGCGTGCAGAACTGAATCAGTCGGAGGAA CTGAGGCGAGCGAGTAGT	1200
Qy		1201	ACTGGAGGGCTTGAGGGGCCACAGACAGATCCATTCATCAGCTCCCTTTTCTTTTTTC	1260
Dd		1201	ACTGGAGGGCTTGAGGGGCCACAGACAGATCCATTCATCAGCTCCCTTTTCTTTTTTC	1260
Qy		1261	CCTTTGAATGTTCTGGCCCTCAGACCAACTCTCTCCTGTATAACTCTCTCTCTGTATAAACC	1320
Dd		1261	CCTTTGAATGTTCTGGCCCTCAGACCAACTCTCTCTCTGTATAACTCTCTCTCTGTATAAACC	1320
Qy		1321	CCACTTTGCCAAGCTTTCTTCTACAACAGAGCCGCCCAACAATGATGATTAACACCTGA	1380
Dd		1321	CCACTTTGCCAAGCTTTCTTCTACAACAGAGCCGCCCAACAATGATGATTAACACCTGA	1380
Qy		1381	CACATCTTGCA	1391
Dd		1381	CACATCTTGCA	1391

RESULT 5	
AAAD36952	
ID	AAAD36952 standard; cDNA; 1391 BP.
XX	
XX	
AC	
AAAD36952;	
XX	
DT	27-AUG-2002 (first entry)
XX	
DE	Human receptor for advanced glycosylation end product (RAGE) cDNA.
XX	
KW	Human; Receptor for advanced glycosylation end product; RAGE; cardiatic;
KW	tissue growth; neointimal formation; blood vessel; restenosis; diabetes;
KW	myocardial infarction; angioplasty; peripheral vascular surgery; angina;
KW	transgenic animal; acute thrombotic stroke; venous thrombosis; gene; ss.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FH	1. .1215
CDS	/*tag= a
FT	
FT	

FT /product= "Human RAGE protein"
FT /note= "CDS does not include start codon"
FT /partial
FT polyA_signal 1368..1373
FT FT /*tag= b
FT polyA_site 1391
FT FT /*tag= c
XX
PN WO200230889-A2.
XX
XX 18-APR-2002.
XX
XX 12-OCT-2001; 2001WO-US032036.
XX PF
XX 13-OCT-2000; 2000US-00687528.
XX PR
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX PA
XX Stern DM, Schmidt A, Marso S, Topol E, Lincoff AM;
PI
XX WPI; 2002-426260/45.
DR P-PSDB; AAE23219.
XX
XX Inhibiting new tissue growth or neointimal formation in blood vessels of
PT subject suffering from diabetes, stroke and preventing restenosis,
PT comprises administering inhibitor of receptor for advance glycation end
PT product.
XX
XX Disclosure; Page 16-17; 43pp; English.
XX
XX The invention relates to a method for inhibiting new tissue growth or
CC neointimal formation in blood vessels in a subject that has experienced
CC blood vessel injury and preventing exaggerated restenosis in a diabetic
CC subject. The method comprises administering an inhibitor of receptor for
CC advanced glycation/glycosylation end product (RAGE), so as to inhibit new
CC tissue growth or neointimal formation in subject's blood vessels and
CC preventing restenosis in the subject. The method is useful for inhibiting
CC new tissue growth or neointimal formation in blood vessels in a subject
CC like non-human animal, a transgenic non-human animal or a human suffering
CC from diabetes, acute thrombotic stroke, venous thrombosis, unstable
CC angina, myocardial infarction, abrupt closure following angioplasty or
CC stent placement, or thrombosis as a result of peripheral vascular surger
CC The method is also useful for preventing restenosis and for determining
CC whether a compound inhibits new tissue growth in a blood vessel in a
CC subject. The present sequence is human RAGE receptor for advanced
CC glycosylation end product (RAGE) cDNA
XX
XX Sequence 1391 BP: 305 A: 407 C: 418 G: 261 T: 0 U: 0 Other:

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/product= "Human RAGE protein"
/note= "CDS does not include start codon"
/partial
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1368..1373
/*tag= b
1391
polyA_site
/*tag= c

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/product= "Human RAGE protein"
/note= "CDS does not include start codon"
/partial
polyA_signal
1368..1373
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polyA_site
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QY 361 CCTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACTCAGCGTGGTGTTCCTCAATAAG 420
Db 361 CCTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACTCAGCGTGGTGTTCCTCAATAAG 420
QY 421 GTGGGACATGTGTGTGTCAGAGGAAAGCTACCCCTCGAGGAGCTCTAGCTGGCACTTTGGAT 480
Db 421 GTGGGACATGTGTGTGTCAGAGGAAAGCTACCCCTCGAGGAGCTCTAGCTGGCACTTTGGAT 480
QY 481 GGAAGCCCTGTGCTTAATGAGAGGAGATCTGTGAAGAACAGACAGGAGACAC 540
Db 481 GGAAGCCCTGTGCTTAATGAGAGGAGATCTGTGAAGAACAGACAGGAGACAC 540
QY 541 CCTGAGACAGGCTCTTCACTGCACTGCGAGCTAATGTGTGACCCAGCCGCGGAGGA 600
Db 541 CCTGAGACAGGCTCTTCACTGCACTGCGAGCTAATGTGTGACCCAGCCGCGGAGGA 600
QY 601 GATCCCGCTCCCACTTCTCTGTAGCTTCAGCCCAAGGCTTCCCGACACCGGGCTTG 660
Db 601 GATCCCGCTCCCACTTCTCTGTAGCTTCAGCCCAAGGCTTCCCGACACCGGGCTTG 660
QY 661 CGCACAGCCCTCATCAGCCCTGTCTGGAGCCTGTGCTCTGGAGGAGTCCAAATTG 720
Db 661 CGCACAGCCCTCATCAGCCCTGTCTGGAGCCTGTGCTCTGGAGGAGTCCAAATTG 720
QY 721 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTGCTGTGGAACCGTACCCCTGACCTGTGA 780
Db 721 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTGCTGTGGAACCGTACCCCTGACCTGTGA 780
QY 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAAGGATGGTGTGCCCTTGGCCCTT 840
Db 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAAGGATGGTGTGCCCTTGGCCCTT 840
QY 841 CCCCCAGCCCTGTGTGATCTCTCTGATAGATAGGCTCTCAGCAAGGAACTTACAGC 900
Db 841 CCCCCAGCCCTGTGTGATCTCTCTGATAGATAGGCTCTCAGCAAGGAACTTACAGC 900
QY 901 TGTGTGGCCACCATTTCCAGCCAGGGCCCGCCAGGAAAGCGTGTCTGACGATCAGATC 960
Db 901 TGTGTGGCCACCATTTCCAGCCAGGGCCCGCCAGGAAAGCGTGTCTGACGATCAGATC 960
QY 961 ATCGAACAGGCGAGGAGGGCCCAACTGCAAGGCTCTGTGGAGGATCAGGGCTGGAACT 1020
Db 961 ATCGAACAGGCGAGGAGGGCCCAACTGCAAGGCTCTGTGGAGGATCAGGGCTGGAACT 1020
QY 1021 CTAGCCCTGGCCCTGGGATCTCTGGAGGCTCTGGGACAGCCGCTCTCATTTGGGTC 1080
Db 1021 CTAGCCCTGGCCCTGGGATCTCTGGAGGCTCTGGGACAGCCGCTCTCATTTGGGTC 1080
QY 1081 ATCTTGTGCAAGGCGGCAACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
Db 1081 ATCTTGTGCAAGGCGGCAACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY 1141 GAAGAGGAGGAGGCGTGCAGAACTGAACTCAGTTCGAGGAACTCAGGAGCGGAGAGTAGT 1200
Db 1141 GAAGAGGAGGAGGCGTGCAGAACTGAACTCAGTTCGAGGAACTCAGGAGCGGAGAGTAGT 1200
QY 1201 ACTGGAGGCGCTTGGAGGGCCCAACAGACAGATCCCATCATCAGTCCCTTTCTTTTC 1260
Db 1201 ACTGGAGGCGCTTGGAGGGCCCAACAGACAGATCCCATCATCAGTCCCTTTCTTTTC 1260
QY 1261 CTTGAACTGTTTGGCCTCAGACCACTCTCTCTGTATATCTCTCTCTCTCTCTATAACC 1320
Db 1261 CTTGAACTGTTTGGCCTCAGACCACTCTCTCTGTATATCTCTCTCTCTCTCTATAACC 1320
QY 1321 CCACCTTGCCAAAGCTTCTTCTACAAACAGAGGCCCCCAATGATGATTAAACACCTGA 1380
Db 1321 CCACCTTGCCAAAGCTTCTTCTACAAACAGAGGCCCCCAATGATGATTAAACACCTGA 1380
QY 1381 CACATCTTGA 1391
```

```
Db 1381 CACATCTTGA 1391
RESULT 6
AD59952
ID AD59952 standard; DNA; 1391 BP.
XX AD59952;
XX 18-DEC-2003 (first entry)
XX Human RAGE (receptor for advanced glycation end product) DNA.
XX Transgenic mouse; transgenic; nerve tissue specific promoter; nootropic;
XX receptor for advanced glycation end product; RAGE; neurological disorder;
XX Alzheimer's disease; amnesia; amyotrophic lateral sclerosis; neuroleptic;
XX brain injury; cerebral senility; degenerative disorder; Down's syndrome;
XX chronic peripheral neuropathy; cognitive disability; memory dysfunction;
XX electric shock; Guillain-Barre syndrome; head trauma; mental retardation;
XX Huntington's disease; learning disability; dyslexia; Tourette's syndrome;
XX neuromuscular disorder; Parkinson's disease; myasthenia gravis; dementia;
XX Pick's disease; human; gene; ds.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
CDS 1..1215
FT /tag= a
FT /product= "Human RAGE protein"
FT /note= "No start codon"
FT /partial
FT polyA_signal 1368..1373
FT /tag= b
XX US6563015-B1.
XX 13-MAY-2003.
XX 14-AUG-2000; 2000US-00638649.
XX 14-AUG-2000; 2000US-00638649.
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX Stern DM, Schmidt AM, Yan SD;
XX WPI; 2003-687217/65.
XX P-PSDB; AAE39510.
XX Transgenic mouse whose genome contain recombinant deoxyribonucleic acid
XX sequence, comprises nerve tissue specific promoter encoding human
XX receptor for advanced glycation end products, and mutant human amyloid
XX precursor protein.
XX Disclosure; Col 6-7; 40pp; English.
XX The invention relates to a transgenic mouse whose genome contain a
XX recombinant DNA sequence, comprising a nerve tissue specific promoter
XX operatively linked to a DNA sequence, which encodes human receptor for
XX advanced glycation end products (RAGE), and a mutant human amyloid
XX precursor protein hAPP695, hAPP751, and hAPP770 bearing mutations linked
XX to familial Alzheimer's disease in humans. The transgenic animal is used
XX for evaluation of the potential therapeutic effect of an agent for
XX treating Alzheimer's disease in a human. It is useful for screening of
XX compounds, which would be useful in the treatment of neurological
XX disorders in humans, e.g. amnesia, amyotrophic lateral sclerosis, a brain
XX injury, cerebral senility, chronic peripheral neuropathy, a cognitive
XX disability, a degenerative disorder associated with learning, Down's
XX syndrome, dyslexia, electric shock induced amnesia or amnesia, Guillain-
XX Barre syndrome, head trauma, Huntington's disease, a learning disability,
XX a memory deficiency, memory loss, a mental illness, mental retardation,
XX memory or cognitive dysfunction, multi-infarct dementia and senile
```

CC	dementia, mvasthenia gravis, a neuromuscular disorder, Parkinson's
CC	disease, Pick's disease, a reduction in spatial memory retention,
CC	senility, or Tourette's syndrome. The present sequence is human RAGE DNA
XX	
SQ	Sequence 1391 BP; 305 A; 407 C; 418 G; 261 T; 0 U; 0 Other;
	Query Match 99.8%; Score 1387.8; DB 10; Length 1391;
	Best Local Similarity 99.9%; Pred. No. 0;
	Matches 1389; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 GGGGACGCGGACACAGCTTGGAGCTCGGTGCTGCTCCTCAGTCTGTGGGGGAGTA 60
DB	1 GGGGACGCGGACACAGCTTGGAGCTCGGTGCTGCTCCTCAGTCTGTGGGGGAGTA 60
QY	61 GTAGTGTCTCAAAACATCAGCCCGGATTGGGAGCCACTGGTGTGAAGTGAAGGGG 120
DB	61 GTAGTGTCTCAAAACATCAGCCCGGATTGGGAGCCACTGGTGTGAAGTGAAGGGG 120
QY	121 GCGCCCAAGAAACACCCAGCGGCTGGAAATGGAACCTGAACACAGGCCGGACAGAGCT 180
DB	121 GCGCCCAAGAAACACCCAGCGGCTGGAAATGGAACCTGAACACAGGCCGGACAGAGCT 180
QY	181 TGAAGGTCTGTCTCTCCAGGAGGAGGCCCTCTGGGACAGTGTGGCTGTGTCTTCCC 240
DB	181 TGAAGGTCTGTCTCTCCAGGAGGAGGCCCTCTGGGACAGTGTGGCTGTGTCTTCCC 240
QY	241 AAGGCTCTCTCTCTCTCGGCTGTGCGGATCCAGGATGAGGGATTTCCGGTGCAGG 300
DB	241 AAGGCTCTCTCTCTCTCGGCTGTGCGGATCCAGGATGAGGGATTTCCGGTGCAGG 300
QY	301 GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTCTTACAGATT 360
DB	301 GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTCTTACAGATT 360
QY	361 CTGGGAAGCCGAAATTTAGATTCTGCTCTGAACTCAAGCTCAAGCTGCTGCTTCCATAAG 420
DB	361 CTGGGAAGCCGAAATTTAGATTCTGCTCTGAACTCAAGCTCAAGCTGCTGCTTCCATAAG 420
QY	421 GTGGGACATGTGTGTCAGAGGGAAGCTACCTGACGGGACTTTAGCTGGCACTTGGAT 480
DB	421 GTGGGACATGTGTGTCAGAGGGAAGCTACCTGACGGGACTTTAGCTGGCACTTGGAT 480
QY	481 GGGAAAGCCCTGTGCTTAATGAGAAGGAGTATCTGTGAAGAAACAGACACAGGAGAC 540
DB	481 GGGAAAGCCCTGTGCTTAATGAGAAGGAGTATCTGTGAAGAAACAGACACAGGAGAC 540
QY	541 CTGAGACAGGGCTCTTCACTGACGTGCGAGCTAATGTGACCCACCCAGCGGGAGGA 600
DB	541 CTGAGACAGGGCTCTTCACTGACGTGCGAGCTAATGTGACCCACCCAGCGGGAGGA 600
QY	601 GATCCCGTCCCACTTCTCTGCTAGCTTCCAGCCAGGCTTCCCGACACCGGGCTTG 660
DB	601 GATCCCGTCCCACTTCTCTGCTAGCTTCCAGCCAGGCTTCCCGACACCGGGCTTG 660
QY	661 CGCACAGCCCCCATCCAGCCCCGTGTCTGGAGCTTGTGCTCTGGAGGAGTCCAATTG 720
DB	661 CGCACAGCCCCCATCCAGCCCCGTGTCTGGAGCTTGTGCTCTGGAGGAGTCCAATTG 720
QY	721 GTGGTGGAGCCAGAAAGGTGAGCAGTAGCTCTGTGTGGAACCGTAACCCCTGACCTGAA 780
DB	721 GTGGTGGAGCCAGAAAGGTGAGCAGTAGCTCTGTGTGGAACCGTAACCCCTGACCTGAA 780
QY	781 GTCCTGCGCCAGCCCTCTCTCAATCCACTGTGATGAAGTGTGCTGCTGCCCCCTT 840
DB	781 GTCCTGCGCCAGCCCTCTCTCAATCCACTGTGATGAAGTGTGCTGCTGCCCCCTT 840
QY	841 CCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGGCTCAGGACAGGGAACCTACAG 900
DB	841 CCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGGCTCAGGACAGGGAACCTACAG 900
QY	901 TGTGTGCGCAACCATTCAGCCACAGGCCCCAGGAAAGCGTCTGTACGATCAGCATC 960
DB	901 TGTGTGCGCAACCATTCAGCCACAGGCCCCAGGAAAGCGTCTGTACGATCAGCATC 960

RESULT 7

ADG32021
ID ADG32021 standard; DNA; 1391 BP.

XX	ADG32021;
XX	AC
XX	ADG32021;
DT	26-FEB-2004 (first entry)
XX	Human DNA homologue of the lung-specific RAGE protein SeqID49.
DE	human; tissue specific; targeted delivery; therapeutic complex; epilepsy;
XX	schizophrenia; bipolar disorder; Parkinson's disease; bacterial;
KW	fungal infection; asthma; cystic fibrosis; pulmonary oedema; diabetes;
KW	pancreatitis; endocrine tumour; pancreatic cancer; infarction;
KW	coronary heart disease; arrhythmia; nootropic; neuroprotective;
KW	antiparkinsonian; cerebroprotective; cytostatic; antibacterial;
KW	fungicidal; antiasthmatic; immunosuppressive; gene; ds.
OS	Homo sapiens.
XX	WO200308469-A2.
PN	16-OCT-2003.
XX	
XX	31-MAR-2003; 2003WO-US010195.
PF	
XX	01-APR-2002; 2002US-0369452P.
PR	
XX	(UTAH-) UTAH VENTURES II LP.
PA	
XX	Roben PW, Stevens AC;
PI	
XX	WPI; 2003-804234/75.
DR	P-PSDB; ADG32004.
XX	New brain-specific, heart-specific, lung-specific, and pancreas-specific
PT	therapeutic complexes, useful for treating or alleviating diseases that
PT	affect the brain, heart, lungs, or pancreas.
XX	

PS	XX	Example 4; SEQ ID NO 49; 127pp; English.	
CC	CC	This invention relates to novel tissue specific endothelial membrane proteins. Specifically, it relates to the targeted delivery of therapeutics to defined organs, tissues or cells using, for example, brain-, heart-, lung- or pancreas-specific complexes. Furthermore, these complexes can be used in smaller amounts than in conventional treatment such that there is reduced chance of associated toxicity and side effects. The present invention describes this therapeutic complex as comprising a ligand that binds to a tissue-specific luminally expressed protein, a therapeutic moiety and linker. As such, the therapeutic complexes are useful for treating or alleviating diseases that affect the brain (e.g. epilepsy, schizophrenia, bipolar disorder and Parkinson's disease), the lungs (e.g. bacterial or fungal infections, asthma, cystic fibrosis and pulmonary oedema), the pancreas (e.g. diabetes, pancreatitis, endocrine tumour and pancreatic cancer) or the heart (e.g. infarction, coronary heart disease and arrhythmia). Accordingly, these compositions exhibit neurotropic, neuroprotective, antiparkinsonian, cerebroprotective, cytostatic, antibacterial, fungicidal, antitachmatic and immunosuppressive activities. This polynucleotide is the DNA sequence encoding a human homologue of a lung-specific luminally expressed protein, used in a therapeutic complex of the invention.	
XX	XX	Sequence 1391 BP; 305 A; 407 C; 418 G; 261 T; 0 U; 0 Other;	
SEQ			
		Query Match 99.8%; Score 1387.8; DB 10; Length 1391;	
		Best Local Similarity 99.9%; Pred. No. 0;	
		Matches 1399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1	GGGGAGCGGAAACAGCAGTGGAGCTGGTCTGGTCTCTAGTCTGTGGGGGAGTA 60	
DB	1	GGGGAGCGGAAACAGCAGTGGAGCTGGTCTGGTCTCTAGTCTGTGGGGGAGTA 60	
QY	61	GTAGTGTCTCAAAACATCAGACCGGATTTGGGAGCCACTGGTGTGAAGTCTAAGGG 120	
DB	61	GTAGTGTCTCAAAACATCAGACCGGATTTGGGAGCCACTGGTGTGAAGTCTAAGGG 120	
QY	121	GCCCCAAGAAACACCCAGCGGCTGGAATGGAATCTGAACACAGCCGGAAGAAGCT 180	
DB	121	GCCCCAAGAAACACCCAGCGGCTGGAATGGAATCTGAACACAGCCGGAAGAAGCT 180	
QY	181	TGGAAGTCTGTCTCCAGGAGAGAGCCCTGGGACGTGGTCTGTCTCTTCCC 240	
DB	181	TGGAAGTCTGTCTCCAGGAGAGAGCCCTGGGACGTGGTCTGTCTCTTCCC 240	
QY	241	AACGGTCTCTCTCTCCGCTGTGGATCCAGATCCAGATGAGGGATTTCCGTCGAG 300	
DB	241	AACGGTCTCTCTCTCCGCTGTGGATCCAGATCCAGATGAGGGATTTCCGTCGAG 300	
QY	301	GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGT 360	
DB	301	GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGT 360	
QY	361	CTTGGGAAGCAGAAATTTAGATTCTGCTCTGAACTACAGGCTGGTGTTCCTCAATAG 420	
DB	361	CTTGGGAAGCAGAAATTTAGATTCTGCTCTGAACTACAGGCTGGTGTTCCTCAATAG 420	
QY	421	GTGGGACATGTGTCTCAGAGGAAGCTACCTCGAGGGACTCTTAGCTGGCACTTGGAT 480	
DB	421	GTGGGACATGTGTCTCAGAGGAAGCTACCTCGAGGGACTCTTAGCTGGCACTTGGAT 480	
QY	481	GGGAAGCCCTGTGTCTAATGAGAGGGAGTATCTGTGAAGGAACAGACCAGGAGACAC 540	
DB	481	GGGAAGCCCTGTGTCTAATGAGAGGGAGTATCTGTGAAGGAACAGACCAGGAGACAC 540	
QY	541	CTTGAGACAGGGCTCTTCACTGCACTGCGAGCTAATGTGACCCAGCCCGGGAGGA 600	
DB	541	CTTGAGACAGGGCTCTTCACTGCACTGCGAGCTAATGTGACCCAGCCCGGGAGGA 600	
QY	601	GATCCCGTCCCACTTCTCTGTAGCTTCAGCCAGGGCTTCCCGACACCGGGCTTG 660	
DB	601	GATCCCGTCCCACTTCTCTGTAGCTTCAGCCAGGGCTTCCCGACACCGGGCTTG 660	

QY	661	CGCAGAGCCCCCATTCAGGCCCTGTGTGGAGCCTGTGCTCTGAGAGAGGTCCAATTG 720	
DB	661	CGCAGAGCCCCCATTCAGGCCCTGTGTGGAGCCTGTGCTCTGAGAGAGGTCCAATTG 720	
QY	721	GTGGTGGAGCCAGAGGTGAGCAGTAGTCTCTGTGGGAACCGTAACCTGACCTGTGAA 780	
DB	721	GTGGTGGAGCCAGAGGTGAGCAGTAGTCTCTGTGGGAACCGTAACCTGACCTGTGAA 780	
QY	781	GTCCCTGSCCAGCCCTCTCTCAATCCACTGTGATGAAGGATGGTGTGCCCTTGCCTT 840	
DB	781	GTCCCTGSCCAGCCCTCTCTCAATCCACTGTGATGAAGGATGGTGTGCCCTTGCCTT 840	
QY	841	CCCCCAGCCCTGTGTGTGATCTCTCCCTGAGATAGGCTCAGACACAGGAACTCAGC 900	
DB	841	CCCCCAGCCCTGTGTGTGATCTCTCCCTGAGATAGGCTCAGACACAGGAACTCAGC 900	
QY	901	TGTGTGGCCACCATTTCCAGCCACGGGCCCCCAGGAAAGCGTCTGTCTCAGCATCAGCATC 960	
DB	901	TGTGTGGCCACCATTTCCAGCCACGGGCCCCCAGGAAAGCGTCTGTCTCAGCATCAGCATC 960	
QY	961	ATCGAACCAAGGAGGAGGGGGCCAACTGTGAGGCTCTGTGGGAGATCAGGGCTGGAACT 1020	
DB	961	ATCGAACCAAGGAGGAGGGGGCCAACTGTGAGGCTCTGTGGGAGATCAGGGCTGGAACT 1020	
QY	1021	CTAGCCCTGGCCCTGGGATCTCTGGAGGCTTGGGACAGCCCTCTGTCTATTGGGGTC 1080	
DB	1021	CTAGCCCTGGCCCTGGGATCTCTGGAGGCTTGGGACAGCCCTCTGTCTATTGGGGTC 1080	
QY	1081	ATCTTGTGCAAGGGCGCAACCGCCAGGAGAGGAGAGAGCCCCAGAAACCAAGGAG 1140	
DB	1081	ATCTTGTGCAAGGGCGCAACCGCCAGGAGAGGAGAGAGCCCCAGAAACCAAGGAG 1140	
QY	1141	GAAAGAGGAGCGTGTGAGAACTGAATCAGTGGAGGAACTGAGGACGCGAGAGTAGT 1200	
DB	1141	GAAAGAGGAGCGTGTGAGAACTGAATCAGTGGAGGAACTGAGGACGCGAGAGTAGT 1200	
QY	1201	ACTGAGGCGCTTGAGGGGCCCAACAGACAGATCCCATCATCAGTCTCTTTCTTTTTC 1260	
DB	1201	ACTGAGGCGCTTGAGGGGCCCAACAGACAGATCCCATCATCAGTCTCTTTCTTTTTC 1260	
QY	1261	CCTTGAAGTGTCTGGCCCTCAGACCAACTCTCTCTGTATAATCTCTCTCTGTATAACC 1320	
DB	1261	CCTTGAAGTGTCTGGCCCTCAGACCAACTCTCTCTGTATAATCTCTCTCTGTATAACC 1320	
QY	1321	CCACCTTGGCAAGCTTTCTTCTACACCAAGAGCCCCCAATGATGATTAACACCTGA 1380	
DB	1321	CCACCTTGGCAAGCTTTCTTCTACACCAAGAGCCCCCAATGATGATTAACACCTGA 1380	
QY	1381	CACATCTTGCA 1391	
DB	1381	CACATCTTGCA 1391	

RESULT 8

AAH57444

ID AAH57444 standard; cDNA; 1582 BP.

XX

AC AAH57444;

XX

DT 10-SEP-2001 (first entry)

XX

DE Human lung cell specific cDNA sequence SEQ ID NO:284.

XX

KW Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;

KW liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;

KW metabolic disease; developmental disease; cytostatic; immunomodulatory;

KW neuroprotective; gene therapy; cancer; immunopathology; neuropathology.

OS Homo sapiens.

XX WO200132927-A2.

PN

XX 10-MAY-2001.

PD

KW amyloidosis; cancer; Crohn's disease; diabetes; Alzheimer's disease;
KW chronic inflammatory disease; osteoarthritis; irritable bowel disease;
XX multiple sclerosis; psoriasis; ss.
OS Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH CDS 1.1436
FT /*tag= a
FT /product= "RAGE"
XX
XX WO2004016229-A2.
XX
XX 26-FEB-2004.
XX
XX 18-AUG-2003; 2003WO-US025996.
XX
XX 16-AUG-2002; 2002US-0404205P.
XX
XX (AMHP) WYETH.
XX
XX Pittman DD, Clancy B, Larsen G, Trepicchio WL, Brennan FM;
PI Feldmann M, Foxwell BJM, Feldman JL;
PI
XX
XX WPI; 2004-192067/18.
XX
XX P-PSDB; ADK00129.
XX
XX New fusion protein comprising a Receptor for Advanced Glycation End
XX Product Ligand Binding Element (RAGE-LBE) and an immunoglobulin element,
XX useful for preparing a composition for treating e.g., Alzheimer's
XX disease.
XX
XX Disclosure; SEQ ID NO 44; 100pp; English.
XX
XX The present invention relates to a new fusion protein comprises a
XX Receptor for Advanced Glycation End Product Ligand Binding Element (RAGE-
XX LBE) and an immunoglobulin element. The fusion protein is useful for
XX preparing a composition for treating RAGE-associated disorder such as
XX amyloidosis, cancer, Crohn's disease, diabetes, complications of
XX diabetes, prion-related disorders, vasculitis, nephropathies,
XX retinopathies and/or neuropathies; Alzheimer's disease, chronic
XX inflammatory disease e.g., rheumatoid arthritis, osteoarthritis,
XX irritable bowel disease, multiple sclerosis, psoriasis or lupus, acute
XX inflammatory disease e.g., sepsis, or cardiovascular disease, e.g.,
XX atherosclerosis or restenosis. The present sequence represents human RAGE
XX protein encoding sequence.
XX
XX Sequence 1436 BP; 340 A; 411 C; 422 G; 263 T; 0 U; 0 Other;
XX
XX Query Match 98.7%; Score 1373; DB 12; Length 1436;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 1384; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
QY 3 GGAGCCGGAAACAGCAGTTGGAGCCCTGGGTGCTGCTCAGTCTGTGGGGGCGAGTAGT 62
DB 22 GGAGCCGGAAACAGCAGTTGGAGCCCTGGGTGCTGCTCAGTCTGTGGGGGCGAGTAGT 81
QY 63 AGGTGCTCAAAACATCACAGCCCGGATGGCGAGCCACTGGTCTGAGTGTAAAGGGGC 122
DB 82 AGGTGCTCAAAACATCACAGCCCGGATGGCGAGCCACTGGTCTGAGTGTAAAGGGGC 141
QY 123 CCCCAAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTG 182
DB 142 CCCCAAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTG 201
QY 183 GAAGGTCTCTGTCCTCCAGGAGAGGCCCTCGGACAGTGTGGCTCGTGTCTTCCCAA 242
DB 202 GAAGGTCTCTGTCCTCCAGGAGAGGCCCTCGGACAGTGTGGCTCGTGTCTTCCCAA 261
QY 243 CGGCTCCCTCTTCTTCCGCTGTCCGATCCAGGATGAGGGGATTTCCGGTGCCAGGC 302
DB 262 CGGCTCCCTCTTCTTCCGCTGTCCGATCCAGGATGAGGGGATTTCCGGTGCCAGGC 321

QY 303 AATGAACAGGAATGGAAGAGAGCAAGTCCAACTACCGAGTCCGTGTCTTACAGATTCC 362
DB 322 AATGAACAGGAATGGAAGAGAGCAAGTCCAACTACCGAGTCCGTGTCTTACAGATTCC 381
QY 363 TGGGAAGCCAGAAATTTGTAGATTCTGCCTCTGAACCTACCGGCTGGTGTCCCAATAGGT 422
DB 382 TGGGAAGCCAGAAATTTGTAGATTCTGCCTCTGAACCTACCGGCTGGTGTCCCAATAGGT 441
QY 423 GGGGACATGTGTGTCAGAGGGAAGCTACCTCGCAGGAGCTCTTTAGCTGGCACTTGGATGG 482
DB 442 GGGGACATGTGTGTCAGAGGGAAGCTACCTCGCAGGAGCTCTTTAGCTGGCACTTGGATGG 501
QY 483 GAAAGCCCTGGTGCCTTAATGAGGAAGGAGTATCTGTGAAGAAACAGACAGGACACCC 542
DB 502 GAAAGCCCTGGTGCCTTAATGAGGAAGGAGTATCTGTGAAGAAACAGACAGGACACCC 561
QY 543 TGAGACAGGGCTCTTTCACACTGCGAGTCTGAGCTTAATGTTGACCCAGCCCGGGAGGAGA 602
DB 562 TGAGACAGGGCTCTTTCACACTGCGAGTCTGAGCTTAATGTTGACCCAGCCCGGGAGGAGA 621
QY 603 TCCCGCTCCACCTTCTCTGTAGCTTTCAGCCCGAGGCTTCCCGGACACCGGGCTTGGC 662
DB 622 TCCCGCTCCACCTTCTCTGTAGCTTTCAGCCCGAGGCTTCCCGGACACCGGGCTTGGC 681
QY 663 CACAGCCCCCATCCAGCCCGCTGTCTGGAGGCTGTGCTCTCTGGAGAGGTCCAAATGGT 722
DB 682 CACAGCCCCCATCCAGCCCGCTGTCTGGAGGCTGTGCTCTCTGGAGAGGTCCAAATGGT 741
QY 723 GGTGGAGCCAGAAAGTGGAGCAGTACTCTCTGTGTAACCGTAACTGACCTGTGAGT 782
DB 742 GGTGGAGCCAGAAAGTGGAGCAGTACTCTCTGTGTAACCGTAACTGACCTGTGAGT 801
QY 783 CCTGCCCCAGCCCTCTCTCAAAATCCACTGAGTGAAGAGTGTGCTTGCCTTTCGCCCTTCC 842
DB 802 CCTGCCCCAGCCCTCTCTCAAAATCCACTGAGTGAAGAGTGTGCTTGCCTTTCGCCCTTCC 861
QY 843 CCCCAGCCCTGTGCTGATCTCTCCCTGAGATAGGGCTCTCAGGACCCAGGAACTACAGCTG 902
DB 862 CCCCAGCCCTGTGCTGATCTCTCCCTGAGATAGGGCTCTCAGGACCCAGGAACTACAGCTG 921
QY 903 TGTGGCCACCCATTCAGCCACCGGGCCCAAGAAACCGTGTCTGAGCATCAGCATCAT 962
DB 922 TGTGGCCACCCATTCAGCCACCGGGCCCAAGAAACCGTGTCTGAGCATCAGCATCAT 981
QY 963 CGAACCCAGCGAGGAGGGGCAACTCGAGCTCTGTGGAGGATCAGGGCTGGGAACTCT 1022
DB 982 CGAACCCAGCGAGGAGGGGCAACTCGAGCTCTGTGGAGGATCAGGGCTGGGAACTCT 1041
QY 1023 AGCCCTGGCCCTGGGGATCTTGGAGGCTTGGGAGCAGCGCCCTGCTCAATGGGGTTCAT 1082
DB 1042 AGCCCTGGCCCTGGGGATCTTGGAGGCTTGGGAGCAGCGCCCTGCTCAATGGGGTTCAT 1101
QY 1083 CTTTGGCAAGAGCGGCAACCGCGAGGAGAGAGAGAGGCCCCAGAAAACAGAGGGA 1142
DB 1102 CTTTGGCAAGAGCGGCAACCGCGAGGAGAGAGAGAGGCCCCAGAAAACAGAGGGA 1161
QY 1143 AGAGGAGGAGCGTGCAGAACTGAATCAGTCGGAGGAACTGAGGCGAGGAGAGTAGTAC 1202
DB 1162 AGAGGAGGAGCGTGCAGAACTGAATCAGTCGGAGGAACTGAGGCGAGGAGAGTAGTAC 1221
QY 1203 TGGAGGGCTTGGAGGGGCCACAGACAGATCCCATCCATCAGCTCCCTTTTCTTTTCCC 1262
DB 1222 TGGAGGGCTTGGAGGGGCCACAGACAGATCCCATCCATCAGCTCCCTTTTCTTTTCCC 1281
QY 1263 TTGAACCTGTGTGGCCCTCAGACCAACTCTCTCTGTATTAATCTCTCTCTGTATAACCCC 1322
DB 1282 TTGAACCTGTGTGGCCCTCAGACCAACTCTCTCTGTATAATCTCTCTCTGTATAACCCC 1341
QY 1323 ACCTTGCCCAAGCTTTCTCTACAACCCAGAGCCCCCACAATGATGATTAACACCTTGACA 1382
DB 1342 ACCTTGCCCAAGCTTTCTCTACAACCCAGAG -CCCCACAATGATGATTAACACCTTGACA 1400

QY 1383 CATCT 1387
Db 1401 CATCT 1405

RESULT 10
ABQ99598
ID ABQ99598 standard; cDNA; 1463 BP.
XX
AC ABQ99598;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human coding sequence SEQ ID 331.
XX
DE Human; expressed sequence tag; EST; chromosome 6p21.3;
KW haematopoietic disorder; central nervous system disease; viral infection;
KW peripheral nervous system disease; non-healing wound; infectious disease;
KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;
KW fungal infection; autoimmune disorder; coagulation disorder; neutropenic;
KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;
KW cytostatic; haemostatic; virucide; antibacterial; fungicide;
KW immunostimulant; cerebroprotective; gene therapy; gene, ss.
XX
OS Homo sapiens.
XX
XX WO200259260-A2.
XX
XX 01-AUG-2002.
XX
XX 16-NOV-2001; 2001WO-US042950.
XX
XX 17-NOV-2000; 2000US-00714936.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;
XX Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX WPI; 2002-590824/63.
XX N-PSDB; ABP65012.
XX
XX New isolated polynucleotide, useful in research, diagnostic or
XX therapeutic methods, e.g. preventing or treating disorders involving
XX aberrant protein expression or biological activity.
XX
XX Claim 1; SEQ ID NO 331; 394pp; English.
XX
XX The present invention relates to novel human coding sequences (ABQ99268-
XX ABQ99608) and proteins (ABP64682-ABP65022). The sequences are useful in
XX therapeutic, diagnostic and research methods. The polynucleotides may be
XX used in the field of molecular biology as hybridisation probes, primers
XX for PCR, for chromosome and gene mapping, for the recombinant production
XX of protein, or in generation of anti-sense DNA or RNA. The
XX polynucleotides are useful in diagnostics as expressed sequence tags
XX (ESTs) for identifying expressed genes or for physical mapping of the
XX human genome. The proteins may be used as molecular weight markers, or as
XX nutritional sources or supplements. The proteins may be used to maintain
XX and expand cell population in a totipotent or pluripotent state,
XX useful for re-engineering damaged or diseased tissues, transplantation,
XX manufacture of bio-pharmaceuticals or the development of bio-sensors. The
XX polynucleotides and proteins are useful for preventing, treating or
XX ameliorating disorders involving aberrant protein expression or
XX biological activity, e.g. haematopoietic disorders, central/peripheral
XX nervous system diseases, mechanical and traumatic disorders, non-healing
XX wounds, immune deficiencies and disorders, infectious diseases caused by
XX viral, bacterial or fungal infection, autoimmune disorders, allergic
XX reactions and conditions, coagulation disorders, or cancer. The
XX polynucleotide sequences of the invention were assembled from ESTs
XX isolated mainly by sequencing by hybridisation, and in some cases,
XX sequences obtained from one or more public databases. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1463 BP; 332 A; 420 C; 443 G; 268 T; 0 U; 0 Other;
Query Match 95.7%; Score 1331; DB 6; Length 1463;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1389; Conservative 0; Mismatches 0; Indels 48; Gaps 1;
QY 3 GGACGCCGGAACAGCAGATTGGAGCCCTGGTGTCTCTCAGTCTGTGGGGGCGAGTAGT 62
Db 27 GGCAGCCGGAACAGCAGATTGGAGCCCTGGTGTCTCTCAGTCTGTGGGGGCGAGTAGT 86
QY 63 AGGTGCTCAAAACATCACAGCCCGATTGGCGAGCCACTGGTGTCTCAAGTGAAGGGGCG 122
Db 87 AGGTGCTCAAAACATCACAGCCCGATTGGCGAGCCACTGGTGTCTCAAGTGAAGGGGCG 146
QY 123 CCCCAAGAAACACCCAGCCGCTGGATGGAATGGAATGGAACACAGCCGCGGACAGAGCTTG 182
Db 147 CCCCAAGAAACACCCAGCCGCTGGATGGAATGGAATGGAACACAGCCGCGGACAGAGCTTG 206
QY 183 GAAGGTCTCTCTCTCCAGGAGGAGGCCCTCGGACACAGTGTGGTCTGTCTCTTCCCAA 242
Db 207 GAAGGTCTCTCTCTCCAGGAGGAGGCCCTCGGACACAGTGTGGTCTGTCTCTTCCCAA 266
QY 243 CGGCTCCCTCTTCTCCGCTGTCTGGATCCAGATGAGGGGATTTCCGGTGCACAGC 302
Db 267 CGGCTCCCTCTTCTCCGCTGTCTGGATCCAGATGAGGGGATTTCCGGTGCACAGC 326
QY 303 AATGACAGGAATGGAAGGAGGACCAAGTCCAACTACCGAGTCCGTGTCTACCATTC 362
Db 327 AATGACAGGAATGGAAGGAGGACCAAGTCCAACTACCGAGTCCGTGTCTACCATTC 386
QY 363 TGGGAAGCCAGAAATTTAGATTCTGCCTCTCTGAACTCACGGTGTGTCTTCCCAATA 418
Db 387 TGGGAAGCCAGAAATTTAGATTCTGCCTCTCTGAACTCACGGTGTGTCTTCCCAATA 446
QY 419 -----AGTGGGACATGTGT 434
Db 447 AGTGGGAAGAAAGCAGGAGAAAGTAGAAAACGGCCCTGTGAACAGGAGGTGGGACATGT 506
QY 435 GTACAGGGAAGCTACCTTCAGGAGGACTTTAGCTGGGACTTTGGATGGGAAGCCCTGT 494
Db 507 GTACAGGGAAGCTACCTTCAGGAGGACTTTAGCTGGGACTTTGGATGGGAAGCCCTGT 566
QY 495 GCCTAATGAGAGGAGGATCTGTGAAGGAAACAGACACAGGAGACACCTTGAGACAGGGCT 554
Db 567 GCCTAATGAGAGGAGGATCTGTGAAGGAAACAGACACAGGAGACACCTTGAGACAGGGCT 626
QY 555 CTTTCACTGACGTGCGAGCTAATGTGACCCAGCCCGGGGAGGAGATCCCGTCCCAC 614
Db 627 CTTTCACTGACGTGCGAGCTAATGTGACCCAGCCCGGGGAGGAGATCCCGTCCCAC 686
QY 615 CTTTCTCTGTAGCTTTCAGCCAGGCTTCCCGGACACCGGGCTTTGGCGACAGCCCAT 674
Db 687 CTTTCTCTGTAGCTTTCAGCCAGGCTTCCCGGACACCGGGCTTTGGCGACAGCCCAT 746
QY 675 CCAGCCCGCTGTCTGGAGCCCTGTCTCTGAGGAGGCTTCAATTTGGTGGAGCAGA 734
Db 747 CCAGCCCGCTGTCTGGAGCCCTGTCTCTGAGGAGGCTTCAATTTGGTGGAGCAGA 806
QY 735 AGGTGAGCAGTAGCTCTGTGGAAACCGTAACCTGTGACCTGTGAAGTCCCTGCCAGCC 794
Db 807 AGGTGAGCAGTAGCTCTGTGGAAACCGTAACCTGTGACCTGTGAAGTCCCTGCCAGCC 866
QY 795 CTTCTCTCAATCCACTGTGATGAAGGATGTGTGCTGCTTCCCGCTTCCCGCCAGCCCTGT 854
Db 867 CTTCTCTCAATCCACTGTGATGAAGGATGTGTGCTGCTTCCCGCTTCCCGCCAGCCCTGT 926
QY 855 GCTGATCTCTCTGAGATAGGGCTTCAGGAACAGGAAACCTTACAGTGTGTGGCCACCCA 914
Db 927 GCTGATCTCTCTGAGATAGGGCTTCAGGAACAGGAAACCTTACAGTGTGTGGCCACCCA 986
QY 915 TTCCAGCCACGGGGCCCGGAAAGCCGTGTCTGTACGATCAGCATCATCGAACCGGCA 974

Qy	371	CAGAAATTGTAGATTCTTGCTCTCTGAACTCAGCGGTGTGTGTCTCCAAATAAGGTGGGGACAT	430
Db	505	CAGAAAATTGTAGATTCTTGCTCTCTGAACTCAGCGGTGTGTGTCTCCAAATAAGGTGGGGACAT	564
Qy	431	GTGTGTCTCAGAGGGAAGCTTACCTTCGACGGACTCTTAGCTGCGACTTTCGGATGGGAAGCCCC	490
Db	565	GTGTGTCTCAGAGGGAAGCTTACCTTCGACGGACTCTTAGCTGCGACTTTCGGATGGGAAGCCCC	624
Qy	491	TGTTGCCCTTAATGAGAAAGGGAGTATCTCTGTAAGGAACACAGACAGGAGACACCCCTTGACAG	550
Db	625	TGTTGCCCTTAATGAGAAAGGGAGTATCTCTGTAAGGAACACAGACAGGAGACACCCCTTGACAG	684
Qy	551	GGCTCTTTCACACTGCTCAGTCGGAGTAAATGTTGACCCCGACCGCGGGAGGAGATCCCGCTC	610
Db	685	GGCTCTTTCACACTGCTCAGTCGGAGTAAATGTTGACCCCGACCGCGGGAGGAGATCCCGCTC	744
Qy	611	CCACCTTCTCTCTGTAGCTTTCAGCCCGACGGCTTCCCGACACCGGGCCCTTGGCGACAGCCCC	670
Db	745	CCACCTTCTCTCTGTAGCTTTCAGCCCGACGGCTTCCCGACACCGGGCCCTTGGCGACAGCCCC	804
Qy	671	CCATCCAGCCCCGTTGTTCTGG-----GAGCCTGTGCTCTGGAAGGAGTCCCAATTG	720
Db	805	CCATCCAGCCCCGTTGTTCTGGGGTGTAGCATAGAGCCTGTGCTCTGGAAGGAGTCCCAATTG	864
Qy	721	GTGTGTGAGCCAGAAAGTGTGAGCAGTAGTCTCTGGTGGAAACCGTTAACCCCTGACTGTGAA	780
Db	865	GTGTGTGAGCCAGAAAGTGTGAGCAGTAGTCTCTGGTGGAAACCGTTAACCCCTGACTGTGAA	924
Qy	781	GTCCCTGCCACGCCCTCTCTCTCAAAATCCACTGGATGAAGATGTTGTCCTTGGCCCCCTT	840
Db	925	GTCCCTGCCACGCCCTCTCTCTCAAAATCCACTGGATGAAGATGTTGTCCTTGGCCCCCTT	984
Qy	841	CCCCCGAGCCCTGTGCTGATCCTCCCTGAGATAGGGCCTCAGGACACAGGGAACCTACAGC	900
Db	985	CCCCCGAGCCCTGTGCTGATCCTCCCTGAGATAGGGCCTCAGGACACAGGGAACCTACAGC	1044
Qy	901	TGTTGTGCCCAACCAATTCAGCCACGGGCCCCAGAGAAAGCCGTGTGTCAGCATCAGCATC	960
Db	1045	TGTTGTGCCCAACCAATTCAGCCACGGGCCCCAGAGAAAGCCGTGTGTCAGCATCAGCATC	1104
Qy	961	ATCGAAACAGCGGAGAGAGGGGCCAACTGCGAGGCTCTGTGGAGGATCAGGGCTGGGAACCT	1020
Db	1105	ATCGAAACAGCGGAGAGAGGGGCCAACTGCGAGGCTCTGTGGAGGATCAGGGCTGGGAACCT	1164
Qy	1021	CTAGCCCTGGCCCTTGGGGATCCTTGGGAGGCTGGGGACAGCCGCCCTGCTCATTTGGGGTC	1080
Db	1165	CTAGCCCTGGCCCTTGGGGATCCTTGGGAGGCTTGGGGACAGCCGCCCTGCTCATTTGGGGTC	1224
Qy	1081	ATCTTGTGGCAAGCGCGCAACCGCGGAGGAGAGAGGAAGGCCCCAGAAAAACCGAGG	1140
Db	1225	ATCTTGTGGCAAGCGCGCAACCGCGGAGGAGAGAGGAAGGCCCCAGAAAAACCGAGG	1284
Qy	1141	GAAGAGAGGAGCGTGCAGAACTCAATCAGTTCGAGGAACTCTGAGGCAGCGGAGAGTAGT	1200
Db	1285	GAAGAGAGGAGCGTGCAGAACTCAATCAGTTCGAGGAACTCTGAGGCAGCGGAGAGTAGT	1344
Qy	1201	ACTGGAGGGCCTTGAAGGGGCCACAGACAGATCCCATCAGCTCCCTTTTCTTTTTC	1260
Db	1345	ACTGGAGGGCCTTGAAGGGGCCACAGACAGATCCCATCAGCTCCCTTTTCTTTTTC	1404
Qy	1261	CTTTGAATGTTCTTGGCCTCAGACCAACTCTCTCTGTATAATCTCTCTCTGTATAACC	1320
Db	1405	CTTTGAATGTTCTTGGCCTCAGACCAACTCTCTCTGTATAATCTCTCTCTGTATAACC	1464
Qy	1321	CCACCTTGGCAAGCTTCTTCTCTAAACAGAGCCCCCACAATGATGATTAACACCTCTGA	1380
Db	1465	CCACCTTGGCAAGCTTCTTCTCTAAACAGAGCCCCCACAATGATGATTAACACCTCTGA	1524
Qy	1381	CACATCTTGCA	1391
Db	1525	CACATCTCGGA	1535

RESULT 12	
ACC59907	
ID	ACC59907 standard; cDNA; 1678 BP.
XX	
XX	ACC59907;
XX	
XX	07-JUL-2003 (first entry)
DT	
XX	
XX	Human REMAP-20 encoding cDNA SEQ ID NO:56.
XX	
XX	Human; receptor and membrane-associated protein; REMAP; cytosolic;
KW	antiarteriosclerotic; anticonvulsant; neurotropic; neuroprotective;
KW	cerebroprotective; anti-HIV; anti-allergic; anti-inflammatory; cancer;
KW	thyromimetic; gene therapy; cell proliferative disorder; atherosclerosis;
KW	neurological disorder; epilepsy; Huntington's disease; stroke; AIDS;
KW	immune disorder; inflammatory disorder; allergy; developmental disorder;
KW	hypothyroidism; Cushing's syndrome; infection; gene; ss.
XX	
OS	Homo sapiens.
XX	
XX	
Key	Location/Qualifiers
FF	108..1373
FT	/tag= a
FT	/product= "REMAP-20"
FT	
XX	
XX	WO2003025130-A2.
XX	
XX	
XX	27-MAR-2003.
XX	
XX	12-SEP-2002; 2002WO-US029220.
XX	
XX	14-SEP-2001; 2001US-0322157P.
XX	
XX	28-SEP-2001; 2001US-0326029P.
PR	
PR	05-OCT-2001; 2001US-0327380P.
PR	
PR	12-OCT-2001; 2001US-0329198P.
PR	
PR	19-OCT-2001; 2001US-0343742P.
PR	
PR	02-NOV-2001; 2001US-0343906P.
PR	
PR	02-NOV-2001; 2001US-0343980P.
PR	
PR	16-NOV-2001; 2001US-0332426P.
PR	
PR	13-MAR-2002; 2002US-0364338P.
PR	
PR	15-MAR-2002; 2002US-0364494P.
PR	
PR	29-MAR-2002; 2002US-0369248P.
XX	
XX	(INCY-) INCYTE GENOMICS INC.
PA	
XX	
XX	Warren BA, Gietzen KJ, Lal PG, Xu Y, Tran UK, Lee S;
PI	Borowsky ML, Becha SD, Sanjanwala MM, Thangavelu K, Tang YT;
PI	Honchell CD, Yue H, Elliott VS, Richardson TW, Azimzai Y, Chawla NK;
PI	Baughn WR, Lu DAM, Nguyen DB, Kalafus DP, Saperstein SK;
PI	Ramkumar J, Lehr-Mason PM, Griffin JA, Duggan BM, Lee SY;
PI	Zebarradian Y, Hafalia AJA, Gururajan R, Swarnakar A, Lee EA;
PI	Marquis JP, Khare R, Emerling BM, Jlang X, Jackson AA;
XX	
XX	WPI; 2003-354596/33.
DR	
DR	P-PSDB; ABR43188.
XX	
XX	New human receptors and membrane-associated proteins (REMAP), useful for
PT	diagnosing, treating and preventing diseases or conditions associated
PT	with the aberrant REMAP expression e.g. cancer, AIDS, atherosclerosis,
PT	infections.
PT	
XX	
XX	
PS	Claim 5; Page 230-231; 241pp; English.
XX	
CC	ACC5988 to ACC59923 encode the human receptor and membrane-associated
CC	proteins given in ABR43169 to ABR43204 and designated REMAP-1 to REMAP-36
CC	(1). (I) have cytosolic, antiarteriosclerotic, anticonvulsant,
CC	neurotropic, neuroprotective, cerebroprotective, anti-HIV, anti-allergic,
CC	anti-inflammatory and thyromimetic activities, and can be used in gene
CC	therapy. The REMAP polypeptides and polynucleotides are useful in
CC	diagnosing, treating and preventing diseases or conditions associated
CC	with the decreased expression or overexpression of REMAP, such as cell
CC	proliferative (e.g. cancer, atherosclerosis), neurological (e.g.

CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS, CC allergies) and developmental (e.g. hypothyroidism, Cushing's syndrome) CC disorders, or infections. They are also useful in assessing the effects CC of exogenous compounds on the expression of nucleic acid and amino acid CC sequences of REMAP. The REMAPs or their fragments are useful in screening CC compounds for effectiveness as agonist or antagonist of the polypeptides, CC or in altering the expression of the target polynucleotide and compounds CC that specifically bind to or modulate the activity of the polypeptide XX
SQ Sequence 1678 BP; 471 A; 438 C; 480 G; 289 T; 0 U; 0 Other;
Query Match 93.08; Score 1293.4; DB 9; Length 1678;
Best Local Similarity 96.99; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 1; Indels 42; Gaps 1;
QY 3 GGCAAGCCGGAACAGCAGTCTGGAGCCTGGGCTGCTCCTCAGTCTCTGGGGGGCAGTAGT 62
DB 203 GGCAGCCGGAACAGCAGTCTGGAGCCTGGGCTGCTCCTCAGTCTCTGGGGGGCAGTAGT 262
QY 63 AGTGCTCAAAAATACACAGCCGGATTTGGCGAGCCACTGGTCTGTAAGTGTAAAGGGGC 122
DB 263 AGTGCTCAAAAATACACAGCCGGATTTGGCGAGCCACTGGTCTGTAAGTGTAAAGGGGC 322
QY 123 CCCAAGAACACCCAGCGCTGGATGTAAGTGAACCTGAAACACAGGCGGACAGAGCTTG 182
DB 323 CCCAAGAACACCCAGCGCTGGATGTAAGTGAACCTGAAATGGAACCT----- 358
QY 183 GAAGTGCTGTCTCTCCAGGAGGAGGCGCCCTGGGACAGTGTGGCTGTCTCTCCCAA 242
DB 359 -----GGAGAGGCGCCCTGGGACAGTGTGGCTGTCTCTCCCAA 400
QY 243 CGGCTCCCTCTCTCTCCGCTGTGGGATCCAGGATGAGGGGATTTCCGGTGCACAGGC 302
DB 401 CGGCTCCCTCTCTCTCCGCTGTGGGATCCAGGATGAGGGGATTTCCGGTGCACAGGC 460
QY 303 AATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTC 362
DB 461 AATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTC 520
QY 363 TGGGAAGCCAGAAATGTAGATTTCTGCTCTGAACTCAGGCTGGTGTTCCTCAATAAGGT 422
DB 521 TGGGAAGCCAGAAATGTAGATTTCTGCTCTGAACTCAGGCTGGTGTTCCTCAATAAGGT 580
QY 423 GGGGACATGTGTCTAGAGAGGAAGTACCTCTGAGGAGCTCTTGTAGCTGGCAGCTTGGATGG 482
DB 581 GGGGACATGTGTCTAGAGAGGAAGTACCTCTGAGGAGCTCTTGTAGCTGGCAGCTTGGATGG 640
QY 483 GAAGCCCTGGTGCCTTAATGAGAAGGGAGTATCTGTGAAGGAACAGACAGGAGACACCC 542
DB 641 GAAGCCCTGGTGCCTTAATGAGAAGGGAGTATCTGTGAAGGAACAGACAGGAGACACCC 700
QY 543 TGAGACAGGGCTCTTCACTCAGCTCGGAGCTAATGGTGACCCAGCCCGGGGAGGAGA 602
DB 701 TGAGACAGGGCTCTTCACTCAGCTCGGAGCTAATGGTGACCCAGCCCGGGGAGGAGA 760
QY 603 TCCCGCTCCACCTCTCTCTGTAGCTTACGCCAGGCGCTTCCCGGACACCGGCGCTTTGG 662
DB 761 TCCCGCTCCACCTCTCTCTGTAGCTTACGCCAGGCGCTTCCCGGACACCGGCGCTTTGG 820
QY 663 CAGAGCCCTCATCAGCCCGCTGTCTGGAGAGCTGTGCTCTGTGGAGAGGTCCAATTGGT 722
DB 821 CAGAGCCCTCATCAGCCCGCTGTCTGGAGAGCTGTGCTCTGTGGAGAGGTCCAATTGGT 880
QY 723 GGTGGAGCCAGAGGTGGAGCAGTGTCTCTGTGGAGCGGTAAACCGTGAACCTGACCTGCAAGT 782
DB 881 GGTGGAGCCAGAGGTGGAGCAGTGTCTCTGTGGAGCGGTAAACCGTGAACCTGACCTGCAAGT 940
QY 783 CCTGCGCCAGCCCTCTCTCAAAATCAACTGGATGAGAGTGTGTGCTTGGCCCTTGCCTTCC 842
DB 941 CCTGCGCCAGCCCTCTCTCAAAATCAACTGGATGAGAGTGTGTGCTTGGCCCTTGCCTTCC 1000
QY 843 CCCAGCCCTGTCTGATCTCTCTCTGAGATAGGGCTTCAGGACCAAGGAACTTACAGTGG 902
|||||

DB 1001 CCCAGCCCTGTGCTGATCTCTCTGAGATAGGGCTCTAGGACCAAGGAACTTACAGTGG 1060
QY 903 TGTGGCCACCCATTTCCAGCCAGCGGGCCCGAGGAAAGCCGTGTGTCTGAGCATCAGCATCAT 962
DB 1061 TGTGGCCACCCATTTCCAGCCAGCGGGCCCGAGGAAAGCCGTGTGTCTGAGCATCAGCATCAT 1120
QY 963 CGAACAGGCGAGGAGGGGCGCAACTGCAAGCTCTGTGGAGGATCAGGGCTGGGAACTCT 1022
DB 1121 CGAACAGGCGAGGAGGGGCGCAACTGCAAGCTCTGTGGAGGATCAGGGCTGGGAACTCT 1180
QY 1023 AGCCCTGGCCCTGGGGATCTCTGGGAGCCTTGGGAGCAGCGCCCTGCTCATTTGGGGTCTAT 1082
DB 1181 AGCCCTGGCCCTGGGGATCTCTGGGAGCCTTGGGAGCAGCGCCCTGCTCATTTGGGGTCTAT 1240
QY 1083 CTTTGTGCGCAAGGCGGCAACGCCGAGGAGAGGAGAGGCGCCCGAGAAACCCAGGAGGA 1142
DB 1241 CTTTGTGCGCAAGGCGGCAACGCCGAGGAGAGGAGAGGCGCCCGAGAAACCCAGGAGGA 1300
QY 1143 AGAGGAGGAGCGTGCAGAACTGAACTCAGTTCGAGGAGAACTTGAAGGCGAGGAGTAGTAC 1202
DB 1301 AGAGGAGGAGCGTGCAGAACTGAACTCAGTTCGAGGAGAACTTGAAGGCGAGGAGTAGTAC 1360
QY 1203 TGGAGGCGCTTGGGGGCGCCACAGACAGATCCCATCATCAGCTCCCTTTCTTTTTCCTCC 1262
DB 1361 TGGAGGCGCTTGGGGGCGCCACAGACAGATCCCATCATCAGCTCCCTTTCTTTTTCCTCC 1420
QY 1263 TTGAACCTGTTGGGCTCAGACCAACTCTCTCTGTATAATCTCTCTCTCTCTCTCTCTCTCT 1322
DB 1421 TTGAACCTGTTGGGCTCAGACCAACTCTCTCTGTATAATCTCTCTCTCTCTCTCTCTCTCT 1480
QY 1323 ACCTTGCCTAAGCTTTCTTCTAACCAGAGCGCCCGCCCAATGATGATTAACAACCTTGACA 1382
DB 1481 ACCTTGCCTAAGCTTTCTTCTAACCAGAGCGCCCGCCCAATGATGATTAACAACCTTGACA 1540
QY 1383 CATCTTGA 1391
DB 1541 CATCTTGA 1549
RESULT 13
ADP19665
ID ADP19665 standard; cDNA; 1329 BP.
XX
AC ADP19665;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human LP2005 encoding cDNA SEQ ID NO:11.
XX
KW human; LP2005; antidiabetic; neuroprotective; nootropic;
KW antiinflammatory; antirheumatic; antiarthritic; vulnery; cytostatic;
KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;
KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;
KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;
KW systemic lupus erythematosus; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 46..1206
FT /tag= b
FT /product= "LP2005"
FT /note= "the present sequence only seems to encodes amino
FT acids 1 to 386 of the LP2005 protein"
FT sig_peptide 46..114
FT /tag= a
FT mat_peptide 115..1203
FT /tag= c
XX
PN WO2004044126-A2.
XX
PD 27-MAY-2004.
XX

QY 1263 TTGAACGTGTTCTGGCCTCAGACCA 1286
 Db 1304 TTGAACGTGTTCTGGCCTCAGACCR 1327

RESULT 14
 ADP19667
 ID ADP19667 standard; cDNA; 1323 BP.
 AC ADP19667;
 DT 12-AUG-2004 (first entry)
 XX Human LP2006 encoding cDNA SEQ ID NO:13.
 XX human; LP2006; antidiabetic; neuroprotective; nootropic;
 KW antiinflammatory; antirheumatic; antiarthritic; vulnery; cytosstatic;
 KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;
 KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;
 KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;
 KW systemic lupus erythematosus; gene; ss.
 XX Homo sapiens.

OS
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 46..414
 FT /*tag= b
 FT /product= "LP2006"
 FT /note= "the present sequence only seems to encodes amino
 FT acids 1 to 122 of the LP2006 protein"
 FT sig_peptide 46..414
 FT /*tag= a
 FT mat_peptide 115..411
 FT /*tag= c
 FT WO2004044126-A2.
 PN
 XX
 XX
 PD 27-MAY-2004.
 XX
 XX
 PF 05-NOV-2003; 2003WO-US032734.
 XX
 XX
 PR 14-NOV-2002; 2002US-0426253P.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Na S, Perkins DR;
 XX
 XX WPI; 2004-411705/38.
 DR P-PSDB; ADP19668.
 XX
 XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or
 PT LP2003) for diagnosing or treating disorders associated with aberrant
 PT levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome
 PT identification.
 XX
 PS Claim 1; SEQ ID NO 13; 111pp; English.

XX The present sequence encodes human LP2006, which is used in the
 CC exemplification of the present invention. The present invention
 CC describes: (1) an isolated nucleic acid (1) comprising DNA having at
 CC least 95% sequence identity to a polynucleotide selected from the group
 CC consisting of: (a) a polynucleotide having a nucleotide sequence as shown
 CC in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a
 CC polypeptide or mature form of a polypeptide having the amino acid
 CC sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide
 CC fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide
 CC having a nucleotide sequence which is complementary to the nucleotide
 CC sequence of a polynucleotide as in (a), (b) or (c); (2) a vector
 CC comprising (1); (3) a host cell comprising the vector; (4) producing an
 CC LP polypeptide; (5) an isolated polypeptide produced by the above method
 CC and comprising an amino acid sequence comprising about 95% sequence
 CC identity to a sequence of amino acid residues comprising LP2001, LP2003,
 CC LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric

CC molecule comprising an LP polypeptide fused to a heterologous amino acid
 CC sequence; (7) an antibody which specifically binds to an LP polypeptide
 CC described above; (8) a composition (C) comprising a therapeutic amount of
 CC an active agent selected from an LP polypeptide, an agonist to an LP
 CC polypeptide, an antagonist to an LP polypeptide, an LP polypeptide
 CC antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a
 CC polynucleotide in combination with a pharmaceutical carrier; and (9)
 CC diagnosing or treating a mammal suffering from a disease, condition or
 CC disorder associated with aberrant levels of an LP-polypeptide. (C) has
 CC antidiabetic, neuroprotective, nootropic, antiinflammatory,
 CC antirheumatic, antiarthritic, vulnery, cytosstatic, immunosuppressive,
 CC nephrotropic and dermatological activities, and can be used in gene
 CC therapy. The compositions (C) and methods are useful for diagnosing or
 CC treating disorders associated with aberrant levels of an LP polypeptide,
 CC such as diabetes and its complications, Alzheimer's disease,
 CC inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple
 CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They
 CC may also be used for chromosome identification. The LP polypeptide can
 CC also be used in manufacturing a medicament for the treatment of the above
 CC -mentioned diseases, conditions or disorders associated with aberrant
 CC levels of the LP polypeptide.
 XX
 SQ Sequence 1323 BP; 292 A; 375 C; 423 G; 231 T; 0 U; 2 Other;

Query Match 89.9%; Score 1250; DB 12; Length 1323;
 Best Local Similarity 99.0%; Pred. No.:0;
 Matches 1273; Conservative 0; Mismatches 0; Indels 13; Gaps 1;
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 Db 48 GG CAG CCG GAA CAG CAG TGG AG CCG TGG TGG TCT C CAG TCT GTG GGG GCG CAG TAG T 107
 QY 63 AG GTG CT CAAA A C A T C A C A G C C C G G A T T G G C G A G C C A C T G T G T G A A G T G T A A G G G G C 122
 Db 108 AG GTG CT CAAA A C A T C A C A G C C C G G A T T G G C G A G C C A C T G T G A A G T G T A A G G G G C 167
 QY 123 C C C C A A G A A A C C A C C C C A G C G G C T G G A A T G G A A C T G A A C A C A G G C C G G A C A G A G C T T G 182
 Db 168 C C C C A A G A A A C C A C C C C A G C G G C T G G A A T G G A A C T G A A C A C A G G C C G G A C A G A G C T T G 227
 QY 183 G A A G T C C T G T C T C C C C A G G A G G G C C C C T G G G A C A G T G T G G C T G T C T C T C C A A 242
 Db 228 G A A G T C C T G T C T C C C C A G G A G G G C C C C T G G G A C A G T G T G G C T G T C T C T C C A A 287
 QY 243 C G G C T C C C T C T T C C T T C C G G C T G T C G G G A T C C A G A T G A G G G A T T T C G G T G C C A G G C 302
 Db 288 C G G C T C C C T C T T C C T T C C G G C T G T C G G A T C C A G A T G A G G G A T T T C C G G T G C C A G G C 347
 QY 303 A T G A A C A G A A T G G A A G A G A C C A A G T C C A A C T A C C A G T C C G T G T C T A C C A G A T T C C 362
 Db 348 A A T G A A C A G A A T G G A A G A G A C C A A G T C C A A C T A C C G A - - - - - A G A T T C C 394
 QY 363 T G G G A G C C A G A A A T T G T A G A T T C T G C C T C T G A A C T C A C G G C T G T G T T C C C A A T A A G T 422
 Db 395 T G G G A G C C A G A A A T T G T A G A T T C T G C C T C T G A A C T C A C G G C T G T G T T C C C A A T A A G T 454
 QY 423 G G G G A C A T G T G T C A G A G G A A G C T A C C C T G C A G G G A C T C T T A G C T G G C A C T T G G A T G G 482
 Db 455 G G G G A C A T G T G T C A G A G G A A G C T A C C C T G C A G G G A C T C T T A G C T G G C A C T T G G A T G G 514
 QY 483 G A A G C C C T G G T G C C T A A T A G A A G G A G A T A T C T G T A A G G A A C A C A C A G A C A G A C A C C 542
 Db 515 G A A G C C C T G G T G C C T A A T A G A A G G A G A T A T C T G T A A G G A A C A C A C A G A C A G A C A C C 574
 QY 543 T G A G A C A G G G C T T T C A C A C T C A G C C G A G C T A A T G T G A C C C A G C C G G G G A G A 602
 Db 575 T G A G A C A G G G C T T T C A C A C T C A G C C G A G C T A A T G T G A C C C A G C C G G G G A G A 634
 QY 603 T C C C C T C C C A C C T C T C C T G T A G C T T C A G C C C A G G C C T T C C C C A C A C A C G G G C C T T G C G 662
 Db 635 T C C C C T C C C A C C T C T C C T G T A G C T T C A G C C C A G G C C T T C C C C A C A C A C G G G C C T T G C G 694
 QY 663 C A C A G C C C C A T C C A G C C C C G T G T C T G G A G A G C C T G T G C C T C T G G A G A G G T C C A A T T G T 722

Qy	603	TCCCGCTCCACCTTCTCTGTAGCTTACGCCAGGCTTCCCGACACCGGCTTGG	662
Db	627	TCCCGCTCCACCTTCTCTGTAGCTTACGCCAGGCTTCCCGACACCGGCTTGG	686
Qy	663	CACAGCCCCCATCAGCCCCGTCTGGGAGCCTGTGCCCTCTGGAGGAGGTCCAAATTGGT	722
Db	687	CACAGCCCCCATCAGCCCCGTCTGGGAGCCTGTGCCCTCTGGAGGAGGTCCAAATTGGT	746
Qy	723	GGTGGAGCCAGAGGTTGGAGCAGTAGCTCTGTGTGAAACCGTAAACCTGTGAAAGT	782
Db	747	GGTGGAGCCAGAGGTTGGAGCAGTAGCTCTGTGTGAAACCGTAAACCTGTGAAAGT	806
Qy	783	CCCTGCCAGCCCTCTCTCAATCACTGGATGAAGATGGTGGCCCTTGGCCCTTCC	842
Db	807	CCCTGCCAGCCCTCTCTCAATCACTGGATGAAGATGGTGGCCCTTGGCCCTTCC	866
Qy	843	CCCAGCCCTGTGTGATCTCCTCCTGAGATAGGCTCTCAGGACAGGGAACCTACAGCTG	902
Db	867	CCCAGCCCTGTGTGATCTCCTCCTGAGATAGGCTCTCAGGACAGGGAACCTACAGCTG	926
Qy	903	TGTGGCCACCCATTCCAGCCACCGGGCCCCAGGAAAGCGTGTGTGAGCATCAGCATCAT	962
Db	927	TGTGGCCACCCATTCCAGCCACCGGGCCCCAGGAAAGCGTGTGTGAGCATCAGCATCAT	986
Qy	963	CGAACAGGCGAGGAGGCGCAACTGGAGGCTCTGTGGAGGATCAGGCTGGGAACTCT	1022
Db	987	CGAACAGGCGAGGAGGCGCAACTGGAGGCTCTGTGGAGGATCAGGCTGGGAACTCT	1046
Qy	1023	AGCCCTGGCCCTGGGATCTCTGGAGGCTTGGGACAGCCGCTGTCTCATTTGGGTCTAT	1082
Db	1047	AGCCCTGGCCCTGGGATCTCTGGAGGCTTGGGACAGCCGCTGTCTCATTTGGGTCTAT	1106
Qy	1083	CTTGTGGCAAGCGCGCAACCGCGAGGAGAGGAGAGGCGCCCAAGAAACCAAGGAGGA	1142
Db	1107	CTTGTGGCAAGCGCGCAACCGCGAGGAGAGGAGAGGCGCCCAAGAAACCAAGGAGGA	1166
Qy	1143	AGAGGAGGAGCTGCAGAACTGAATCAGTCCGAGGAACCTGAGGCGAGGAGAGTAGTAC	1202
Db	1167	AGAGGAGGAGCTGCAGAACTGAATCAGTCCGAGGAACCTGAGGCGAGGAGAGTAGTAC	1226
Qy	1203	TGGAGGCGCTTGGAGGGCCCCACAGACAGATCCCATCCATCAG	1244
Db	1227	TGGAGGCGCTTGGAGGGCCCCACAGACAGATCCCATCCATCAG	1268

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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1387.8	99.8	1391	4	US-09-638-648-4
3	1348.2	96.9	1405	4	US-08-755-235-3
4	1213	87.2	1215	4	US-09-949-016-5154
5	1018	73.2	1023	2	US-08-633-148-1
6	950.8	68.4	957	2	US-08-633-148-3
7	944.8	67.9	1426	4	US-09-638-649-2
8	944.8	67.9	1426	4	US-09-638-648-2
9	901.4	64.8	1438	4	US-08-755-235-1
10	826.4	59.4	1347	4	US-09-638-648-6
11	826.4	59.4	1348	4	US-09-638-649-6
12	281.4	20.2	5816	4	US-09-949-016-16900
13	281.4	20.2	7080	4	US-09-949-016-16896
14	108.6	7.8	601	4	US-09-949-016-178939
15	93	6.7	601	4	US-09-949-016-178940
16	72.6	5.2	601	4	US-09-949-016-178938
17	55.4	4.0	7218	1	US-08-232-463-14
18	42.6	3.1	1614	4	US-09-616-289-45
19	41.4	3.0	247781	4	US-09-949-016-14193
20	41	2.9	169998	3	US-09-676-6108-24
21	41	2.9	197496	4	US-09-877-177A-10
22	40	2.9	601	4	US-09-949-016-178941
23	39.8	2.9	485	5	PT-US95-05741-10
24	39.6	2.8	561	4	US-09-702-705-72
25	39.6	2.8	561	4	US-09-736-457-72
26	39.6	2.8	561	4	US-09-614-124B-72
27	39.6	2.8	561	4	US-09-671-325-72

28	39.6	2.8	561	4	US-09-589-184-72	Sequence 72, Appl
29	39.6	2.8	561	4	US-09-658-824-72	Sequence 72, Appl
30	39.6	2.8	2539	2	US-08-432-016-1	Sequence 1, Appl
31	39.6	2.8	2539	2	US-08-684-594-1	Sequence 1, Appl
32	39.6	2.8	2539	4	US-09-023-655-1496	Sequence 1496, Ap
33	39.6	2.8	2539	4	US-09-949-016-3677	Sequence 3677, Ap
34	39.6	2.8	4235	4	US-09-702-705-317	Sequence 317, App
35	39.6	2.8	4235	4	US-09-736-457-317	Sequence 317, App
36	39.6	2.8	4235	4	US-09-614-124B-317	Sequence 317, App
37	39.6	2.8	4235	4	US-09-671-325-317	Sequence 317, App
38	39.6	2.8	4235	4	US-09-589-184-317	Sequence 317, App
39	39.6	2.8	4235	4	US-09-658-824-317	Sequence 317, App
40	39.6	2.8	23796	4	US-09-949-016-17581	Sequence 17581, A
41	39.2	2.8	6108	4	US-09-949-016-12213	Sequence 12213, A
42	38.4	2.8	22218	4	US-09-949-016-14240	Sequence 14240, A
43	38	2.7	1416	4	US-09-902-540-4687	Sequence 4687, Ap
44	38	2.7	3991	3	US-08-506-296B-3	Sequence 3, Appl
45	38	2.7	28558	4	US-09-902-540-1231	Sequence 1231, Ap

ALIGNMENTS

RESULT 1
US-09-638-649-4
; Sequence 4, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1391
; TYPE: DNA
; ORGANISM: Human
US-09-638-649-4

Query Match	99.8%;	Score 1387.8;	DB 4;	Length 1391;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1389;	Conservative	0;	Mismatches 2;	Indels 0;
Gaps 0;				
QY	1	GGGGCAGCGGAAACAGCAGTGGAGCTGGGTCTGGTCTCTCAGTCTGTGGGGGCGAGTA	60	
DB	1	GGGGCAGCGGAAACAGCAGTGGAGCTGGGTCTGGTCTCTCAGTCTGTGGGGGCGAGTA	60	
QY	61	GTAGTGTCTCAAAACATCAGCCCGGATGGGAGCCACTGGTCTGAAGTCTAAGGG	120	
DB	61	GTAGTGTCTCAAAACATCAGCCCGGATGGGAGCCACTGGTCTGAAGTCTAAGGG	120	
QY	121	GGCCCCAAGAAACACCCAGCGGCTGGAACTGAACACAGCCGCGACAGAGCT	180	
DB	121	GGCCCCAAGAAACACCCAGCGGCTGGAACTGAACACAGCCGCGACAGAGCT	180	
QY	181	TGGAAGTCTCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGTCTGTCTTCCC	240	
DB	181	TGGAAGTCTCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGTCTGTCTTCCC	240	
QY	241	AACGGTCTCTCTCTTCTCCCGGTGTCGGATTCAGGATGAGGGGATTTTCCGGTCCAG	300	
DB	241	AACGGTCTCTCTCTTCTCCCGGTGTCGGATTCAGGATGAGGGGATTTTCCGGTCCAG	300	
QY	301	GCAATCAACAGGAATGGAAGGAGCAAGTCCAACTACCGAGTCCGTCTGTCTACCAAGATT	360	
DB	301	GCAATCAACAGGAATGGAAGGAGCAAGTCCAACTACCGAGTCCGTCTGTCTACCAAGATT	360	

QY 721 GTGGTGGAGCCAGAGGTGGAGCAGTAGCTCTCTGGTGGAAACCTGAACCTGTGA 780
DB 721 GTGGTGGAGCCAGAGGTGGAGCAGTAGCTCTCTGGTGGAAACCTGAACCTGTGA 780
QY 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGGATGAAGATGGTGGCCCTT 840
DB 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGGATGAAGATGGTGGCCCTT 840
QY 841 CCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGGCTCAGAACAGGAACTACAGC 900
DB 841 CCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGGCTCAGAACAGGAACTACAGC 900
QY 901 TGTGTGGCCACCCATTCAGCCACGGGCCCCAGGAAAGCGTGTCTGAGCATCAGCATC 960
DB 901 TGTGTGGCCACCCATTCAGCCACGGGCCCCAGGAAAGCGTGTCTGAGCATCAGCATC 960
QY 961 ATCGAACAGGCGAGGAGGGGCCAACTGACGGCTCTGTGGAGGATCAGGGCTGGAACT 1020
DB 961 ATCGAACAGGCGAGGAGGGGCCAACTGACGGCTCTGTGGAGGATCAGGGCTGGAACT 1020
QY 1021 CTAGCCCTGGCCCTGGGATCTCTGGAGGCTTGGGACAGCCCTCTGCTCATTTGGGTC 1080
DB 1021 CTAGCCCTGGCCCTGGGATCTCTGGAGGCTTGGGACAGCCCTCTGCTCATTTGGGTC 1080
QY 1081 ATCTTGTGCCAAAGCGGCAACGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
DB 1081 ATCTTGTGCCAAAGCGGCAACGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY 1141 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1200
DB 1141 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1200
QY 1201 ACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1260
DB 1201 ACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1260
QY 1261 CTTGAACTGTCTGGCCCTCAGACCAACTCTCTCTGTATATCTCTCTCTGTATAACC 1320
DB 1261 CTTGAACTGTCTGGCCCTCAGACCAACTCTCTCTGTATATCTCTCTCTGTATAACC 1320
QY 1321 CCACCTTGGCAGCTTCTTCTACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1380
DB 1321 CCACCTTGGCAGCTTCTTCTACACAGGAGGAGGAGGAGGAGGAGGAGGAGT 1380
QY 1381 CACATCTTGA 1391
DB 1381 CACATCTTGA 1391

RESULT 3

US-08-755-235-3
; Sequence 3, Application US/08755235
; Patent No. 6790443
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755, 235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1405
; TYPE: DNA
; ORGANISM: Human
US-08-755-235-3

Query Match 96.9%; Score 1348.2; DB 4; Length 1405;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1383; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 1 GGGGCAGCCGGAACACAGACTTGGAGCCTGGGTGCTGGTCTCTCAGTCTGTGGGGGAGTA 60
DB 1 GGGGCAGCCGGAACACAGACTTGGAGCCTGGGTGCTGGTCTCTCAGTCTGTGGGGGAGTA 60
QY 61 GTAGTGTCTCAAAACATCAACAGCCCGGATTTGGGAGCCACTGGTGTGAAGTGTAAAGGG 120
DB 61 GTAGTGTCTCAAAACATCAACAGCCCGGATTTGGGAGCCACTGGTGTGAAGTGTAAAGGG 120
QY 121 GCCCCCAAGAACACACCCAGCGGCTGGAAATGGAACACTGAAACACAGCCGCGACAGAAGCT 180
DB 121 GCCCCCAAGAACACACCCAGCGGCTGGAAATGGAACACTGAAACACAGCCGCGACAGAAGCT 180
QY 181 TGGAAAGTCTGTCTCTCCCAAGGAGAGGCCCTCTGGGACAGTGTGGCTCGTGTCTTCCC 240
DB 181 TGGAAAGTCTGTCTCTCCCAAGGAGAGGCCCTCTGGGACAGTGTGGCTCGTGTCTTCCC 240
QY 241 AACGGCT 300
DB 241 AACGGCT 300
QY 301 GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCCTGTCTACCAAGATT 360
DB 301 GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCCTGTCTACCAAGATT 360
QY 361 CTTGGGAAAGCCAGAAATTTGTAGATTCTGCTCTGAACTCACCGCTGGTGTTCCTCAATAAG 420
DB 361 CTTGGGAAAGCCAGAAATTTGTAGATTCTGCTCTGAACTCACCGCTGGTGTTCCTCAATAAG 420
QY 421 GTGGGACATGT 480
DB 421 GTGGGACATGT 480
QY 481 GGGAAAGCCCTCTGTCT 540
DB 481 GGGAAAGCCCTCTGTCT 540
QY 541 CTTGAGACAGGCTCTTTCACATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 600
DB 541 CTTGAGACAGGCTCTTTCACATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 600
QY 601 GATCCCGCTCCACACTTCT 660
DB 601 GATCCCGCTCCACACTTCT 660
QY 661 CGCACAGCCCT 719
DB 661 CGCACAGCCCT 719
QY 720 GGTGTGGAGCCAGAGGTGGAGCAGTAGTCTCTGTGGAAACCGTAAACCTGTGAGTGTGA 779
DB 720 GGTGTGGAGCCAGAGGTGGAGCAGTAGTCTCTGTGGAAACCGTAAACCTGTGAGTGTGA 779
QY 780 AGTCCCTGCCAGCCCT 839
DB 780 AGTCCCTGCCAGCCCT 839
QY 840 TCCCCCAGCCCTGTGTCTGATCTCTCTCTGAGATAGGGCTCAGGACACAGGAACTACAG 899
DB 840 TCCCCCAGCCCTGTGTCTGATCTCTCTCTGAGATAGGGCTCAGGACACAGGAACTACAG 899
QY 900 CTTGTGTGGCCACCCATTCAGCCACGGGCCCCAGGAAAGCGTGTGTGTGTGTGTGTGTGT 959
DB 900 CTTGTGTGGCCACCCATTCAGCCACGGGCCCCAGGAAAGCGTGTGTGTGTGTGTGTGTGT 959
QY 960 CATCGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1019
DB 960 CATCGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1019
QY 1020 TCTAGCCCTGGCCCTGGGGATCTCTGGAGGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGG 1079
DB 1020 TCTAGCCCTGGCCCTGGGGATCTCTGGAGGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGG 1079

	Query Match	100.0%;	Score 1391;	DB 16;	Length 1391;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 1391;	Conservative	0;	Mismatches	0; Indels
					0; Gaps
Qy	1	GGGGCAGCCGGAACAGCAGTTGGAGCTGGGTCTGGTCTCAGTCTGTGGGGGAGTA	60		
Db	1	GGGGCAGCCGGAACAGCAGTTGGAGCTGGGTCTGGTCTCAGTCTGTGGGGGAGTA	60		
Qy	61	GTAGGTGCTCAAAACATCAGCCCCGGATTGGCGGCCACTGGTGTCTGAAGTCTAAGGGG	120		
Db	61	GTAGGTGCTCAAAACATCAGCCCCGGATTGGCGGCCACTGGTGTCTGAAGTCTAAGGGG	120		

QY 121 G C C C C A A G A A A C C A C C C C A G C G G C T G G A A T G G A A A C T G A A C A C A G C C C G G A C A G A G C T 180
Db 121 G C C C C A A G A A A C C A C C C C A G C G G C T G G A A T G G A A A C T G A A C A C A G C C C G G A C A G A G C T 180
QY 181 T G G A G G T C C T G T C T C C C A G G A G A G A G C C C C T G G A C A G T G T G G C T C G T G C T T C C C 240
Db 181 T G G A G G T C C T G T C T C C C A G G A G A G A G C C C C T G G A C A G T G T G G C T C G T G C T T C C C 240
QY 241 A A C G G C T C C C T C T C C T T C C G G C T G T C G G A T C C A G G A T G A G G G A T T T T C C G G T G C C A G 300
Db 241 A A C G G C T C C C T C T C T T C C G G C T G T C G G A T C C A G G A T G A G G G A T T T T C C G G T G C C A G 300
QY 301 G C A A T G A A C A G A A T G G A A G A G A C C A A G T C C A A C T A C G A G T C C G T G T C T A C A G A T T 360
Db 301 G C A A T G A A C A G A A T G G A A G A G A C C A A G T C C A A C T A C G A G T C C G T G T C T A C A G A T T 360
QY 361 C T T G G A A G C C A G A A A T T C A G A T T C T G C C T C T G A A C T A C C G C T G T T C C C A T A G 420
Db 361 C T T G G A A G C C A G A A A T T C A G A T T C T G C C T C T G A A C T A C C G C T G T T C C C A T A G 420
QY 421 G T G G G A C A T G T G T C A G A G G A A G C T A C C C T G C A G G A C T C T T A G C T G G C A C T T G G A T 480
Db 421 G T G G G A C A T G T G T C A G A G G A A G C T A C C C T G C A G G A C T C T T A G C T G G C A C T T G G A T 480
QY 481 G G G A A C C C C T G T G C T A T A G A A G G A G A T A T C T G T G A A G A A C A G A C C A G G A C A C 540
Db 481 G G G A A C C C C T G T G C T A T A G A A G G A G A T A T C T G T G A A G A A C A G A C C A G G A C A C 540
QY 541 C C T G A C A C A G G C T C T T C A C T G C A G T C G G A G C T A A T G T G A C C C C A G C C C G G G A G A 600
Db 541 C C T G A C A C A G G C T C T T C A C T G C A G T C G G A G C T A A T G T G A C C C C A G C C C G G G A G A 600
QY 601 G A T C C C C G T C C A C C T C T C T G A C T T C A G C C C A G G C T T C C C C G A C A C C G G G C T T G 660
Db 601 G A T C C C C G T C C A C C T C T C T G A C T T C A G C C C A G G C T T C C C C G A C A C C G G G C T T G 660
QY 661 C G C A G C C C C A T C A G C C C C G T G T C G G A G C T G T G C T T G A G A G A G T C C A A T T G 720
Db 661 C G C A G C C C C A T C A G C C C C G T G T C G G A G C T G T G C T T G A G A G A G T C C A A T T G 720
QY 721 G T G G T G G C C A G A G G T G G A G C A G T A G C T C T G T G G A C C G T A A C C T G A C C T G T G A A 780
Db 721 G T G G T G G C C A G A G G T G G A G C A G T A G C T C T G T G G A C C G T A A C C T G A C C T G T G A A 780
QY 781 G T C C C T G C C C A G C C C T C T C T C A A A T C C A T G A T G A A G A T G T G T G C C T T G C C C C T T 840
Db 781 G T C C C T G C C C A G C C C T C T C T C A A A T C C A T G A T G A A G A T G T G T G C C T T G C C C C T T 840
QY 841 C C C C C A G C C C T G T G T A T C T C C C T G A T A G G G C C T C A G A C C A G G A A C C T A C A C 900
Db 841 C C C C C A G C C C T G T G T A T C T C C C T G A T A G G G C C T C A G A C C A G G A A C C T A C A C 900
QY 901 T G T G T G G C C A C C A T T C C A G C C A G C G G C C C C A G G A A G C G T G C T C A G C A T C A G A T C 960
Db 901 T G T G T G G C C A C C A T T C C A G C C A G C G G C C C C A G G A A G C G T G C T C A G C A T C A G A T C 960
QY 961 A T C G A A C C A G C C A G A G G G C C A A C T G C A G G C T C T G T G G A G E A T C A G G C T G G G A A C T 1020
Db 961 A T C G A A C C A G C C A G A G G G C C A A C T G C A G G C T C T G T G G A G E A T C A G G C T G G G A A C T 1020
QY 1021 C T A G C C C T G C C C T G G G A T C T T G G A G C C T G G G A C A C C C C C T G C T A T T G G G G T C 1080
Db 1021 C T A G C C C T G C C C T G G G A T C T T G G A G C C T G G G A C A C C C C C T G C T A T T G G G G T C 1080
QY 1081 A T C T T T G C C A A G G C G C A C C C C A G A G A G A G A G A G C C C C A G A A A C C A G G A G 1140
Db 1081 A T C T T T G C C A A G G C G C A C C C C A G A G A G A G A G A G A G A G A G A G A G A G A G A G A G 1140
QY 1141 G A A G A G A G A G C G T C A G A A C T G A A T C A G T C G G A G A A C C T G A G C A G C C G A G A G T A G T 1200
Db 1141 G A A G A G A G A G C G T C A G A A C T G A A T C A G T C G G A G A A C C T G A G C A G C C G A G A G T A G T 1200
QY 1201 A C T G G A G G C C T T G A G G G C C C A C A G A G A T C C C A T C C A T C A G T C C C T T T T T T T T T T T C 1260

RESULT 2

US-10-115-635-351
; Sequence 351, Application US/10115635
; Publication No. US20040137434A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 797CON
; CURRENT APPLICATION NUMBER: US/10/115,635
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/714,936
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 362
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 351
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(1239)
US-10-115-635-351

Query Match 99.9%; Score 1389; DB 18; Length 1415;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCAGCCGAAACAGCAGTTGGAGCCCTGGGTGCTGCTCAGTCTGTGGGGGGCAGTAGT 62
Db 27 GGCAGCCGAAACAGCAGTTGGAGCCCTGGGTGCTCCTCAGTCTGTGGGGGGCAGTAGT 86
QY 63 AGGTGCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTGAAGTAAAGGGGC 122
Db 87 AGGTGCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTGAAGTAAAGGGGC 146
QY 123 CCCCAGAAACACACCCAGCGCTGGAATGGAACCTGAAACACAGGCCGGAAGAGCTTG 182
Db 147 CCCCAGAAACACACCCAGCGCTGGAATGGAACCTGAAACACAGGCCGGAAGAGCTTG 206
QY 183 GAAGTCTGTCTCTCCCAAGGAGAGGCCCTTGGGACAGTGTGGCTGTGCTCTTCCCAA 242
Db 207 GAAGTCTGTCTCTCCCAAGGAGAGGCCCTTGGGACAGTGTGGCTGTGCTCTTCCCAA 266
QY 243 CGGCTCCCTCTTCTCCGCTGTGGGATCCAGGATGAGGGGATTTCCGGTGCCAGGC 302

Db 267 CGGCTCCCTCTTCCGCTGTGGGATCCAGGATGAGGGGATTTTCGGTGCCAGGC 326
Qy 303 AATGAACAGGAATGGAAGAGAGACCAAGTCAACTACCGAGTCCGTGTCTTACAGATTC 362
Db 327 AATGAACAGGAATGGAAGAGAGAGACCAAGTCAACTACCGAGTCCGTGTCTTACAGATTC 386
Qy 363 TGGGAAGCCAGAAATGTAGATTCTGGCTCTGAACCTACCGCTGGTGTTCCTCAATAAGGT 422
Db 387 TGGGAAGCCAGAAATGTAGATTCTGGCTCTGAACCTACCGCTGGTGTTCCTCAATAAGGT 446
Qy 423 GGGGACATGTGTCTCAGAGGAAGTACCTCGAGGAGCTCTTAGCTGGCAGCTTGGATGG 482
Db 447 GGGGACATGTGTCTCAGAGGAAGTACCTCGAGGAGCTCTTAGCTGGCAGCTTGGATGG 506
Qy 483 GAAGCCCTGGTCCCTAATGAGAAGGAGTATCTGTGAAGAAACAGACAGGAGACACCC 542
Db 507 GAAGCCCTGGTCCCTAATGAGAAGGAGTATCTGTGAAGAAACAGACAGGAGACACCC 566
Qy 543 TGAGACAGGGCTCTTCACTGACAGTCCGAGCTAATGGTGACCCAGCCGGGGAGGAGA 602
Db 567 TGAGACAGGGCTCTTCACTGACAGTCCGAGCTAATGGTGACCCAGCCGGGGAGGAGA 626
Qy 603 TCCCGCTCCACCTCTTCTCTGTAGCTTACGCCAGGCTTCCCGGACACCGGGCTTTGG 662
Db 627 TCCCGCTCCACCTCTTCTCTGTAGCTTACGCCAGGCTTCCCGGACACCGGGCTTTGG 686
Qy 663 CACAGCCCTCCATCAGCCCGCTGTCTGGAGCTGTGCCTCTGGAGAGGTCCAAATGGT 722
Db 687 CACAGCCCTCCATCAGCCCGCTGTCTGGAGCTGTGCCTCTGGAGAGGTCCAAATGGT 746
Qy 723 GGTGAGCCAGAGGTGGAGCAGTAGTCTGTGTGAACCGTAAACCTGACCTGTGAAGT 782
Db 747 GGTGAGCCAGAGGTGGAGCAGTAGTCTGTGTGAACCGTAAACCTGACCTGTGAAGT 806
Qy 783 CCTGCGCCAGCCCTCTCTCAATCACTGATGAAGAGTGTGCTTGCCTTGCCTTCC 842
Db 807 CCTGCGCCAGCCCTCTCTCAATCACTGATGAAGAGTGTGCTTGCCTTGCCTTCC 866
Qy 843 CCCCAGCCCTGTCTGATCTCTCCCTGAGATAGGCTCTCAGGACAGGGAACCTACAGCTG 902
Db 867 CCCCAGCCCTGTCTGATCTCTCTCTGAGATAGGCTCTCAGGACAGGGAACCTACAGCTG 926
Qy 903 TGTGGCCACCCATTCCAGCCACCGGGCCCGAGGAAGCGTGTGTGAGCATCAGATCAT 962
Db 927 TGTGGCCACCCATTCCAGCCACCGGGCCCGAGGAAGCGTGTGTGAGCATCAGATCAT 986
Qy 963 CGAACCCAGCGAGGGGCGCAACTCAGGCTCTGTGGGAGGATCAGGCTGGGAACTCT 1022
Db 987 CGAACCCAGCGAGGGGCGCAACTCAGGCTCTGTGGGAGGATCAGGCTGGGAACTCT 1046
Qy 1023 AGCCCTGGCCCTGGGGATCTGGGAGGCTTGGGACAGCGCCCTGTCTCAATGGGGTCA 1082
Db 1047 AGCCCTGGCCCTGGGGATCTGGGAGGCTTGGGACAGCGCCCTGTCTCAATGGGGTCA 1106
Qy 1083 CTTGTGGCAAGCGCGCAACCGCGAGAGAGAGAGAGGCGCCCGAGAAACAGAGGA 1142
Db 1107 CTTGTGGCAAGCGCGCAACCGCGAGAGAGAGAGAGGCGCCCGAGAAACAGAGGA 1166
Qy 1143 AGAGGAGGAGCGTGCAGAACTGAATCAGTCGGAGGAACCTGAGGCGAGGAGTAGTAC 1202
Db 1167 AGAGGAGGAGCGTGCAGAACTGAATCAGTCGGAGGAACCTGAGGCGAGGAGTAGTAC 1226
Qy 1203 TGGAGGGCTTGAAGGGGCCACAGACAGATCCCATCAGCTCCCTTTCTTTTCCC 1262
Db 1227 TGGAGGGCTTGAAGGGGCCACAGACAGATCCCATCAGCTCCCTTTCTTTTCCC 1286
Qy 1263 TTGAACGTGTCTGGCTCAGACCAACTCTCTCTGTATATCTCTCTCTGTATTAACCC 1322
Db 1287 TTGAACGTGTCTGGCTCAGACCAACTCTCTCTGTATATCTCTCTCTGTATTAACCC 1346
Qy 1323 ACCTTGGCAGCTTCTTCTAACAACAGAGCCCGCCACATGATGATTAACAACCTGACA 1382
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Qy 1383 CATCTTGCA 1391
Db 1407 CATCTTGCA 1415

RESULT 3

US-08-905-709-3
; Sequence 3, Application US/08905709
; Publication No. US20010039256A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David
; APPLICANT: Schmidt, Ann M.
; TITLE OF INVENTION: A METHOD TO PREVENT ACCELERATED
; ; TITLE OF INVENTION: ATHEROSCLEROSIS USING (SRAE) SOLUBLE RECEPTOR FOR
; ; TITLE OF INVENTION: ADVANCED GLYCATION ENDPRODUCTS
; ; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,709
; FILING DATE: 05-AUG-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/52876
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-905-709-3

Query Match 96.9%; Score 1348.2; DB 8; Length 1405;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1383; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

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Db 61 GTAGGTGCTCAAAACATCAAGCCCGATTGGCGAGCCACTGCTGCTGAAGTGTAAAGGG 120
Qy 121 GCGCCCAAGAAACACCCAGCGGCTGGAAATGGAACCTGAACACAGCCCGGACAGAGCT 180
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QY 1080 CATCTTGTGGCAAGGGGGGCAACCCGAGGAGAGGAGAGAGCCCGAGAAACACAGGA 1139
Db 1080 CATCTTGTGGCAAGGGGGGCAACCCGAGGAGAGGAGAGG - AGGCCCCAGAAAAACACAGGA 1138
QY 1140 GGAAGAGAGGAGAGCTGCAGAACTGAATCAGTCGGAGGAACTTGGAGCAGCGAGAGTAG 1199
Db 1139 GGAAGAGAGGAGAGCTGCAGAACTGAATCAGTCGGAGGAACTTGGAGCAGCGAGAGTAG 1198
QY 1200 TACTGGAGGCGCTTGGAGGGCCACAGACAGATCCATCCATCAGCTCCCTTTTCTTTTT 1259
Db 1199 TACTGGAGGCGCTTGGAGGGCCACAGACAGATCCCATCAGCTCCCTTTTCTTTTT 1258
QY 1260 CCCTTGAACCTGCTCGCCCTCAGACCACTCTCTCTGTATATCTCTCTCTCTCTCTCTCT 1319
Db 1259 CCCTTGAACCTGCTCGCCCTCAGACCACTCTCTCTGTATATCTCTCTCTCTCTCTCTCT 1318
QY 1320 CCACCTTGGCAAGCTTTCTTACAAACAGAGCCGCCCAACATGATGATTAACACCTG 1379
Db 1319 CCACCTTGGCAAGCTTTCTTACAAACAGAGCCGCCCAACATGATGATTAACACCTG 1378
QY 1380 ACACATCTT 1388
Db 1379 ACACATCTT 1387

RESULT 6

US-10-115-635-352
; Sequence 352, Application US/10115635
; Publication No. US20040137434A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyang
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 797CON
; CURRENT APPLICATION NUMBER: US/10/115,635
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/714,936
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 362
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 352
; LENGTH: 1463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(1287)
US-10-115-635-352

Query Match 95.7%; Score 1331; DB 18; Length 1463;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1389; Conservative 0; Mismatches 0; Indels 48; Gaps 1;

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Db 87 AGGTGCTCAAAACATCACAGCCCGGATTTGGGAGCCACTGGTGTCTGAAAGTGAAGGGGCG 146
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Db 147 CCCAAGAAACCAACCCAGCGCTGGAATGGAATGGAACACTGAACACAGGCCGACAGAGCTTG 206
QY 183 GAAGTCTCTGCTCTCCACAGGAGGAGGCCCCCTGGGACAGTGTGGTCTGTCTTCTTCCAA 242
Db 207 GAAGTCTCTGCTCTCCACAGGAGGAGGCCCCCTGGGACAGTGTGGTCTGTCTTCTTCCAA 266
QY 243 CGGCTCCCTCTCTCTCCGCTGTGGGATCCAGATGAGGGGATTTTCCGGTGCAGGCG 302
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QY 303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTC 362
Db 327 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTC 386
QY 363 TGGGAAGCCAGAAATTTAGATTCTGCTCTCAACTCAGGCTGTGTCTTCCCAATA --- 418
Db 387 TGGGAAGCCAGAAATTTAGATTCTGCTCTCAACTCAGGCTGTGTCTTCCCAATAAGGT 446
QY 419 -----AGGTGGGACATGTGT 434
Db 447 AGTGAAGAAACAGGAGAGAGTAGAAACGGGCCCTGTGAACAGGAGGTGGGACATGTGT 506
QY 435 GTCAGAGGAGACTACCTTCAGGAGACTCTTAGCTGGGACACTTGGATGGGAGCCCTGTGT 494
Db 507 GTCAGAGGAGACTACCTTCAGGAGACTCTTAGCTGGGACACTTGGATGGGAGCCCTGTGT 566
QY 495 GCCTAATGAGAGGAGATATCTGCAAGGAAACAGACAGGAGACACCTTGAGACAGGCT 554
Db 567 GCCTAATGAGAGGAGATATCTGCAAGGAAACAGACAGGAGACACCTTGAGACAGGCT 626
QY 555 CTTCACTGACGTGCGAGCTAATGGTCAACCCAGCCCGGGAGGAGATCCCTGCCAC 614
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QY 615 CTTCTCTGTAGCTTACGCCAGAGCTTCCCGGACACCGGGCTTGGCAGACAGCCCAT 674
Db 687 CTTCTCTGTAGCTTACGCCAGAGCTTCCCGGACACCGGGCTTGGCAGACAGCCCAT 746
QY 675 CCAGCCCGCTGTCTGGGAGCTTGCCTCTGGAGAGGTCCAATTTGGTGTGGAGCCAGA 734
Db 747 CCAGCCCGCTGTCTGGGAGCTTGCCTCTGGAGAGGTCCAATTTGGTGTGGAGCCAGA 806
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Db 807 AGGTGGAGCAGTAGCTCTGTGTGGAACCGTAAACCTGACCTGTGAAGTCCCTGCCAGCC 866
QY 795 CTTCTCTCAAAATCCAATGGAATGGAAGGATGTGCTTCCCTTCCCTCCCGAGCCCTGT 854
Db 867 CTTCTCTCAAAATCCAATGGAATGGAAGGATGTGCTTCCCTTCCCTCCCGAGCCCTGT 926
QY 855 GCTGATCTCTCTGAGATAGGGCTCTCAGGACAGGGAACCTTACAGCTGTGTGGGACCCA 914
Db 927 GCTGATCTCTCTGAGATAGGGCTCTCAGGACAGGGAACCTTACAGCTGTGTGGGACCCA 986
QY 915 TTCCAGCCACCGGCCCCAGGAAAGCCCTGTGTGAGCATCAGCATCATCGAACACAGGCGA 974
Db 987 TTCCAGCCACCGGCCCCAGGAAAGCCCTGTGTGAGCATCAGCATCATCGAACACAGGCGA 1046
QY 975 GGAGGGGCCAACTGCAGGCTCTGTGGGAGGATCAGGGCTGGGAACTCTAGGCCCTGGCCCT 1034
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QY 1035 GGGGATCTTGGGAGGCTTGGGGAACAGCGCCCTGCTCATTTGGGGTCTATTTGTGGCAAG 1094
Db 1107 GGGGATCTTGGGAGGCTTGGGGAACAGCGCCCTGCTCATTTGGGGTCTATTTGTGGCAAG 1166
QY 1095 GCGCAACCGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1154

[illegible][illegible]

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1106	Qy	GAGGAGAGGAGAGGAAGCGCCCCAGAAAACC--AGGAGGAGAGGAGGAGCGTGCAGAAC	1167
1146	Db	AAGGACAGGAGAGAGAGGTCCCGAANAACGAGGAGGAGAGGAGGAGAGGACGCGAAC	1207
1163	Qy	TGAATCAGTCGGAGGAACCTTGAGCGAGCGAGAGTAGTACTGGAGGGCTTTTGAGGGGGCC	1227
1206	Db	TGAACCAAGCCAGAGGAGGCCCGAGCGCGCAGAGAGCAGCACAGGAGGGCTTTGAGGAGGCC	1266
1223	Qy	ACAGACAGATCCCATCCATCAGCTCCCTTTTCTTTTCCCTTGAACCTGTCTCTGGGCTCAG	1287
1266	Db	ACGCCACAGACCCGATCCATCAG--CCCTCTTTTCTTTTCCCACTCTCTTTCTGGGCCCCAG	1327
1283	Qy	ACCAACTCTCTCCTGTGATAATCTCTCTCTGTATAAACCCCAACCTTGCCCAAGCTTTTCTTCT	1347
1324	Db	ACCAGTTCTCTCTGTATATATCTC-----CAGCCCAACATCTCCCAACATTCTTCTCC	1377

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RESULT 13
US-08-755-235-1
; Sequence 1, Application US/08755235
; Publication No. US20030059423A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1438
; TYPE: DNA
; ORGANISM: Bovine
US-08-755-235-1
Query Match      64.8%; Score 901.4; DB 8; Length 1438;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

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Minimum DB seq length: 0

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1355	97.4	1436	9 BC020669	BC020669 Homo sapi
2	1289	92.7	1391	6 AR321600	AR321600 Sequence
3	1289	92.7	1391	9 HUMRAGE	M91211 Human recep
4	1242	89.3	1268	9 AB036432	AB036432 Homo recep
5	1193	85.8	1451	9 AB061669	AB061669 Homo sapi
6	990	71.2	1223	6 BD176670	BD176670 Soluble R
7	990	71.2	1223	9 AB061668	AB061668 Homo sapi
8	821	59.0	1218	6 CQ730900	CQ730900 Sequence
9	623	44.8	1250	9 HSA133822	HA133822 Homo sapi
10	466	33.5	698	6 AX795283	AX795283 Sequence
11	466	33.5	698	9 AF537303	AF537303 Homo sapi
12	290	20.8	511	6 AX795282	AX795282 Sequence
13	230	20.8	511	9 AF536237	AF536237 Homo sapi
14	274	19.7	5062	9 HSM808526	BM848378 Homo sapi
15	274	19.7	10108	9 HUMHXRAGE	D28769 Human HOX12
16	274	19.7	56747	9 AL845464	AL845464 Human DNA
17	274	19.7	62944	6 AX334775	AX334775 Sequence
18	274	19.7	62944	6 AX336090	AX336090 Sequence
19	274	19.7	62944	9 HSMHC3W5A	U89336 Homo sapien

C	20	274	19.7	80063	9	EX284686	EX284686 Human DNA
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C	22	274	19.7	102588	9	EX927239	EX927239 Human DNA
C	23	274	19.7	103327	9	AL662830	AL662830 Human DNA
C	24	274	19.7	137335	9	AL662884	AL662884 Human DNA
C	25	274	19.7	200685	2	AP001455	AP001455 Homo sapi
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C	27	273	19.6	653	9	AF536236	AF536236 Homo sapi
C	28	223	16.0	197811	2	AC009833	AC009833 Homo sapi
C	29	181	13.0	610	6	AX333424	AX333424 Sequence
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C	31	176	12.7	176	11	G06703	G06703 human STS
C	32	167	12.0	747	9	HSR238896	HSR238896 Homo sapi
C	33	136	9.8	159822	9	AC148714	AC148714 Macaca mu
C	34	123	8.8	123	6	BD190119	BD190119 Polypepti
C	35	97	7.0	189424	9	AC148664	AC148664 Macaca mu
C	36	60	4.3	60	6	CQ544915	CQ544915 Sequence
C	37	58	4.2	255	9	HSR012753	HSR012753 Homo sapi
C	38	51	3.7	51	6	AX161745	AX161745 Sequence
C	39	51	3.7	483	4	AY370908	AY370908 Sus scro
C	40	45	3.2	1704	9	AF001095	AF001095 Homo sapi
C	41	42	3.0	1426	4	BOVRAGE	M91212 Cow recepto
C	42	42	3.0	1426	6	AR321599	AR321599 Sequence
C	43	37	2.7	127266	4	AL773562	AL773562 Pig DNA
C	44	33	2.4	51	9	AF065212	AF065212 Homo sapi
C	45	33	2.4	1832	9	AF208289	AF208289 Homo sapi

ALIGNMENTS

RESULT 1	BC020669	Homo sapiens advanced glycosylation and product-specific receptor, transcript variant 1, mRNA (CDNA clone MGC:22357 IMAGE:4718076), complete cds.	1436 bp	mRNA	linear	PRI 29-JUN-2004
LOCUS	BC020669					
DEFINITION	BC020669					
ACCESSION	BC020669					
VERSION	BC020669.1	GI:18088362				
KEYWORDS	MGC.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 1436)					
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Lequellano, N.A., Peters, G.J., Abramson, R.D., Mullah, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.					
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences					
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99	(26)			16899-16903 (2002)
PUBMED	12477932					
REFERENCE	2 (bases 1 to 1436)					
AUTHORS	Strausberg, R.					
TITLE	Direct Submission					
JOURNAL	Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,					

REMARK
COMMENT

USA
NIH-MGC Project URL: <http://mgc.mci.nih.gov>
Contact: MGC help desk
Email: cgapbe-re@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) med@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 37 Row: e Column: 17
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 26787960.

FEATURES
source

Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="Lung"
/clone_lib="NIH MGC 77"
/lab_host="DH10B"
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/translation="MAAGTAVGAWLVLSLWGANVGAQNTARIQEPVLVKCKGAPKK
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ORIGIN

Query Match 97.4%; Score 1355; DB 9; Length 1436;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCGAGCGGAACAGCAGTGGAGCCTGGGTGCTGCTCAGTCTGTGGGGGCGAGTAGT 62
DB 22 GGCGAGCGGAACAGCAGTGGAGCCTGGGTGCTGCTCAGTCTGTGGGGGCGAGTAGT 81
QY 63 AGGTGCTCAAAACATCAGACCCCGGATTGGCGAGCCACTGGTCTGAAAGTGAAGGGGC 122
DB 82 AGGTGCTCAAAACATCAGACCCCGGATTGGCGAGCCACTGGTCTGAAAGTGAAGGGGC 141
QY 123 CCCAAGAAACACACCCAGCGGCTGGAATGGAACTGAACACAGGCGGCACAGAGCTTG 182
DB 142 CCCAAGAAACACACCCAGCGGCTGGAATGGAACTGAACACAGGCGGCACAGAGCTTG 201
QY 183 GAAGTCTGTCTCCCAAGGAGGAGCCCTGGGACAGTGTGGTCTGTCTTCCCA 242
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QY 243 CGGCTCCCTCTTCCCTTCCGCTGTCCGGATCCAGGATGAGGGGATTTTCCGGTCCAGGC 302
DB 262 CGGCTCCCTCTTCCCTTCCGCTGTCCGGATCCAGGATGAGGGGATTTTCCGGTCCAGGC 321
QY 303 ATGGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACAGATCC 362
DB 322 ATGGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACAGATCC 381
QY 363 TGGGAGCCAGAAATTTGTAGATCTTCCCTCTGAACTCAGCGCTGGTGTTCCTCAATAGGT 422
DB 382 TGGGAGCCAGAAATTTGTAGATCTTCCCTCTGAACTCAGCGCTGGTGTTCCTCAATAGGT 441
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DB 442 GGGGACATGTGTCTCAGAGGAGGATACCTCTCAGGAGCTTTAGTGGCACTTTGATCG 501
QY 483 GAAGCCCTGGTGTCTTAATGAGAGGAGTATCTGTGAAGGAAACAGACAGGAGACACCC 542
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QY 543 TGAGACAGGCTCTTCACTGCTGAGTCCGAGCTATGTTGAGCCCGGCGGAGGAGA 602
DB 562 TGAGACAGGCTCTTCACTGCTGAGTCCGAGCTATGTTGAGCCCGGCGGAGGAGA 621
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DB 742 GGTGAGCCAGAAAGTGGAGCAGTAGTCTCTGTTGGAACCGTAACCTGTGAACT 801
QY 783 CCTGCCAGCCCTCTCTCAATCCACTGGAATGAAGATGTTGCTGCTTGGCCCTTCC 842
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VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
PUBMED				

AUTHORS Yonekura, H., Yamamoto, Y., Sakurai, S., Petrova, R. G., Abedin, Md. J., Li, H., Yasui, K., Takeuchi, M., Makita, Z., Takasawa, S., Okamoto, H., Watanabe, T. and Yamamoto, H.

TITLE Novel splice variants of the receptor for advanced glycation end-products expressed in human vascular endothelial cells and pericytes, and their putative roles in diabetes-induced vascular injury

JOURNAL Biochem. J. 370 (Pt 3), 1097-1109 (2003)

MEDLINE 22510265

PUBMED 12495433

REFERENCE 2 (bases 1 to 1451)

AUTHORS Yonekura, H., Yamamoto, Y., Sakurai, S. and Yamamoto, H.

TITLE Direct Submission

JOURNAL Submitted (11-MAY-2001) Hideto Yonekura, Kanazawa University, Graduate School of Medical Science; 13-1 Takara-machi, Kanazawa, Ishikawa 920-8640, Japan (E-mail: hyone@med.kanazawa-u.ac.jp, Tel: 81-76-285-2182, Fax: 81-76-234-4226)

FEATURES

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BD176670

LOCUS

DEFINITION Soluble RAGE protein.

ACCESSION BD176670

VERSION BD176670.1 GI:29122380

KEYWORDS WO 02074805-A/1.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1223)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Yamamoto, H., Yonekura, H., Yamamoto, Y., Sakurai, S. and Watanabe, T.

TITLE Soluble RAGE protein

JOURNAL Patent: WO 02074805-A 1 26-SEP-2002;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: gb_est1:*
 - 2: gb_est2:*
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 - 4: gb_est3:*
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 - 7: gb_est6:*
 - 8: gb_gse1:*
 - 9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1149	82.6	1163	9	AY421474 Pan trogl
3	800.4	57.5	1209	9	AY421475 Mus muscu
4	779.4	56.0	1296	7	CF110468 Shultzoni
5	753.4	54.2	1347	3	AK004802 Mus muscu
6	714.8	51.4	1194	5	BQ067161 AGENCOURT
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15	640.4	46.0	729	4	CG545652 602572917
16	610.6	43.9	755	4	CG529866 602558957
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ALIGNMENTS

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LOCUS Homo sapiens AGER gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY421473
VERSION AY421473.1 GI:39748335
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1215)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1215)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
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them based on alignment.
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DEFINITION genomic survey sequence.
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VERSION AY421474.1 GI:39748336
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 1163)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1163)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity 99.1%; Pred. No. 3.6e-285;
Matches 1152; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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QY 113 GTAAGGGGGCCCCAAGAAAACACCCAGCGGCTGGAATGGAACCTGAACACAGGCCGA 172
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Db 121 CAGAGCTTGAAGGTCTGTCTCCCGAGGAGGAGGCCCTTGGACAGTGTGGCTCGTG 180
QY 233 TCCTTCCCAACGGCTCCCTCTTCTTCCGGCTGTCCGGATCCAGGATGAGGGATTTTCC 292
Db 181 TCCTTCCCAACGGCTCCCTCTTCTTCCGGCTGTCCGGATCCAGGATGAGGGATTTTCC 240
QY 293 GGTGCCAGGCATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCT 352
Db 1163

241	Db	GGTGCCAGGCATGAAACAGGAATGGAAGAGGACCAAGTCAACTACCGAGTCCGTGTCT	300
353	Qy	ACCAAGATTCTGGGAAGCCAGAAATTGTAGATTCTGCTCTCTGAACTCACGGCTGGTGTTC	412
301	Db	ACCAGATTCTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACTCACGGCTGGTGTTC	360
413	Qy	CCAAATAGGTGGGAATATGTGTGTCTGAGGGAAGCTACCTCTGCAGGGACTCTTTAGCTGGC	472
361	Db	CCAAATAGGTGGGACATGTGTGTNNNNNGAAGCTACCTCTGCAGGGACTCTTTAGTTGGC	420
473	Qy	ACTTTGATGGGAAGCCCTCGTCTCTAATGAGAAGGAGTATCTGTCAAGGAAACAGACCA	532
421	Db	ACTTTGATGGGAAGCCCTCGTCTCTAATGAGAAGGAGTATCTGTGAAGAAACAGACCA	480
533	Qy	GGAGACACCTCTGAGACAGGGCTCTTTCACACTGCAGTCTGAGCTAATGGTGAACCCAGCCC	592
481	Db	GGAGACACCTCTGAGACAGGGCTCTTTCACACTGCAGTCTGAGCTAATGGTGAACCCAGCCC	540
593	Qy	GGGAGAGATATCCCGTCCACCTTCTCTGTAGCTTTCAGCCAGGCTCTCCCGGACACC	652
541	Db	GGGAGAGATATCCCGTCCACCTTCTCTGTAGCTTTCAGCCAGGCTCTCCCGGACACC	600
653	Qy	GGGCTTGGCAGACAGCCCCCATCAGAGCCGCTGTCTGGAGCCCTGTGGAGGAGG	712
601	Db	GGGCTTGGCAGACAGCCCCCATCAGAGCCGCTGTCTGGAGCCCTGTGGAGGAGG	660
713	Qy	TCCAAATGGTGGTGGAGCCAGAGGTGGAGCAGTAGCTCTCTGGTGGAAACCGTAACCCCTGA	772
661	Db	TCCAAATGGTGGTGGAGCCAGAGGTGGAGCAGTAGCTCTCTGGTGGAAACCGTAACCCCTGA	720
773	Qy	CTGTGAAGTCCCTGCGCAGCCCTCTCTCAAATCCAATGGAATGGTGTGTCCT	832
721	Db	CTGTGAAGTCCCTGCGCAGCCCTCTCTCAAATCCAATGGAATGGTGTGTCCT	780
833	Qy	TGCCCCCTTCCCGCCAGCCCTGTGTGATCTCTCCCTGAGATAGGCGCTCAGGACCAAGGAA	892
781	Db	TGCCCCCTTCCCGCCAGCCCTGTGTGATCTCTCCCTGAGATAGGCGCTCAGGACCAAGGAA	840
893	Qy	CTTACAGCTGTGTGGCCACCCATTCACAGCCACCGGGCCCCCAGGAAGCCGTCTCAGCA	952
841	Db	CTTACAGCTGTGTGGCCACCCATTCACAGCCACCGGGCCCCCAGGAAGCCGTCTCAGCA	900
953	Qy	TCAGCATATCGAACACAGGCGAGGAGGGCCAACTGCAGGCTCTGTGGGAGGATCAGGGC	1012
901	Db	TCAGCATATCGAACACAGGCGAGGAGGGCCAACTGCAGGCTCTGTGGGAGGATCAGGGC	960
1013	Qy	TGGGAATCTAGCCCTGGCCCTTGGGATCTCTGGAGAGCCCTGGGACAGCGCCCTGCTCA	1072
961	Db	TGGGAATCTAGCCCTGGCCCTTGGGATCTCTGGAGAGCCCTGGGACAGCGCCCTGCTCA	1020
1073	Qy	TTGGGGTCATCTTGTGTGCAAGGGCGGCAACGCGAGGAGGAGGAGGAGGCGCCAGAAA	1132
1021	Db	TTGGGGTCATCTTGTGTGCAAGGGCGGCAACGCGAGGAGGAGGAGGAGGCGCCAGAAA	1080
1133	Qy	ACCAGGAGGAGGAGGAGCGGTGCAGAACTGAATCAATGTCGGAGGAACTCTGAGCGCG	1192
1081	Db	ACCAGGAGGAGGAGGAGCGGTGCAGAACTGAATCAATGTCGGAGGAACTCTGAGCGCG	1140
1193	Qy	AGAGTAGTACTGGAGGGCCCTTGA	1215
1141	Db	AGAGTAGTACTGGAGGGCCCTTGA	1163
RESULT 3			
AY421475	LOCUS	1209 bp	DNA
DEFINITION			linear
ACCESSION			GSS 17-DEC-2003
KEYWORDS			Mus musculus AGER gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ORGANISM			Mus musculus (house mouse)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 21:51:55 ; Search time 813 Seconds
(without alignments)
10128.364 Million cell updates/sec

Title: US-10-091-019-1
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Sequence: 1 999gcagccggaacagcagt.....aacacctgacacattgtgca 1391

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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- 6: Geneseqn2002as:*
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- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1391	100.0	1391	6 ABQ79955	Abq79955 Human RAG
2	1389	99.9	1415	6 ABQ99597	Abq99597 Human cod
3	1355	97.4	1436	12 ADX00130	Adx00130 Human RAG
4	1304	93.7	1582	4 AAH57444	Aah57444 Human lun
5	1289	92.7	1391	6 ABK10856	Abk10856 DNA encod
6	1289	92.7	1391	6 ABK94114	Abk94114 Human CDN
7	1289	92.7	1391	6 AAD36952	Aad36952 Human rec
8	1289	92.7	1391	10 AAD59952	Aad59952 Human RAG
9	1289	92.7	1391	10 ADG32021	Adg32021 Human DNA
10	1242	89.3	1268	10 ADG33024	Adg33024 Human DNA
11	1189	85.5	1678	9 ACC59907	Acc59907 Human REM
12	1182	83.5	1217	10 ADP95563	Adp95563 Human NOV
13	1117	80.3	1329	12 ADP19665	Adp19665 Human LP2
14	1088	78.2	1294	12 ADP19669	Adp19669 Human LP2
15	1044	75.1	1226	10 ADP95565	Adp95565 Human NOV
16	1018	73.2	1023	2 AAV12394	Aav12394 Human sol
17	1018	73.2	1023	2 AAV06517	Aav06517 Human RAG
18	1015	73.0	1173	10 ADP95567	Adp95567 Human NOV
19	1013	72.8	1020	6 ABQ79956	Abq79956 Human sol
20	990	71.2	1223	6 ABV73151	Abv73151 Human sol

21	990	71.2	1223	10	ADG37043	Adg37043 Receptor
22	990	71.2	1291	12	ADP19655	Adp19655 Human LP2
23	977	70.2	1146	13	ADG10302	Adg10302 Human the
24	973	69.9	1463	6	ABQ99598	Abq99598 Human cod
25	954	68.6	957	2	AAV06518	Aav06518 Human RAG
26	933	67.1	1223	12	ADP19667	Adp19667 Human LP2
27	877	63.0	1761	12	ADK00128	Adk00128 Human RAG
28	870	62.5	1384	12	ADP19659	Adp19659 Human LP2
29	852	61.3	957	2	AAV12395	Aav12395 Human mat
30	822	59.1	1239	12	ADP19663	Adp19663 Human LP2
31	820	59.0	1090	12	ADM80824	Adm80824 Human CAD
32	820	59.0	1194	12	ADP19657	Adp19657 Human LP2
33	697	50.1	1539	9	ACC59920	Acc59920 Human REM
34	697	50.1	1627	9	ACC59921	Acc59921 Human REM
35	574	41.3	1339	12	ADP19661	Adp19661 Human LP2
36	466	33.5	698	10	ADD40792	Add40792 Human RAG
37	316	24.2	336	6	ABQ79957	Abq79957 Human RAG
38	290	20.8	511	10	ADD40791	Add40791 Human RAG
39	274	19.7	62944	6	ABL68262	Ab168262 Kidney ca
40	274	19.7	62944	6	ABL66947	Ab166947 Lung canc
41	273	19.6	653	10	ADD40790	Add40790 Human RAG
42	255	18.3	255	4	AAH57236	Aah57236 Human lun
43	197	14.2	203	12	ACH83167	Ach83167 Human gen
44	197	14.2	218	10	ACD96717	Acd96717 Human col
45	197	14.2	553	12	ACH69467	Ach69467 Human gen

ALIGNMENTS

RESULT 1
ABQ79955
ID ABQ79955 standard; DNA; 1391 BP.

XX AC ABQ79955;

DT 23-DEC-2002 (first entry)

DE Human RAGE nucleotide sequence.

XX KW Receptor for Advanced Glycated end product; RAGE; recombinant; nontropic;
KW antiarteriosclerotic; antidiabetic; cytostatic; nephrotropic; vasotropic;
KW neuroprotective; antiinflammatory; gene therapy; human; ds.

OS Homo sapiens.

PN WO200270667-A2.

PD 12-SEP-2002.

PF 05-MAR-2002; 2002WO-US006881.

PR 05-MAR-2001; 2001US-0273418P.

PA (TRAN-) TRANSTECH PHARMA INC.

XX Harris R, Shen J, Shahbaz M;

DR WPI; 2002-713443/77.

XX PT High level expression of recombinant Receptors for Advanced Glycated end products (RAGE) proteins for treating increased levels of advanced glycosylation end products, comprises infecting cells with a high titer recombinant virus.

XX PS Claim 12; Fig 2A; 5lpp; English.

XX CC The invention relates to a method for high level expression of recombinant forms of the Receptor for Advanced Glycated end products (RAGE) or its fragments. The method involves (i) subcloning a nucleotide sequence encoding RAGE or its fragment into a virus; (ii) preparing a high titer stock of recombinant virus; and (iii) infecting host cells with the high titer recombinant virus under conditions such that

CC predetermined levels of RAGE or its fragment is produced, where the
CC predetermined levels of RAGE comprises at least 25 mg recombinant protein
CC per liter of culture. The method is useful for high level expression of
CC recombinant RAGE polypeptide or its fragment which may be useful in
CC preventing, treating or ameliorating diseases associated with increased
CC levels of advanced glycosylation end products, such as atherosclerosis,
CC diabetes and its symptoms, amyloidosis, kidney failure, Alzheimer's
CC disease, inflammation, systemic lupus nephritis, inflammatory lupus
CC nephritis, cancer or erectile dysfunction. The present sequence
CC represents the nucleotide sequence of human RAGE as reported in GenBank
CC /EMBL Accession no. XM004205
XX
SQ Sequence 1391 BP; 305 A; 408 C; 417 G; 261 T; 0 U; 0 Other;
Query Match 100.0%; Score 1391; DB 6; Length 1391;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGACGCGGAAACAGCAGTTGGAGCTGGGTCTGGTCTCCTAGTCTGTGGGGGCGAGTA 60
DB 1 GGGGACGCGGAAACAGCAGTTGGAGCTGGGTCTGGTCTCCTAGTCTGTGGGGGCGAGTA 60
QY 61 GTAGGTGCTCAAAACATCAGACCCCGGATGGGAGCCACTGTGTGAAGTGAAGGG 120
DB 61 GTAGGTGCTCAAAACATCAGACCCCGGATGGGAGCCACTGTGTGAAGTGAAGGG 120
QY 121 GCGCCCAAGAAACACGCCAGCGCTGGAAATGAAACTGAACACAGCCGGAAGAAGCT 180
DB 121 GCGCCCAAGAAACACGCCAGCGCTGGAAATGAAACTGAACACAGCCGGAAGAAGCT 180
QY 181 TGAAGGTCTCTGCTCCGCCAGGAGAGGCCCTCGGACAGTGTGCTGTCTTCC 240
DB 181 TGAAGGTCTCTGCTCCGCCAGGAGAGGCCCTCGGACAGTGTGCTGTCTTCC 240
QY 241 AACGGTCCCTCTCTTCCGGTGTGCGGATCCAGATCAGGGGATTTCCGGTCCAG 300
DB 241 AACGGTCCCTCTCTTCCGGTGTGCGGATCCAGATCAGGGGATTTCCGGTCCAG 300
QY 301 GCAATGAACAGGAATGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGT 360
DB 301 GCAATGAACAGGAATGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGT 360
QY 361 CTTGGGAAGCCAGAAATTTAGATTCTGCTGAACTACGGCTGGTGTTCCTCAATAAG 420
DB 361 CTTGGGAAGCCAGAAATTTAGATTCTGCTGAACTACGGCTGGTGTTCCTCAATAAG 420
QY 421 GTGGGACATGTGTCTCAGAGGAGAGCTACCTGCAGGAGCTCTTAGCTGGCACTTGGAT 480
DB 421 GTGGGACATGTGTCTCAGAGGAGAGCTACCTGCAGGAGCTCTTAGCTGGCACTTGGAT 480
QY 481 GGGAAAGCCCTGTGCTTAATGAGAGGGAGTATCTGTGAAGAAACAGACAGGAGACAC 540
DB 481 GGGAAAGCCCTGTGCTTAATGAGAGGGAGTATCTGTGAAGAAACAGACAGGAGACAC 540
QY 541 CTTGAGACAGGGCTCTTACACTGCACTCGAGCTAATGTGTACCCAGCCCGGGAGGA 600
DB 541 CTTGAGACAGGGCTCTTACACTGCACTCGAGCTAATGTGTACCCAGCCCGGGAGGA 600
QY 601 GATCCCGGTCCACCTTCTCTGTAGCTTACGCCAGGCTTCCCGACACCGGGCTTG 660
DB 601 GATCCCGGTCCACCTTCTCTGTAGCTTACGCCAGGCTTCCCGACACCGGGCTTG 660
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DB 661 CGCACAGCCCTCCAGCCCGGTGTCTGGAGCTGTGCTCTGGAGGAGGTCCAATTG 720
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DB 721 GTGTGGAGCCAGAGGTGGAGCAGTAGCTCTTGGTGGAAACCGTAACCTGACCTGTGAA 780
QY 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAAGATGGTGTGCCCTTGGCCCTT 840
DB 781 GTCCCTGCCAGCCCTCTCTCTCAATCCACTGATGAAGATGGTGTGCCCTTGGCCCTT 840

QY 841 CCCCCAGCCCTGTGTCTGATCTCCTGAGATAGGGCTTCAGGACACAGGAACTTACAGC 900
DB 841 CCCCCAGCCCTGTGTCTGATCTCCTGAGATAGGGCTTCAGGACACAGGAACTTACAGC 900
QY 901 TGTGTGGCCACCCATTCCAGCCACCGGGCCCAAGGAAGCCGTGTGTACGATCAGCATC 960
DB 901 TGTGTGGCCACCCATTCCAGCCACCGGGCCCAAGGAAGCCGTGTGTACGATCAGCATC 960
QY 961 ATCGAACACAGGCGAGGAGGGGCCAACTGTCAGGCTCTGTGGGAGGATCAGGGCTGGGAAT 1020
DB 961 ATCGAACACAGGCGAGGAGGGGCCAACTGTCAGGCTCTGTGGGAGGATCAGGGCTGGGAAT 1020
QY 1021 CTAGCCCTGGCCCTGGGGATCTTGGAGGCTTGGGACACGCCCTCTCATTTGGGGTC 1080
DB 1021 CTAGCCCTGGCCCTGGGGATCTTGGAGGCTTGGGACACGCCCTCTCATTTGGGGTC 1080
QY 1081 ATCTTGTGCAAAAGGGGCAAGCCGAGGAGGAGGAAGGCCCAAGAAACACAGGAG 1140
DB 1081 ATCTTGTGCAAAAGGGGCAAGCCGAGGAGGAGGAAGGCCCAAGAAACACAGGAG 1140
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DB 1141 GAAGGAGGAGCGTGTGACAGAACTGAATCAGTCGAGGAACTCAGGACGCGGAGAGTAGT 1200
QY 1201 ACTGGAGGCGCTTGGAGGGCCCAACAGACAGATCCCATCAGTCCTCTTTCTTTTC 1260
DB 1201 ACTGGAGGCGCTTGGAGGGCCCAACAGACAGATCCCATCAGTCCTCTTTCTTTTC 1260
QY 1261 CTTGAGACTGTCTGGCCCTCAGACCACTCTCTCTGTATAATCTCTCTCTGTATAACC 1320
DB 1261 CTTGAGACTGTCTGGCCCTCAGACCACTCTCTCTGTATAATCTCTCTCTGTATAACC 1320
QY 1321 CCACCTTGGCAAGCTTTCTTCTACACAGAGCCGCCCAATGATGATTAACACCTGA 1380
DB 1321 CCACCTTGGCAAGCTTTCTTCTACACAGAGCCGCCCAATGATGATTAACACCTGA 1380
QY 1381 CACATCTTGA 1391
DB 1381 CACATCTTGA 1391
RESULT 2
ABQ99597
ID ABQ99597 standard; cDNA; 1415 BP.
XX
AC ABQ99597;
XX
DT 25-FEB-2003 (first entry)
XX
Human coding sequence SEQ ID 330.
XX
DE
XX
KW Human; expressed sequence tag; EST; chromosome 6p21.3;
KW haematopoietic disorder; central nervous system disease; viral infection;
KW peripheral nervous system disease; non-healing wound; infectious disease;
KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;
KW fungal infection; autoimmune disorder; coagulation disorder; neutropenic;
KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;
KW cytostatic; haemostatic; virucide; antibacterial; fungicide;
KW immunostimulant; cerebroprotective; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200259260-A2.
XX
PD 01-AUG-2002.
XX
PF 16-NOV-2001; 2001WO-US042950.
XX
PR 17-NOV-2000; 2000US-00714936.
XX
PA (HYSE-) HYSEQ INC.
XX

AC ADK00130;
XX 20-MAY-2004 (first entry)
XX Human RAGE encoding sequence.
XX
XX Advanced Glycation End Product Ligand Binding Element; RAGE-LBE;
XX Cytostatic; Antidiabetic; Nootropic; Antiarthritic; Osteopathic;
XX Neuroprotective; Antiinflammatory; Dermatological; Immunosuppressive;
XX Vasotropic; Antipsoriatic; Antibacterial; Antiarteriosclerotic;
XX amyloidosis; cancer; Crohn's disease; diabetes; Alzheimer's disease;
XX chronic inflammatory disease; osteoarthritis; irritable bowel disease;
XX multiple sclerosis; psoriasis; ss.
XX Homo sapiens.
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
XX CDS 1..1436
XX /*tag= a
XX /product= "RAGE"
XX
XX WO2004016229-A2.
XX
XX 26-FEB-2004.
XX
XX 18-AUG-2003; 2003WO-US025996.
XX
XX 16-AUG-2002; 2002US-0404205P.
XX
XX (AMHP) WYETH.
XX
XX Pittman DD, Clancy B, Larsen G, Trepicchio WL, Brennan FM;
XX Feldmann M, Foxwell BJM, Feldman JL;
XX
XX WPI; 2004-192067/19.
XX P-PSDB; ADK00129.
XX
XX New fusion protein comprising a Receptor for Advanced Glycation End
XX Product Ligand Binding Element (RAGE-LBE) and an immunoglobulin element,
XX useful for preparing a composition for treating e.g., Alzheimer's
XX disease.
XX
XX Disclosure; SEQ ID NO 44; 100pp; English.
XX
XX The present invention relates to a new fusion protein comprises a
XX Receptor for Advanced Glycation End Product Ligand Binding Element (RAGE-
XX LBE) and an immunoglobulin element. The fusion protein is useful for
XX preparing a composition for treating RAGE-associated disorder such as
XX amyloidosis, cancer, Crohn's disease, diabetes, complications of
XX diabetes, prion-related disorders, vasculitis, nephropathies,
XX retinopathies and/or neuropathies; Alzheimer's disease, chronic
XX inflammatory disease e.g., rheumatoid arthritis, osteoarthritis,
XX irritable bowel disease, multiple sclerosis, psoriasis or lupus, acute
XX inflammatory disease e.g., sepsis, or cardiovascular disease, e.g.,
XX atherosclerosis or stenosis. The present sequence represents human RAGE
XX protein encoding sequence.
XX
XX Sequence 1436 BP; 340 A; 411 C; 422 G; 263 T; 0 U; 0 Other;
XX
XX
XX Query Match 97.4%; Score 1355; DB 12; Length 1436;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 3 GGCGCGGACAGAGTTGGAGCCTGGGTGCTGGTCTCCTCAGTCTGTGGGGGCGAGTACT 62
XX
XX 22 GGCGCGGACAGAGTTGGAGCCTGGGTGCTGGTCTCCTCAGTCTGTGGGGGCGAGTACT 81
XX
XX 63 AGGTGCTCAAAAATCATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAAGTGAAGGGGGC 122
XX
XX 82 AGGTGCTCAAAAATCATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAAGTGAAGGGGGC 141
XX
XX 123 CCCAAGAAACCAACCCAGCGGCTGGAAATGGAAACTGAAACAGAGCCGCGACAGAGCTTG 182

142 CCCAAGAAACCAACCCAGCGGCTGGAAATGGAAACTGAAACAGAGCCGCGACAGAGCTTG 201
183 GAAGTCTCTGTCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCTCTCCCAA 242
202 GAAGTCTCTGTCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCTCTCCCAA 261
243 CGGCTCCCTCTCTCTCTCCCGGCTGTCCGGATCCAGATGAGGGGATTTCCGGTCCAGGC 302
262 CGGCTCCCTCTCTCTCTCCCGGCTGTCCGGATCCAGATGAGGGGATTTCCGGTCCAGGC 321
303 ATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACAGATTCC 362
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363 TGGGAGCCAGAAATTTGTAGATTCTGCCTCTGAACTCACGGCTGGTGTCCCAATAAGGT 422
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562 TGAGACAGGGCTCTTACACTGCAGTCCGAGCTTAATGTTGACCCAGCCGCGGGAGGAGA 621
603 TCCCGTCCCACTCTCTCTGTAGTTTACGCCAGGCTTCCCGACACCGGCGCTTGGG 662
622 TCCCGTCCCACTCTCTCTGTAGTTTACGCCAGGCTTCCCGACACCGGCGCTTGGG 681
663 CACAGCCCTCATCCAGCCCGGTGTCTGGAGCCTGTGCCTCTGGAGGAGGTCCAATTGGT 722
682 CACAGCCCTCATCCAGCCCGGTGTCTGGAGCCTGTGCCTCTGGAGGAGGTCCAATTGGT 741
723 GGTGGAGCCAGAAAGTGGAGCAGTAGTCTCTCGTGGAAACCGTAACCTCAGCTGCAAGT 782
742 GGTGGAGCCAGAAAGTGGAGCAGTAGTCTCTCGTGGAAACCGTAACCTCAGCTGCAAGT 801
783 CCCTGCCAGCCCTCTCTCTCAAAATCCACTGGATGAAGATGGTGTGCTCCCTTCCCTCC 842
802 CCCTGCCAGCCCTCTCTCTCAAAATCCACTGGATGAAGATGGTGTGCTCCCTTCCCTCC 861
843 CCCCAGCCCTGTGTGTATCTCTCTGAGATAGGGCTCAGGACAGGGAACCTACAGCTG 902
862 CCCCAGCCCTGTGTGTATCTCTCTGAGATAGGGCTCAGGACAGGGAACCTACAGCTG 921
903 TGTGGCCACCAATTCAGCCACGGCCCGCCAGGAAAGCCGTGTGTGAGCATCAGCATCAT 962
922 TGTGGCCACCAATTCAGCCACGGCCCGCCAGGAAAGCCGTGTGTGAGCATCAGCATCAT 981
963 CGAACCCAGCCAGGAGGGGCGCAACTCTGTGGAGGATCAGGCTCTGGGAACTCT 1022
982 CGAACCCAGGAGGGGCGCAACTCTGTGGAGGATCAGGCTCTGGGAACTCT 1041
1023 AGCCCTGGCCCTGGGGATCTCTGGAGGCTGTGGGACAGCCGCGCTGTCTATTGGGGTCAAT 1082
1042 AGCCCTGGCCCTGGGGATCTCTGGAGGCTGTGGGACAGCCGCGCTGTCTATTGGGGTCAAT 1101
1083 CTTGTGGCAAGGCGCGCAACGCCGAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1142
1102 CTTGTGGCAAGGCGCGCAACGCCGAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1161
1143 AGAGGAGGAGCGTGCAGAACTGAATCAGTTCGAGGAACTCTGAGGAGGAGGAGGAGGAGGAG 1202
1162 AGAGGAGGAGCGTGCAGAACTGAATCAGTTCGAGGAACTCTGAGGAGGAGGAGGAGGAGGAG 1221
1203 TGGAGGCGCTTGGAGGGGCCACAGACAGATCCATCCATCAGCTCGCTTTCTTTTCC 1262

```
Db 1222 TGGAGGGCCTTGAGGGGCCACAGACAGATCCCATCATCAGCTCCCTTTCTTTTCC 1281
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Db 1282 TTGAACCTGTTCTGGCCTCAGACCAACTCTCTCTGTATATCTCTCTCTGTATAACCCC 1341
Qy 1323 ACCTTGCCAAAGCTTCTCTTACAAACAGAGCCCC 1357
Db 1342 ACCTTGCCAAAGCTTCTCTTACAAACAGAGCCCC 1376

RESULT 4
AAH57444
ID AAH57444 standard; cDNA; 1582 BP.
XX
AC AAH57444;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human lung cell specific cDNA sequence SEQ ID NO:284.
XX
KW Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;
KW uterus; ovary; stomach; intestine; kidney; pancreas; es;
KW metabolic disease; developmental disease; cytostatic; immunomodulatory;
KW neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
XX
OS Homo sapiens.
XX
PN WO200132927-A2.
XX
PD 10-MAY-2001.
XX
PF 02-NOV-2000; 2000WO-US030396.
XX
PR 04-NOV-1999; 99US-0163508P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Sornasse T, Seilhamer JJ, Watson GA;
XX
DR WPI; 2001-291057/30.
XX
DR
XX
PT New cell and tissue specific polynucleotides useful for diagnosis,
PT prognosis or monitoring of treatments for disorders where the gene is
PT associated with a cancer, immunopathology or neuropathology.
XX
PS Claim 1; Page 210; 327pp; English.
XX
CC AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
CC sequences (I). (I) can have cytostatic, immunomodulatory and
CC neuroprotective activities, and can be used in gene therapy. (I) and
CC proteins (II) encoded by then are used in high throughput screening
CC assays to select DNA molecules, RNA molecules, peptide nucleic acids,
CC mimetics, peptides, proteins, agonists, antagonists, antibodies or their
CC fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical
CC agents. Expression of (I) in a sample indicates the differentiation of
CC embryonic stem cells into a tissue selected from brain, heart, kidney,
CC liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used
CC to produce an expression profile that defines a metabolic or
CC developmental process, treatment, condition, disease or disorder. The
CC gene profile can be used for diagnosis, prognosis or monitoring of
CC treatments and for investigating a predisposition to a disorder where the
CC gene is associated with a cancer, immunopathology or neuropathology
XX
SQ Sequence 1582 BP; 355 A; 448 C; 486 G; 293 T; 0 U; 0 Other;

Query Match 93.7%; Score 1304; DB 4; Length 1582;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGACGCGGAACAGCAGTGGAGCCCTGGGTGCTGCTCAGTCTGTGGGGGCACTAGT 62
Db 203 GGACGCGGAACAGCAGTGGAGCCCTGGGTGCTGCTCAGTCTGTGGGGGCACTAGT 262
```


841	Db		CCCCCAGCCCTGTCGTGATCTCTCCCTGAGATAGGGCCTCAGGACCAAGGAACTTACAGC	900
901	Qy		TGTGTGCCACCCATTCCAGCCACGGGCCCCAGGAAACCGTGTGTGCAGCATCAGCATC	960
901	Db		TGTGTGCCACCCATTCCAGCCACGGGCCCCAGGAAACCGTGTGTGCAGCATCAGCATC	960
961	Qy		ATCGAACCGCGAGGAGGGGCCNACTGTCAGGCTCTGTGGGAGGATCAGGGCTGGGNACT	1020
961	Db		ATCGAACCGCGAGGAGGGGCCCAACTGCAAGGCTCTGTGGGAGGATCAGGGCTGGGNACT	1020
1021	Qy		CTAGCCCTGGCCCTGGGGATCTCTGGGAGGCTTGGGACAGCGGCCCTGTCTATTGGGGTC	1080
1021	Db		CTAGCCCTGGCCCTGGGGATCTCTGGGAGGCTTGGGACAGCGGCCCTGTCTATTGGGGTC	1080
1081	Qy		ATCTTGTGGCAAGCGCGGCAACGCCGAGGAGAGAGAGGAAGGCCCCAGAAAAACCAAGGAG	1140
1081	Db		ATCTTGTGGCAAGCGCGGCAACGCCGAGGAGAGAGAGGAAGGCCCCAGAAAAACCAAGGAG	1140
1141	Qy		GAGAGGAGGAGCGTGCAGAACTGAATCAGTCCGAGGNACTCTGAGGCAGCGGAGGTAGT	1200
1141	Db		GAGAGGAGGAGCGTGCAGAACTGAATCAGTCCGAGGNACTCTGAGGCAGCGGAGGTAGT	1200
1201	Qy		ACTGGAGGGCCTTGAGGGGCCACAGACAGATCCCATCAGCTCCCTTTCTTTTTC	1260
1201	Db		ACTGGAGGGCCTTGAGGGGCCACAGACAGATCCCATCAGCTCCCTTTCTTTTTC	1260
1261	Qy		CCTTGAACTGTTCTGGGCTCAGACCAACTCTCTCTGTATAACTCTCTCTGTATTAACC	1320
1261	Db		CCTTGAACTGTTCTGGGCTCAGACCAACTCTCTCTGTATAACTCTCTCTGTATTAACC	1320
1321	Qy		CCACTTGGCAAGCTTTCTTCTACAAACAGAGCCCCCACAATGATGATTAAACCACTTGA	1380
1321	Db		CCACTTGGCAAGCTTTCTTCTACAAACAGAGCCCCCACAATGATGATTAAACCACTTGA	1380
1381	Qy		CACATCTTGCA	1391
1381	Db		CACATCTTGCA	1391

RESULT 6
ABK84114
ID ABK84114 standard: CDNA: 1391 BP.

XX	ABK84114;	
XX	AC	
XX		
DT	14-AUG-2002	(first entry)
XX		
DE	Human cDNA differentially expressed in granulocytic cells #685.	

Human; ss; granulocytic cell; DNA chip; bacterial infection;
 viral infection; parasitic infection; protozoal infection;
 fungal infection; sterile inflammatory disease; psoriasis;
 rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 cardiac reperfusion injury; renal reperfusion injury; ARDS;
 adult respiratory distress syndrome; inflammatory bowel disease;
 Crohn's disease; ulcerative colitis; periodontal disease;
 granulocyte activation; chronic inflammation; allergy.

XX
OS
XX
PN

XX
PD
11-APR-2002.XX
PF 03-OCT-2001; 2001WO-US030821.XX
PR 03-OCT-2000: 2000US-0237189P.

XX PA (GENE-) GENE LOGIC INC.

XX PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J; XX

WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.

Claim 1: SEQ ID NO 685: 114pp; English: English.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g., psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published/pct_sequences

Sequence 1391 BP: 305 A: 407 C: 418 G: 261 T: 0 U: 0 Other:

```

every Match      92.7%; Score 1289; DB 6; Length 1391;
1st Local Similarity 99.9%; Pred. No. 0;
Mismatchches 1389; Conservative 0; Mismatchches 2; Indels 0; Gaps 0;

```

1 GGGGAGCCGGAAACAGCAGTTGGAGCTGGGTGCTCGTCCCTCAGTCTGTGGGGGGGAGTA 60
1 GGGGAGCCGGAAACAGCAGTTGGAGCTGGGTGCTCGTCCCTCAGTCTGTGGGGGGGAGTA 60
61 GTAGGTGCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAAGTGTAAAGGG 12
61 GTAGGTGCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAAGTGTAAAGGG 12
121 GCCCCCAAGAAACACACCCACGCGCTGGAAATGAAACTGAAACACAGGCCGGACAGAAGCT 18
121 GCCCCCAAGAAACACACCCACGCGCTGGAAATGAAACTGAAACACAGGCCGGACAGAAGCT 18
181 TGGAAAGTCTGTCTCCCCAGGAGGAGGCCCTGGGACAGTGTGGCTCGTCTCTCC 24
181 TGGAAAGTCTGTCTCCCCAGGAGGAGGCCCTGGGACAGTGTGGCTCGTCTCTCC 24
241 AACGGCTCCCTCTTCTTCCGGCTGTGGGATCCAGGATGAGGGGATTTTCCGGTGCCAG 30
241 AACGGCTCCCTCTTCTTCCGGCTGTGGGATCCAGGATGAGGGGATTTTCCGGTGCCAG 30
301 GCAATGAACAGGAATGAAAGGAGACAAGTCCAACTACCGAGTCCGTCTCTACAGATT 36
301 GCAATGAACAGGAATGAAAGGAGACAAGTCCAACTACCGAGTCCGTCTCTACAGATT 36

QY 1 GGGGACGCGGAAACAGCAGTTGAGCCTGGGTCTCTGCTCTCAGTCTGTGGGGGAGTA 60
 Db 1 GGGGACGCGGAAACAGCAGTTGAGCCTGGGTCTCTGCTCTCAGTCTGTGGGGGAGTA 60
 QY 61 GTAGTGTCTCAAAACATCAGACCCCGATTGGCGAGCCACTGGTCTGAAGTCTAAGGG 120
 Db 61 GTAGTGTCTCAAAACATCAGACCCCGATTGGCGAGCCACTGGTCTGAAGTCTAAGGG 120
 QY 121 GCCCCAAAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGGCCCGGACAGAAGCT 180
 Db 121 GCCCCAAAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGGCCCGGACAGAAGCT 180
 QY 181 TGAAGGTCTCTGCTCTCCCAAGGAGAGGCCCTCTGGGACAGTGTGGCTCTGTCTCTTCCC 240
 Db 181 TGAAGGTCTCTGCTCTCCCAAGGAGAGGCCCTCTGGGACAGTGTGGCTCTGTCTCTTCCC 240
 QY 241 AACGGCTCTCTCTCTCTCCGCTGTGGATCCAGATCAGGGGATTTTCCGGTCCAG 300
 Db 241 AACGGCTCTCTCTCTCTCCGCTGTGGATCCAGATCAGGGGATTTTCCGGTCCAG 300
 QY 301 GCAATGAACAGGAATGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATT 360
 Db 301 GCAATGAACAGGAATGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATT 360
 QY 361 CCTGGGAAGCCAGAAATTGTAGATTCTGCCTCTGAACTCACGGCTGGTGTTCCTCAATAAG 420
 Db 361 CCTGGGAAGCCAGAAATTGTAGATTCTGCCTCTGAACTCACGGCTGGTGTTCCTCAATAAG 420
 QY 421 GTGGGACATGTGTCTCAGAGGAGACTACCTGCAGGAGCTCTTAGCTGGCACTTGGAT 480
 Db 421 GTGGGACATGTGTCTCAGAGGAGACTACCTGCAGGAGCTCTTAGCTGGCACTTGGAT 480
 QY 481 GGAAGCCCTGTGTCTTAAGAGGAGTATCTGTGAAGAAACAGACAGAGACAC 540
 Db 481 GGAAGCCCTGTGTCTTAAGAGGAGTATCTGTGAAGAAACAGACAGAGACAC 540
 QY 541 CCTGAGACAGGCTCTTTCACATGTCAGTCCGAGCTAATGTGACCCCGCGGGAGGA 600
 Db 541 CCTGAGACAGGCTCTTTCACATGTCAGTCCGAGCTAATGTGACCCCGCGGGAGGA 600
 QY 601 GATCCCCGTCACCTTCTCTGTAGTTTACGCCAGGCTTCCCGACACCGGGCCTTG 660
 Db 601 GATCCCCGTCACCTTCTCTGTAGTTTACGCCAGGCTTCCCGACACCGGGCCTTG 660
 QY 661 CGCACAGCCCTCCACAGCCCGTGTCTGGAGCCTGTGCTCTGGAGGAGTCCCAATTG 720
 Db 661 CGCACAGCCCTCCACAGCCCGTGTCTGGAGCCTGTGCTCTGGAGGAGTCCCAATTG 720
 QY 721 GTGTGGAGCCAGAAAGTGGAGCAGTAGCTCCTGGTGGAAACCGTAACCTGACCTGTGAA 780
 Db 721 GTGTGGAGCCAGAAAGTGGAGCAGTAGCTCCTGGTGGAAACCGTAACCTGACCTGTGAA 780
 QY 781 GTCCCTGCCAGCCCTCTCTCAAAATCCATGGAATGAAGATGGTGTGCCCTTGCCCTTT 840
 Db 781 GTCCCTGCCAGCCCTCTCTCAAAATCCATGGAATGAAGATGGTGTGCCCTTGCCCTTT 840
 QY 841 CCCCCAGCCCTGTGTGATCTCCCTGAGTATGGGCTCAGGACAGGGAACCTACAGC 900
 Db 841 CCCCCAGCCCTGTGTGATCTCCCTGAGTATGGGCTCAGGACAGGGAACCTACAGC 900
 QY 901 TGTGTGGCCACCCATTCCAGCCAGCGGCCCCAGGAAAGCCGTGTGTGAGCATCAGCATC 960
 Db 901 TGTGTGGCCACCCATTCCAGCCAGCGGCCCCAGGAAAGCCGTGTGTGAGCATCAGCATC 960
 QY 961 ATCGAAACAGCGAGAGGGGCGCAACTGCGAGGCTCTGTGGAGGATCAGGGCTGGGAAT 1020
 Db 961 ATCGAAACAGCGAGAGGGGCGCAACTGCGAGGCTCTGTGGAGGATCAGGGCTGGGAAT 1020
 QY 1021 CTAGCCCTGGCCCTGGGAGTCTGGGAGGCTGGGGACAGCCGCTGCTCATTTGGGTC 1080
 Db 1021 CTAGCCCTGGCCCTGGGAGTCTGGGAGGCTGGGGACAGCCGCTGCTCATTTGGGTC 1080

RESULT 8

AAD59952

ID AAD59952 standard; DNA; 1391 BP.

XX AAD59952;

AC AAD59952;

XX DT 18-DEC-2003 (first entry)

XX DT 18-DEC-2003 (first entry)

XX DT 18-DEC-2003 (first entry)

XX DT 18-DEC-2003 (first entry)

XX DT 18-DEC-2003 (first entry)

XX DT 18-DEC-2003 (first entry)

XX DT 18-DEC-2003 (first entry)

XX DT 18-DEC-2003 (first entry)

XX DT 18-DEC-2003 (first entry)

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XX DT 18-DEC-2003 (first entry)

XX DT 18-DEC-2003 (first entry)

XX DT 18-DEC-2003 (first entry)

XX DT 18-DEC-2003 (first entry)

XX DT 18-DEC-2003 (first entry)

Human RAGE (receptor for advanced glycation end product) DNA.

Transgenic mouse; transgenic; nerve tissue specific promoter; nootropic;
 receptor for advanced glycation end product; RAGE; neurological disorder;
 Alzheimer's disease; amnesia; amyotrophic lateral sclerosis; neuroleptic;
 brain injury; cerebral senility; degenerative disorder; Down's syndrome;
 chronic peripheral neuropathy; cognitive disability; memory dysfunction;
 electric shock; Guillain-Barre syndrome; head trauma; mental retardation;
 Huntington's disease; learning disability; dyslexia; Tourette's syndrome;
 neuromuscular disorder; Parkinson's disease; myasthenia gravis; dementia;
 Pick's disease; human; gene; ds.

Homo sapiens.

Key Location/Qualifiers

CDS 1..1215

FT /*tag= a

FT /product= "Human RAGE protein"

FT /note= "No start codon"

FT /partial

FT polyA_signal 1368..1373

FT /*tag= b

XX US6563015-B1.

XX 13-MAY-2003.

XX 14-AUG-2000; 2000US-00638649.

XX 14-AUG-2000; 2000US-00638649.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Stern DM, Schmidt AM, Yan SD;

XX WPI; 2003-687217/65.

XX P-PSDB; AAE39510.

XX Transgenic mouse whose genome contain recombinant deoxyribonucleic acid

XX sequence, comprises nerve tissue specific promoter encoding human

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

receptor for advanced glycation end products, and mutant human amyloid precursor protein.

Disclosure; Col 6-7; 40pp; English.

The invention relates to a transgenic mouse whose genome contain a recombinant DNA sequence, comprising a nerve tissue specific promoter operatively linked to a DNA sequence, which encodes human receptor for advanced glycation end products (RAGE), and a mutant human amyloid precursor protein hAPP695, hAPP751, and hAPP770 bearing mutations linked to familial Alzheimer's disease in humans. The transgenic animal is used for evaluation of the potential therapeutic effect of an agent for treating Alzheimer's disease in a human. It is useful for screening of compounds, which would be useful in the treatment of neurological disorders, which would be useful in the treatment of neurological injury, cerebral senility, chronic peripheral neuropathy, a cognitive disability, a degenerative disorder associated with learning, Down's syndrome, dyslexia, electric shock induced amnesia or amnesia, Guillain-Barre syndrome, head trauma, Huntington's disease, a learning disability, a memory deficiency, memory loss, a mental illness, mental retardation, memory or cognitive dysfunction, multi-infarct dementia and senile dementia, myasthenia gravis, a neuromuscular disorder, Parkinson's disease, Pick's disease, a reduction in spatial memory retention, senility, or Tourette's syndrome. The present sequence is human RAGE DNA Sequence 1391 BP: 305 A; 407 C; 418 G; 261 T; 0 U; 0 Other;

Sequence 1391 BP; 305 A; 407 C; 418 G; 261 T; 0 U; 0 Other;

Query Match	92.7%	Score 1289	DB 10	Length 1391	
at Local Similarity	99.9%	Prod. No. 0			
ches 1389	Conservative	0	Mismatches 2	Indels 0	Gaps 0
1	GGGCGACGCCGAAACAGCAGTGTGGAGCCTGGGTGCTGGTCCCTCAGTCTGTGGGGGGCAGTA	60			
1	GGGCGACGCCGAAACAGCAGTGTGGAGCCTGGGTGCTGGTCCCTCAGTCTGTGGGGGGCAGTA	60			
61	GTAGTGCTCAAAACATCACAGCCCGGATTCGGCAGGCCACTTGGTCTGTAAGTGAAGGGG	120			
61	GTAGTGCTCAAAACATCACAGCCCGGATTCGGCAGGCCACTTGGTCTGTAAGTGAAGGGG	120			
121	GCCCCCAAGAAACACCCACGCGGTGGAATGGAAAACGTGAACACAGGCCGACAGAGCT	180			
121	GCCCCCAAGAAACACCCACGCGGTGGAATGGAAAACGTGAACACAGGCCGACAGAGCT	180			
181	TGGAAGGTCCTGTCTCCCCAGGAGGAGGCCCTTGGGACAGTGTGGCTCTGTCTCTCCC	240			
181	TGGAAGGTCCTGTCTCCCCAGGAGGAGGCCCTTGGGACAGTGTGGCTCTGTCTCTCCC	240			
241	AACGGCTCCCTCTTCTCCGCTGTCCGGATCCAGGATGAGGGGATTTCCGGTGGCCAG	300			
241	AACGGCTCCCTCTTCTCCGCTGTCCGGATCCAGGATGAGGGGATTTCCGGTGGCCAG	300			
301	GCAATGACAGGAATGGAAGAGGACCAAGTCCAACTACCCAGTCCGTGTCTACAGATT	360			
301	GCAATGACAGGAATGGAAGAGGACCAAGTCCAACTACCCAGTCCGTGTCTACAGATT	360			
361	CCTGGGAAGCCAGAAATGTAGATTCTGCCCTCGAACTCACGGCTGGTGTCCCAATAAG	420			
361	CCTGGGAAGCCAGAAATGTAGATTCTGCCCTCGAACTCACGGCTGGTGTCCCAATAAG	420			
421	GTGGGACATGTGTCTCAGAGGGAAGCTACCCCTCAGGGACTCTTAGCTGGCACTTGGAT	480			
421	GTGGGACATGTGTCTCAGAGGGAAGCTACCCCTCAGGGACTCTTAGCTGGCACTTGGAT	480			
481	GGGAAGCCCTGGTGCCCTAAATGAGAGGGAGTATCTGTGAAGGAACAGACACAGAGACAC	540			
481	GGGAAGCCCTGGTGCCCTAAATGAGAGGGAGTATCTGTGAAGGAACAGACACAGAGACAC	540			
541	CCTGAGACAGGGCTCTTCACACTGCAGTCGGAGCTAATGGTGAACCCAGCCCGGGAGGA	600			
541	CCTGAGACAGGGCTCTTCACACTGCAGTCGGAGCTAATGGTGAACCCAGCCCGGGAGGA	600			
601	GATCCCGTCCACCTTCTCTAGTCTCAGCCCAAGCCCTTCCCGCACACCCGGGCCCTTG	660			

OS	Homo sapiens.		
PN	W02003084469-A2.		
PD	16-OCT-2003.		
XX			
XX	31-MAR-2003; 2003WO-US010195.		
PF	01-APR-2002; 2002US-0369452P.		
XX	(UTAH-) UTAH VENTURES II LP.		
PA	Roben PW, Stevens AC;		
XX			
PI	WPI; 2003-804234/75.		
XX	P-PSDB; ADG32004.		
DR			
XX	New brain-specific, heart-specific, lung-specific, and pancreas-specific		
PT	therapeutic complexes, useful for treating or alleviating diseases that		
PT	affect the brain, heart, lungs, or pancreas.		
XX			
PS	Example 4; SEQ ID NO 49; 127pp; English.		
XX			
CC	This invention relates to novel tissue specific endothelial membrane		
CC	proteins. Specifically, it relates to the targeted delivery of		
CC	therapeutics to defined organs, tissues or cells using, for example,		
CC	brain-, heart-, lung- or pancreas-specific complexes. Furthermore, these		
CC	complexes can be used in smaller amounts than in conventional treatment		
CC	such that there is reduced chance of associated toxicity and side		
CC	effects. The present invention describes this therapeutic complex as		
CC	comprising a ligand that binds to a tissue-specific luminally expressed		
CC	protein, a therapeutic moiety and linker. As such, the therapeutic		
CC	complexes are useful for treating or alleviating diseases that affect the		
CC	brain (e.g. epilepsy, schizophrenia, bipolar disorder and Parkinson's		
CC	disease), the lungs (e.g. bacterial or fungal infections, asthma, cystic		
CC	fibrosis and pulmonary edema), the pancreas (e.g. diabetes,		
CC	pancreatitis, endocrine tumour and pancreatic cancer) or the heart (e.g.		
CC	infarction, coronary heart disease and arrhythmia). Accordingly, these		
CC	compositions exhibit neurotropic, neuroprotective, antiparkinsonian,		
CC	cerebroprotective, cytostatic, antibacterial, fungicidal, antiasthmatic		
CC	and immunosuppressive activities. This polynucleotide is the DNA sequence		
CC	encoding a human homologue of a lung-specific luminally expressed		
CC	protein, used in a therapeutic complex of the invention.		
XX			
SQ	Sequence 1391 BP; 305 A; 407 C; 418 G; 261 T; 0 U; 0 Other;		
	Query Match 92.7%; Score 1289; DB 10; Length 1391;		
	Best Local Similarity 99.9%; Pred. No. 0;		
	Matches 1389; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY	1 GGGGAGCCGGACACAGCAGTTGGAGCTGGGCTGCTGCTCCTCAGTCTGTGGGGGGCAGTA 60		
DB	1 GGGGAGCCGGACACAGCAGTTGGAGCTGGGCTGCTGCTCCTCAGTCTGTGGGGGGCAGTA 60		
QY	61 GTAGTGTCTCAAAATCAAGCCCGATTTGGCGACCACTGGTGTGAAGTGAAGGG 120		
DB	61 GTAGTGTCTCAAAATCAAGCCCGATTTGGCGACCACTGGTGTGAAGTGAAGGG 120		
QY	121 GCGCCCAAGAACCAACCCAGCGCTGGATGGAATGGAATGGAATGGAATGGAATGGAATG 180		
DB	121 GCGCCCAAGAACCAACCCAGCGCTGGATGGAATGGAATGGAATGGAATGGAATGGAATG 180		
QY	181 TGAAGGTCTGTCTCCCGAGGAGAGCGCCCTGGGACAGTGTGGCTGTGTCTTCCC 240		
DB	181 TGAAGGTCTGTCTCCCGAGGAGAGCGCCCTGGGACAGTGTGGCTGTGTCTTCCC 240		
QY	241 AACGGTCTCTTCTTCCCGGTGTGGGATCCAGGATGAGGGGATTTTCGGGTCCAG 300		
DB	241 AACGGTCTCTTCTTCCCGGTGTGGGATCCAGGATGAGGGGATTTTCGGGTCCAG 300		
QY	301 GCATGAACAGGATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATT 360		
DB	301 GCAATGAACAGGATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATT 360		

QY	361	CCTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACTCAGCGCTGGTGTTCCTCAATAAG	420
DB	361	CCTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACTCAGCGCTGGTGTTCCTCAATAAG	420
QY	421	GTGGGACATGTGTGTGAGGGAAGCTACCTTGCAGGGACTCTTGTAGCTGGCACTTGGAT	480
DB	421	GTGGGACATGTGTGTGAGGGAAGCTACCTTGCAGGGACTCTTGTAGCTGGCACTTGGAT	480
QY	481	GGGAAGCCCTTGTGTGCTTAATGAGAAGGGAGTATCTGTGAAGGAAACAGACAGGAGACAC	540
DB	481	GGGAAGCCCTTGTGTGCTTAATGAGAAGGGAGTATCTGTGAAGGAAACAGACAGGAGACAC	540
QY	541	CCTGAGACAGGGCTCTTTCACACTGCAGTGGAGCTAATGTGTACCCAGCCCGGGAGGA	600
DB	541	CCTGAGACAGGGCTCTTTCACACTGCAGTGGAGCTAATGTGTACCCAGCCCGGGAGGA	600
QY	601	GATCCCGTCCCACTTCTCTGTAGCTTTCAGCCAGGGCTTCCCGACACCCGGGCTTG	660
DB	601	GATCCCGTCCCACTTCTCTGTAGCTTTCAGCCAGGGCTTCCCGACACCCGGGCTTG	660
QY	661	CGCACAGCCCCCATCCAGCCCCGTGTCTGGAGCCTGTGCTCTGGAGGAGGTCCAATTG	720
DB	661	CGCACAGCCCCCATCCAGCCCCGTGTCTGGAGCCTGTGCTCTGGAGGAGGTCCAATTG	720
QY	721	GTGGTGGAGCCAGAAAGGTGGAGCAGTAGCTCTCTGAGTGAACCTGACCTGTGTAA	780
DB	721	GTGGTGGAGCCAGAAAGGTGGAGCAGTAGCTCTCTGAGTGAACCTGACCTGTGTAA	780
QY	781	GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAAGTGGTGTGCTTGTGCTTGTGCTT	840
DB	781	GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAAGTGGTGTGCTTGTGCTTGTGCTT	840
QY	841	CCCCCAGCCCTGTGTGTGATCTCTCCCTGAGATAGGGCCTCAGGACAGGGAACCTACAGC	900
DB	841	CCCCCAGCCCTGTGTGTGATCTCTCCCTGAGATAGGGCCTCAGGACAGGGAACCTACAGC	900
QY	901	TGTGTGGCCACCCATTTCCAGCCACGGGCCCCCAGGAAAGCGTGTGTGATCAGCATC	960
DB	901	TGTGTGGCCACCCATTTCCAGCCACGGGCCCCCAGGAAAGCGTGTGTGATCAGCATC	960
QY	961	ATCGAACAGGCGAGGAGGGGCGCACTCAGGCTCTGTGGAGGATCAGGGCTGGGNACT	1020
DB	961	ATCGAACAGGCGAGGAGGGGCGCACTCAGGCTCTGTGGAGGATCAGGGCTGGGNACT	1020
QY	1021	CTAGCCCTGGCCCTGGGGATCTTGGGAGCCTGGGACAGCCGCCCTGTCTATTGGGGTC	1080
DB	1021	CTAGCCCTGGCCCTGGGGATCTTGGGAGCCTGGGACAGCCGCCCTGTCTATTGGGGTC	1080
QY	1081	ATCTTGTGGCAAGGCGGCAACGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1140
DB	1081	ATCTTGTGGCAAGGCGGCAACGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1140
QY	1141	GAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1200
DB	1141	GAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1200
QY	1201	ACTTGGAGGCGCTTGGGGGCGGACAGACAGATCCCATCCATCAGTCCCTTTCTTTTTC	1260
DB	1201	ACTTGGAGGCGCTTGGGGGCGGACAGACAGATCCCATCCATCAGTCCCTTTCTTTTTC	1260
QY	1261	CCTTGAACCTGTCTGGCCCTCAGACCAACTCTCTCTGTGTATTAATCTCTCTCTGTATAAC	1320
DB	1261	CCTTGAACCTGTCTGGCCCTCAGACCAACTCTCTCTGTGTATTAATCTCTCTCTGTATAAC	1320
QY	1321	CAACCTTGCAGGCTTTTCTTCAACAGAGGCGCCCGACCAATGTATGATTAACACCTGA	1380
DB	1321	CAACCTTGCAGGCTTTTCTTCAACAGAGGCGCCCGACCAATGTATGATTAACACCTGA	1380
QY	1381	CACATCTTGA 1391	
DB	1381	CACATCTTGA 1391	

RESULT 10	
ADG33024	
ID	ADG33024 standard; DNA; 1268 BP.
XX	
AC	ADG33024;
XX	
DT	26-FEB-2004 (first entry)
XX	
DE	Human DNA differentially expressed in patients with SLE SeqID348.
XX	
KW	human; ds; autoimmune; chronic inflammatory disease; SLE;
KW	systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;
KW	Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;
KW	ulcerative colitis; primary sclerosing cholangitis; appendicitis;
KW	diverticulitis; primary biliary sclerosis.
XX	
OS	Homo sapiens.
XX	
PN	WO2003090694-A2.
XX	
PD	06-NOV-2003.
XX	
PF	24-APR-2003; 2003WO-US013015.
XX	
PR	24-APR-2002; 2002US-00131827.
XX	
PA	(EXPR-) EXPRESSION DIAGNOSTICS INC.
XX	
PI	Wohlgemuth J, Fry K, Woodward R, Ly N;
XX	
DR	WPI; 2003-877243/81.
XX	
PT	Diagnosing or monitoring autoimmune and chronic inflammatory diseases,
PT	such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative
PT	colitis, psoriasis and asthma by detecting the expression level of one or
PT	more genes.
XX	
PS	Claim 18; SEQ ID NO 348; 877pp; English.
XX	
CC	This invention relates to novel methods for diagnosing and monitoring
CC	autoimmune and chronic inflammatory diseases. Specifically, it refers to
CC	the identification of genes that have a clinical utility as diagnostic
CC	tools for the management of, in particular, patients with systemic lupus
CC	erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the
CC	present invention describes a method for determining the levels of
CC	multiple differentially expressed genes of a patient, in a concerted
CC	manner, in order to achieve an improved diagnostic assay with sensitivity
CC	and specificity for the disease in question. As such, these genes are
CC	useful for the diagnosis of various other inflammatory disorders
CC	including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,
CC	ankylosing spondylitis, ulcerative colitis, primary sclerosing
CC	cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.
CC	This polynucleotide is a DNA sequence representing human mRNA that is
CC	differentially expressed in patients with SLE, used in an exemplification
CC	of the invention.
XX	
SQ	Sequence 1268 BP; 280 A; 361 C; 410 G; 217 T; 0 U; 0 Other;
Query Match	89.3%; Score 1242; DB 10; Length 1268;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1242; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	3 GGCGAGCCGGAACAGAGTGGAGCCCTGGGTGGTGGTCTCAGTCTGTGGGGGACAGT 62
DB	27 GGCGAGCCGGAACAGAGTGGAGCCCTGGGTGGTGGTCTCAGTCTGTGGGGGACAGT 86
QY	63 AGGTGCTCAAAACATCACAGCCCGGATGGCGAGCCACCTGGTCTGAAAGTGAAGGGGGC 122
DB	87 AGGTGCTCAAAACATCACAGCCCGGATGGCGAGCCACCTGGTCTGAAAGTGAAGGGGGC 146
QY	123 CCCAAGAAACACCCAGCGGTGAATGGAACTGAACACAGGCGCGACAGACCTTG 182

RESULT 11
ACC59907
ID ACC59907 standard; cDNA; 1678 BP.
XX ACC59907;
AC ACC59907;
XX
DT 07-JUL-2003 . (first entry)
XX
DE Human REMAP-20 encoding cDNA SEQ ID NO:56.
XX
KW Human; receptor and membrane-associated protein; REMAP; cytostatic;
KW antitumor; anticonvulsant; neurotropic; neuroprotective;
KW cerebrotrophic; anti-HIV; anti-allergic; anti-inflammatory; cancer;
KW thymine; gene therapy; cell proliferative disorder; atherosclerosis;
KW neurological disorder; epilepsy; Huntington's disease; stroke; AIDS;
KW immune disorder; inflammatory disorder; allergy; developmental disorder;
KW hypothyroidism; Cushing's syndrome; infection; gene; ss.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 108..1373
FT /*tag= a
FT /product= "REMAP-20"
XX
PN WO2003025130-A2.
XX
XX
PD 27-MAR-2003.
XX
XX
PF 12-SEP-2002; 2002WO-US029220.
XX
PR 14-SEP-2001; 2001US-0322157P.
PR 28-SEP-2001; 2001US-0326029P.
PR 05-OCT-2001; 2001US-0327380P.
PR 12-OCT-2001; 2001US-0329198P.
PR 19-OCT-2001; 2001US-0343742P.
PR 02-NOV-2001; 2001US-0343906P.
PR 02-NOV-2001; 2001US-0343980P.
PR 16-NOV-2001; 2001US-0332426P.
PR 13-MAR-2002; 2002US-0364338P.
PR 15-MAR-2002; 2002US-0364494P.
PR 29-MAR-2002; 2002US-0369248P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
PI Warren BA, Gietzen KJ, Lal PG, Xu Y, Tran UK, Lee S;
PI Borowsky ML, Becha SD, Sanjanwala MM, Thangavelu K, Tang YT;
PI Honchell CD, Yue H, Elliott VS, Richardson TW, Azimzai Y, Chawla NK;
PI Baughn MR, Lu DAM, Nguyen DB, Kalafus DP, Sapperstein SK;
PI Ramkumar J, Lehr-Mason PM, Griffin JA, Duggan BM, Lee SY;
PI Zebartadjan Y, Hafalia AJA, Gururajan R, Swarnakar A, Lee EA;
PI Marquis JP, Khare R, Emerling BM, Jiang X, Jackson AA;
XX
DR WPI; 2003-354596/33.
DR P-PSDB; ABR43188.
XX
XX New human receptors and membrane-associated proteins (REMAP), useful for
PT diagnosing, treating and preventing diseases or conditions associated
PT with the aberrant REMAP expression e.g. cancer, AIDS, atherosclerosis, or
PT infections.
XX
XX Claim 5; Page 230-231; 241pp; English.
PS
XX ACC5988 to ACC59923 encode the human receptor and membrane-associated
CC proteins given in ABR43169 to ABR43204 and designated REMAP-1 to REMAP-36
CC (i). (i) have cytostatic, antitumor, anticonvulsant, anticonvulsant,
CC neurotrophic, neuroprotective, cerebrotrophic, anti-HIV, antiallergic,
CC anti-inflammatory and thymine activities, and can be used in gene
CC therapy. The REMAP polypeptides and polynucleotides are useful in
CC diagnosing, treating and preventing diseases or conditions associated
CC with the decreased expression or overexpression of REMAP, such as cell

CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
CC allergies) and developmental (e.g. hypothyroidism, Cushing's syndrome)
CC disorders, or infections. They are also useful in assessing the effects
CC of exogenous compounds on the expression of nucleic acid and amino acid
CC sequences of REMAP. The REMAPs or their fragments are useful in screening
CC compounds for effectiveness as agonist or antagonist of the polypeptides,
CC or in altering the expression of the target polynucleotide and compounds
CC that specifically bind to or modulate the activity of the polypeptide
XX
SQ Sequence 1678 BP; 471 A; 438 C; 480 G; 289 T; 0 U; 0 Other;

Query Match 85.5%; Score 1189; DB 9; Length 1678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 GGGAGAGAGCCCTGGGACAGTGTGCTCGTGTCTTCCCAACGGCTCCCTCTTCTCTTCC 260
DB 359 GGGAGAGAGCCCTGGGACAGTGTGCTCGTGTCTTCCCAACGGCTCCCTCTTCTCTTCC 418

QY 261 GGCTGTGGGATCCAGGATGAGGGGATTTTCCGGTCCAGGCAATGAACAGGAATGAAA 320
DB 419 GGCTGTGGGATCCAGGATGAGGGGATTTTCCGGTCCAGGCAATGAACAGGAATGAAA 478

QY 321 GGAGACCAAGTCCAACTACCGAGTCCGTGTCTTACAGATTCCTGGGAGGAGGATTTGT 380
DB 479 GGAGACCAAGTCCAACTACCGAGTCCGTGTCTTACAGATTCCTGGGAGGAGGATTTGT 538

QY 381 AGATTCTGCTCTGAACTCACCGCTGTGTCTTCCCAATAGGTGGGACATGTGTGAGA 440
DB 539 AGATTCTGCTCTGAACTCACCGCTGTGTCTTCCCAATAGGTGGGACATGTGTGAGA 598

QY 441 GGGAGCTACCTTCGACGGGACTCTTAGCTGGCACTTTGGATGGGAAGCCCTTGTGTCTAA 500
DB 599 GGGAGCTACCTTCGACGGGACTCTTAGCTGGCACTTTGGATGGGAAGCCCTTGTGTCTAA 658

QY 501 TGAGAGGAGATATCTGTGAAGAACAGACAGGAGACACCTTGAGACAGGGCTCTTTCAC 560
DB 659 TGAGAGGAGATATCTGTGAAGAACAGACAGGAGACACCTTGAGACAGGGCTCTTTCAC 718

QY 561 ACTGCAGTCGGAGCTAATGTGACCCAGCCCGGGAGGAGATCCCGCTCCACCTTCTC 620
DB 719 ACTGCAGTCGGAGCTAATGTGACCCAGCCCGGGAGGAGATCCCGCTCCACCTTCTC 778

QY 621 CTGTAGCTTTCAGCCAGGCTTTCCTCCGACACCGGGCTTTGGGACAGCCCTTCCAGCC 680
DB 779 CTGTAGCTTTCAGCCAGGCTTTCCTCCGACACCGGGCTTTGGGACAGCCCTTCCAGCC 838

QY 681 CCGTGTCTGGAGCTGTGCTCTTGAGAGAGGTCCAATTGGTGGAGCCAGAGGTGG 740
DB 839 CCGTGTCTGGAGCTGTGCTCTTGAGAGAGGTCCAATTGGTGGAGCCAGAGGTGG 898

QY 741 AGCAGTAGCTCTGGTGGAAACCGTAACCTGTGAGTCCCTGCGAGCCAGCCCTCTCC 800
DB 899 AGCAGTAGCTCTGGTGGAAACCGTAACCTGTGAGTCCCTGCGAGCCAGCCCTCTCC 958

QY 801 TCAATCCACTGGATGAAGAGTGTGCTGCTTCCCTTCCCTCCAGCCCTTGTGTGAT 860
DB 959 TCAATCCACTGGATGAAGAGTGTGCTGCTTCCCTTCCCTCCAGCCCTTGTGTGAT 1018

QY 861 CTTCCCTGAGATAGGCTCTCAGAGACAGGAGAACCTTACAGTGTGTGGCCACCATTTCCAG 920
DB 1019 CTTCCCTGAGATAGGCTCTCAGAGACAGGAGAACCTTACAGTGTGTGGCCACCATTTCCAG 1078

QY 921 CCACGGGCCCCAGGAAGCCGTGCTGTAGCATCATGACATCATGAAACAGCCAGGAGGG 980
DB 1079 CCACGGGCCCCAGGAAGCCGTGCTGTAGCATCATGAAACAGCCAGGAGGG 1138

QY 981 GCCAACTGCAGGCTCTGTGGGAGGATCAGGGCTGGGAACCTTAGCCCTTGGCCCTGGGGAT 1040
DB 1139 GCCAACTGCAGGCTCTGTGGGAGGATCAGGGCTGGGAACCTTAGCCCTTGGCCCTGGGGAT 1198

QY 1041 CTTGGAGGCTTGGGAGACAGCCGCTGTCTTATTGGGGTCTATTTGTGGCAAGGGCGCA 1100


```
Db 365 TGGGAGCCAGAAATTGTAGATTCTGCTCTGAACTCAGCGCTGGTGTTCCTCCAAATAGGT 424
Qy 423 GGGGACATGTGTCTCAGAGGGAAGCTACCTCGCAGGACCTCTTAGCTGGCACTTGTGATGG 482
Db 425 GGGGACATGTGTCTCAGAGGGAAGCTACCTCGCAGGACCTCTTAGCTGGCACTTGTGATGG 484
Qy 483 GAAGCCCTTGGTCCCTTAATGAGAAGGAGTATCTGTGAAGGAACAGACAGGAGACACCC 542
Db 485 GAAGCCCTTGGTCCCTTAATGAGAAGGAGTATCTGTGAAGGAACAGACAGGAGACACCC 544
Qy 543 TGAGACAGGGCTCTTACACCTGAGTCGAGCTAATGGTGACCCAGCCCGGGGAGGAGA 602
Db 545 TGAGACAGGGCTCTTACACCTGAGTCGAGCTAATGGTGACCCCGGGGAGGAGA 604
Qy 603 TCCCCCTGCCACCTTCTCTGTAGCTTACGCCAGCCGCTTCCCGGACACCGGGCCCTTGG 662
Db 605 TCCCCCTGCCACCTTCTCTGTAGCTTACGCCAGCCGCTTCCCGGACACCGGGCCCTTGG 664
Qy 663 CACAGCCCCCATCCAGCCCCGTGTCTGGAGCCTGTGCGCTCTGGAGGAGGTCCAAATGGT 722
Db 665 CACAGCCCCCATCCAGCCCCGTGTCTGGAGCCTGTGCGCTCTGGAGGAGGTCCAAATGGT 724
Qy 723 GGTGGAGCCAGAGGTGGAGCACTAGCTCTGTGTGGAACCGTAACCTGACCTGTGAAGT 782
Db 725 GGTGGAGCCAGAGGTGGAGCACTAGCTCTGTGTGGAACCGTAACCTGACCTGTGAAGT 784
Qy 783 CCTGTGCCAGCCCTCTCTCAAAATCCACTGGATGAAGGATGGTGTGCCCTTGGCCCTTCC 842
Db 785 CCTGTGCCAGCCCTCTCTCAAAATCCACTGGATGAAGGATGGTGTGCCCTTGGCCCTTCC 844
Qy 843 CCCAGCCCTGTGCTGATCTCTCCAGATAGGCTCTCAGGACCGGGAACCTACAGCTG 902
Db 845 CCCAGCCCTGTGCTGATCTCTCCAGATAGGCTCTCAGGACCGGGAACCTACAGCTG 904
Qy 903 TGTGGCCACCCATTCCAGCCACGGGCCCCAGGAAGCCGTGTGTGAGCATCAGCATCAT 962
Db 905 TGTGGCCACCCATTCCAGCCACGGGCCCCAGGAAGCCGTGTGTGAGCATCAGCATCAT 964
Qy 963 CGAACCCAGCGAGGAGGGCCAACTCAGGCTCTGTGGAGGATCAGGCTGGGAACCTCT 1022
Db 965 CGAACCCAGCGAGGAGGGCCAACTCAGGCTCTGTGGAGGATCAGGCTGGGAACCTCT 1024
Qy 1023 AGCCCTGGCCCTGGGATCTGGAGGCTCTGGGACAGCGCCCTCTCATTTGGGTCTAT 1082
Db 1025 AGCCCTGGCCCTGGGATCTGGAGGCTCTGGGACAGCGCCCTCTCATTTGGGTCTAT 1084
Qy 1083 CTTGTGGCAAGCGGCAACCGCGAGGAGGAGAGAGGCGCCCGGAGAAACCCAGGAGGA 1142
Db 1085 CTTGTGGCAAGCGGCAACCGCGAGGAGGAGAGAGGCGCCCGGAGAAACCCAGGAGGA 1144
Qy 1143 AGAGGAGGAGCGTGCAGAACTGAATCAGTCGGAGGAACCTGAGGCGAGGAGTAGTATC 1202
Db 1145 AGAGGAGGAGCGTGCAGAACTGAATCAGTCGGAGGAACCTGAGGCGAGGAGTAGTATC 1204
Qy 1203 TGGAGGGCCCTTGA 1215
Db 1205 TGGAGGGCCCTTGA 1217
```

RESULT 13

ADP19665

ID ADP19665 standard; cDNA; 1329 BP.

XX AC ADP19665;

XX AC ADP19665;

XX DT 12-AUG-2004 (first entry)

XX DE Human Lp2005 encoding cDNA SEQ ID NO:11.

XX KW human; Lp2005; antidiabetic; neuroprotective; nootropic;

XX KW antinflammatory; antirheumatic; antiarthritic; vulnerary; cytostatic;

XX KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;

XX KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;

XX KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;

XX KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;

XX KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;

XX KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;

XX KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;

XX KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;

XX KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;

Alzheimer's disease; inflammation; rheumatoid arthritis; wound; autoimmune disease; multiple sclerosis; cancer; lupus nephritis; systemic lupus erythematosus; gene; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 46..1206

/*tag= b

/product= "LP2005"

/note= "the present sequence only seems to encode amino acids 1 to 386 of the LP2005 protein"

46..114

/*tag= a

115..1203

/*tag= c

sig_peptide

mat_peptide

WO2004044126-A2.

27-MAY-2004.

05-NOV-2003; 2003WO-US032734.

14-NOV-2002; 2002US-0426253P.

(ELIL) LILLY & CO ELI.

Na S, Perkins DR;

WPI; 2004-411705/38.

P-PSDB; ADP19666.

New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or LP2003) for diagnosing or treating disorders associated with aberrant levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome identification.

Claim 1; SEQ ID NO 11; 111pp; English.

The present sequence encodes human LP2005, which is used in the exemplification of the present invention. The present invention describes: (1) an isolated nucleic acid (I) comprising DNA having at least 9% sequence identity to a polynucleotide selected from the group consisting of: (a) a polynucleotide having a nucleotide sequence as shown in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a polypeptide or mature form of a polypeptide having the amino acid sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide having a nucleotide sequence which is complementary to the nucleotide sequence of a polynucleotide as in (a), (b) or (c); (2) a vector comprising (1); (3) a host cell comprising the vector; (4) producing an LP polypeptide; (5) an isolated polypeptide produced by the above method and comprising an amino acid sequence comprising about 95% sequence identity to a sequence of amino acid residues comprising LP2001, LP2003, LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric molecule comprising an LP polypeptide fused to a heterologous amino acid sequence; (7) an antibody which specifically binds to an LP polypeptide described above; (8) a composition (C) comprising a therapeutic amount of an active agent selected from an LP polypeptide, an agonist to an LP polypeptide, an antagonist to an LP polypeptide, an LP polypeptide antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a polynucleotide in combination with a pharmaceutical carrier; and (9) diagnosing or treating a mammal suffering from a disease, condition or disorder associated with aberrant levels of an LP-polypeptide. (C) has antidiabetic, neuroprotective, nootropic, antiinflammatory, antirheumatic, antiarthritic, vulnerary, cytostatic, immunosuppressive, nephrotropic and dermatological activities, and can be used in gene therapy. The compositions (C) and methods are useful for diagnosing or treating disorders associated with aberrant levels of an LP polypeptide, such as diabetes and its complications, Alzheimer's disease, inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They may also be used for chromosome identification. The LP polypeptide can

CC also be used in manufacturing a medicament for the treatment of the above
CC -mentioned diseases, conditions or disorders associated with aberrant
CC levels of the LP polypeptide.
XX
SQ Sequence 1329 BP; 289 A; 379 C; 424 G; 235 T; 0 U; 2 Other;
Query Match 80.3%; Score 1117; DB 12; Length 1329;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GGCGCCGGAACAGCAGTGGAGCCCTGGGTCCTCAGTCTGTGGGGGCGAGTAGT 62
Db 48 GGCGCCGGAACAGCAGTGGAGCCCTGGGTCCTCAGTCTGTGGGGGCGAGTAGT 107
QY 63 AGTGTCTCAAAACATCACAGCCCGGATGGCGAGCCACTGGTCTGAAGTGAAGGGGC 122
Db 108 AGTGTCTCAAAACATCACAGCCCGGATGGCGAGCCACTGGTCTGAAGTGAAGGGGC 167
QY 123 CCCAAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAGCTTG 182
Db 168 CCCAAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAGCTTG 227
QY 183 GAAGTCTCTCTCCAGGAGAGAGCCCTCGGACAGTGTGGTCTGTCTTCCCAA 242
Db 228 GAAGTCTCTCTCCAGGAGAGAGCCCTCGGACAGTGTGGTCTGTCTTCCCAA 287
QY 243 CGGCTCCCTCTCTCCGCTCTCGGATCCAGGATGAGGGATTTCCGGTGCCAGGC 302
Db 288 CGGCTCCCTCTCTCCGCTCTCGGATCCAGGATGAGGGATTTCCGGTGCCAGGC 347
QY 303 AATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC 362
Db 348 AATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC 407
QY 363 TGGGAAGCCGAAATGTAGATTCTGCCTTGAACCTACAGCTGGTGTTCCTCAATAGGT 422
Db 408 TGGGAAGCCGAAATGTAGATTCTGCCTTGAACCTACAGCTGGTGTTCCTCAATAGGT 467
QY 423 GGGGACATGTCTCAGAGGAAGTACCTCGAGGACTCTTAGCTGGCATTGGATGG 482
Db 468 GGGGACATGTCTCAGAGGAAGTACCTCGAGGACTCTTAGCTGGCATTGGATGG 527
QY 483 GAAGCCCTGGTCTTAATGAGAAGGAGTATCTGTGAAGGAACAGACAGGAGACACCC 542
Db 528 GAAGCCCTGGTCTTAATGAGAAGGAGTATCTGTGAAGGAACAGACAGGAGACACCC 587
QY 543 TGAGACAGGGCTCTTACACTGAGTCTGAGGCTAATGGTGAACCCAGCCGCGGGAGAGA 602
Db 588 TGAGACAGGGCTCTTACACTGAGTCTGAGGCTAATGGTGAACCCAGCCGCGGGAGAGA 647
QY 603 TCCCGTCCACCTCTCTCTGTAGCTTACGCCAGGCTTCCCGACACCGGGCTTGG 662
Db 648 TCCCGTCCACCTCTCTCTGTAGCTTACGCCAGGCTTCCCGACACCGGGCTTGG 707
QY 663 CACAGCCCTTCCAGCCCTGTCTGGAGCCTGTGCCTCTGGAGAGGTCCAAATGGT 722
Db 708 CACAGCCCTTCCAGCCCTGTCTGGAGCCTGTGCCTCTGGAGAGGTCCAAATGGT 767
QY 723 GGTGAGCCGAGAGGTGGAGCTAGCTCTGTGTGAACCGTGAACCTGACCTGGAAT 782
Db 768 GGTGAGCCGAGAGGTGGAGCTAGCTCTGTGTGAACCGTGAACCTGACCTGGAAT 827
QY 783 CCTGCGCCAGCCCTCTCTCAATCACTGATGAAGGATGGTGCCTTGGCCCTTCC 842
Db 828 CCTGCGCCAGCCCTCTCTCAATCACTGATGAAGGATGGTGCCTTGGCCCTTCC 887
QY 843 CCCAGCCCTGTGCTGATCTTCCCTCAGATPAGGCTCAGGACCGAGGAACCTACAGCTG 902
Db 888 CCCAGCCCTGTGCTGATCTTCCCTCAGATPAGGCTCAGGACCGAGGAACCTACAGCTG 947
QY 903 TGTGGCCACCCATTCAGCCAGGCGCCCGAGGAAGCCGTGCTGTAGCATCAGCATAT 962
Db 948 TGTGGCCACCCATTCAGCCAGGCGCCCGAGGAAGCCGTGCTGTAGCATCAGCATAT 1007

QY 963 CGAAACAGCGCAGGAGGGCCCAACTGCAGGCTCTGTGGAGGATCAGGCTGGAACTCT 1022
Db 1008 CGAACCCAGCGCAGGAGGGCCCAACTGCAGGCTCTGTGGAGGATCAGGCTGGAACTCT 1067
QY 1023 AGCCCTGGCCCTGGGGATCCTGGAGGCTTGGGGACAGCCGCCCTCTCATTTGGGGTCA 1082
Db 1068 AGCCCTGGCCCTGGGGATCCTGGAGGCTTGGGGACAGCCGCCCTCTCATTTGGGGTCA 1127
QY 1083 CTTGTGGCAAGCGCGCAACCGCGAGGAGGAGG 1119
Db 1128 CTTGTGGCAAGCGCGCAACCGCGAGGAGGAGG 1164
RESULT 14
ADP19669
ID ADP19669 standard; cDNA; 1294 BP.
XX
AC ADP19669;
DT 12-AUG-2004 (first entry)
XX
DE Human LP2007 encoding cDNA SEQ ID NO:15.
XX
KW human; LP2007; antidiabetic; neuroprotective; nootropic;
KW antinflammatory; antirheumatic; antiarthritic; vulnerary; cytostatic;
KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;
KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;
KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;
KW systemic lupus erythematosus; gene; ss.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT CDS 46..1218
FT /tag= b
FT /product= "LP2007"
FT sig_peptide 46..114
FT /tag= a
FT mat_peptide 115..1215
FT /tag= c
XX
PN WO2004044126-A2.
XX
XX
PD 27-MAY-2004.
XX
PF 05-NOV-2003; 2003WO-US032734.
XX
PR 14-NOV-2002; 2002US-0426253P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Na S, Perkins DR;
XX
FI WPI; 2004-411705/38.
DR P-PSDB; ADP19670.
XX
PT New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or
PT LP2003) for diagnosing or treating disorders associated with aberrant
PT levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome
PT identification.
XX
PS Example 2; SEQ ID NO 15; 111pp; English.
XX
CC The present sequence encodes human LP2007, which is used in the
CC exemplification of the present invention. The present invention
CC describes: (1) an isolated nucleic acid (1) comprising DNA having at
CC least 95% sequence identity to a polynucleotide selected from the group
CC consisting of: (a) a polynucleotide having a nucleotide sequence as shown
CC in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a
CC polypeptide or mature form of a polypeptide having the amino acid
CC sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide
CC fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide

CC having a nucleotide sequence which is complementary to the nucleotide
 CC sequence of a polynucleotide as in (a), (b) or (c); (2) a vector
 CC comprising (1); (3) a host cell comprising the vector; (4) producing an
 CC LP polypeptide; (5) an isolated polypeptide produced by the above method
 CC and comprising an amino acid sequence comprising about 95% sequence
 CC identity to a sequence of amino acid residues comprising LP2001, LP2003,
 CC LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric
 CC molecule comprising an LP polypeptide fused to a heterologous amino acid
 CC sequence; (7) an antibody which specifically binds to an LP polypeptide
 CC described above; (8) a composition (C) comprising a therapeutic amount of
 CC polypeptide, an agonist to an LP polypeptide, an antagonist to an LP
 CC polypeptide, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a
 CC antibody, in combination with a pharmaceutical carrier; and (9)
 CC diagnosing or treating a mammal suffering from a disease, condition or
 CC disorder associated with aberrant levels of an LP-polypeptide. (C) has
 CC antidiabetic, neuroprotective, nootropic, antiinflammatory,
 CC antirheumatic, antiarthritic, vulnerary, cytostatic, immunosuppressive,
 CC nephrotropic and dermatological activities, and can be used in gene
 CC therapy. The compositions (C) and methods are useful for diagnosing or
 CC treating disorders associated with aberrant levels of an LP polypeptide,
 CC such as diabetes and its complications, Alzheimer's disease,
 CC inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple
 CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They
 CC may also be used for chromosome identification. The LP polypeptide can
 CC also be used in manufacturing a medicament for the treatment of the above
 CC -mentioned diseases, conditions or disorders associated with aberrant
 CC levels of the LP polypeptide.

SQ Sequence 1294 BP; 282 A; 367 C; 414 G; 229 T; 0 U; 2 Other;

Query Match 78.2%; Score 1088; DB 12; Length 1294;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 GCGAGAGGCCCTGGGACAGTGGCTCGTGTCTTCCCAACGGCTCTCTTCCTCC 260
 DB 204 GCGAGAGGCCCTGGGACAGTGGCTCGTGTCTTCCCAACGGCTCTCTTCCTCC 263
 QY 261 GGCTGTGGGATCAGGATCAGGGGATTTTCCGGTGCAGGCAATGAACAGGAATGAAA 320
 DB 264 GGCTGTGGGATCAGGATCAGGGGATTTTCCGGTGCAGGCAATGAACAGGAATGAAA 323
 QY 321 GGAGACCAAGTCCAATACCGAGTCCGTGTCTACCAAGATTCCTGGGAAGCCAGAAATTGT 380
 DB 324 GGAGACCAAGTCCAATACCGAGTCCGTGTCTACCAAGATTCCTGGGAAGCCAGAAATTGT 383
 QY 381 AGATTCTGCTCTGAATCAGGCTGGTGTCTCCATTAAGTGGGACATGTGTGCAGA 440
 DB 384 AGATTCTGCTCTGAATCAGGCTGGTGTCTCCATTAAGTGGGACATGTGTGCAGA 443
 QY 441 GCGAAGCTACCCGCGAGGACTTTAGCTGGCACTTGGATGGGAAGCCCTGGTGCTAA 500
 DB 444 GCGAAGCTACCCGCGAGGACTTTAGCTGGCACTTGGATGGGAAGCCCTGGTGCTAA 503
 QY 501 TGAGAAGGGAGTATCTGTGAAGAAACAGACAGGAGACACCCCTGAGACAGGGCTCTTTCAC 560
 DB 504 TGAGAAGGGAGTATCTGTGAAGAAACAGACAGGAGACACCCCTGAGACAGGGCTCTTTCAC 563
 QY 561 ACTGCAGTCCGAGCTAATGTGATACCCAGCCCGGGAGGAGATCCCGTCCCACTTCTTC 620
 DB 564 ACTGCAGTCCGAGCTAATGTGATACCCAGCCCGGGAGGAGATCCCGTCCCACTTCTTC 623
 QY 621 CTGTAGCTTCAGCCAGGCTCTCCCGACACCGGGCTTGGCGACAGCCCGCCATCCAGCC 680
 DB 624 CTGTAGCTTCAGCCAGGCTCTCCCGACACCGGGCTTGGCGACAGCCCGCCATCCAGCC 683
 QY 681 CCCTGTCTGGAGCTGTGCTCTGAGAGAGGTCCAATTGGTGGTGGAGCCAGAGGTGG 740
 DB 684 CCCTGTCTGGAGCTGTGCTCTGAGAGAGGTCCAATTGGTGGTGGAGCCAGAGGTGG 743
 QY 741 AGCAGTAGCTCTCTGGTGGAAACCGTAACCTTGACTGTGAAGTCCCTGGCCAGCCCTCTCC 800

DB 744 AGCAGTAGCTCTCTGGTGGAAACCGTAACCTGACCTGTGAAGTCCCTGCCCAGCCCTCTCC 803
 QY 801 TCAAAATCCATCGATGAAGATGCTGTGCTCCCTTCCCTCCCTCCCTCCCTGCTGTGCTGAT 860
 DB 804 TCAAAATCCATCGATGAAGATGCTGTGCTCCCTTCCCTCCCTCCCTGCTGTGCTGAT 863
 QY 861 CTCTCCCTGATAGGAGCTCTCAGACACAGGAACTTACAGCTGTGTGGCCACCCATTCAG 920
 DB 864 CTCTCCCTGATAGGAGCTCTCAGACACAGGAACTTACAGCTGTGTGGCCACCCATTCAG 923
 QY 921 CCACGGGCCCCAGGAAAGCCGCTCTGTACGATCAGCATCATCGAACCCAGCCGAGGAGG 980
 DB 924 CCACGGGCCCCAGGAAAGCCGCTCTGTACGATCAGCATCATCGAACCCAGCCGAGGAGG 983
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 XX AC ADE95565;
 XX AC AC
 XX DT 12-FEB-2004 (first entry)
 XX DT
 XX DE Human NOVX16d protein cDNA sequence.
 KW NOVX protein; biochemical stimulation; physiological stimulation;
 KW cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
 KW antirheumatic; antiarthritic; antidiabetic; nephrotropic; dermatological;
 KW immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;
 KW nootropic; antipsoriatic; antiparkinsonian; antidiabetic; neuroleptic;
 KW antidepressant; antiallergic; gynaecological; gene therapy; vaccine;
 KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;
 KW cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;
 KW psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;
 KW Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;
 KW depression; allergy; fertility disorder; gene; ss; NOVX16d.
 XX Homo sapiens.
 XX OS
 XX WO2003050245-A2.
 XX PN
 XX PD 19-JUN-2003.
 XX PF
 XX 03-DEC-2002; 2002WO-US038594.
 XX PR
 XX 05-DEC-2001; 2001US-0336600P.
 XX PR 07-DEC-2001; 2001US-0338285P.
 XX PR 12-DEC-2001; 2001US-0341346P.
 XX PR 17-DEC-2001; 2001US-0341477P.

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PR 15-MAY-2002; 2002US-0380981P.
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XX
XX (CURA-) CURAGEN CORP.
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XX Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru RA;
PI Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X;
PI Jeffers ME, Ji W, Li L, Malvankar UM, Miller CE, Murphy R;
PI Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG;
PI Smithson G, Scarling R, Taupier RJ, Voss EZ, Zhong H, Zhong M;
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DR WPI; 2003-513974/48.
DR P-PSDB; ADE95566.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 20; SEQ ID NO 97; 211bp; English.
XX
XX This invention relates to novel NOVX proteins, and the DNA sequence which
CC encode them, having properties related to stimulation of biochemical or
CC physiological responses in a cell, a tissue, an organ or an organism.
CC Compounds which modulate the proteins of the invention may have cardiac,
CC antiarrhythmic, hypotensive, cytostatic, anorectic, antirheumatic,
CC antiarthritic, antidiabetic, nephrotropic, dermatological,
CC immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,
CC nootropic, antipsoriatic, antiparkinsonian, antiasthmatic, neuroleptic,
CC antidepressant, antiallergic or gynaecological activities. The DNA
CC sequences of the invention may be useful for gene therapy whilst the
CC protein sequences may allow the development of a vaccine. The protein is
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease. The invention may be useful in
CC diagnosing, treating or preventing NOVX-associated disorders, for example
CC cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
CC rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin
CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
CC Parkinson's disease, asthma, schizophrenia, depression, allergies or
CC fertility disorders. The nucleic acids may further be used as
CC hybridisation probes, in chromosome mapping, tissue typing, preventive
CC medicine, and pharmacogenomics. The present sequence is the cDNA sequence
CC which encodes the human NOVX16d protein of the invention.
XX
SQ Sequence 1226 BP; 270 A; 348 C; 397 G; 211 T; 0 U; 0 Other;

Query Match 75.1%; Score 1044; DB 10; Length 1226;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1044; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1018	73.2	1023	2	US-08-633-148-1
5	873	62.8	1405	4	US-08-755-235-3
6	852	61.3	957	2	US-08-633-148-3
7	274	19.7	5816	4	US-09-949-016-16900
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ALIGNMENTS

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US-09-638-649-4
; Sequence 4, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Van, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1391
; TYPE: DNA
; ORGANISM: Human
US-09-638-649-4

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				Indels	0;
				Gaps	0;
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; Patent No. 6825164
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; APPLICANT: Zlokovic, Berislav
; TITLE OF INVENTION: A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID
; FILE REFERENCE: 0575/62097
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1391
; TYPE: DNA
; ORGANISM: Human
US-09-638-648-4
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Query Match 92.7%; Score 1289; DB 4; Length 1391;
Best Local Similarity 99.9%; Pred. No. 0;
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Db ACTGAGGAGGCTTGGAGGGCCACAGACAGATCCCATCCATCAGCTCCCTTTCTTTTTC 1260
QY 1261 CTTGAACTGTTTGGCCCTCAGACCAACTCTCTCTGTATATAATCTCTCTCTGTATAACC 1320
Db CTTGAACTGTTTGGCCCTCAGACCAACTCTCTCTGTATATAATCTCTCTCTGTATAACC 1320
QY 1321 CCACCTTGCAGGCTTCTTCAACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1380
Db CCACCTTGCAGGCTTCTTCAACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1380
QY 1381 CACATCTTGCA 1391
Db CACATCTTGCA 1391

RESULT 3
US-09-949-016-5154
; Sequence 5154, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5154
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Human

US-09-949-016-5154

Query Match 87.2%; Score 1213; DB 4; Length 1215;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAGCCGGAAACAGCAGTTGGAGCCCTGGGTGCTCTCAGTCTGTGGGGGGCAGTAGT 62
Db 3 GGAGCCGGAAACAGCAGTTGGAGCCCTGGGTGCTCTCAGTCTGTGGGGGGCAGTAGT 62
QY 63 AGGTGCTCAAAACATCACAGCCGGATTCGCGAGCCACTGGTCTGAAGTGAAGGGGGC 122
Db 63 AGGTGCTCAAAACATCACAGCCGGATTCGCGAGCCACTGGTCTGAAGTGAAGGGGGC 122
QY 123 CCCAAGAAACACACCCCGAGCGCTGGAATGGAACCTGAAACACAGGCGGACAGAGCTTG 182
Db 123 CCCAAGAAACACACCCCGAGCGCTGGAATGGAACCTGAAACACAGGCGGACAGAGCTTG 182
QY 183 GAAGTCTCTGTCTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 242
Db 183 GAAGTCTCTGTCTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 242
QY 243 CGGCTCCCTCTCTCTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 302
Db 243 CGGCTCCCTCTCTCTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 302
QY 303 AATGAACAGGAAATGGAAGGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTTACCAGATTCC 362
Db 303 AATGAACAGGAAATGGAAGGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTTACCAGATTCC 362
QY 363 TGGGAAGCCAGAAATTTGTAGATTCTGCTCTGAACTCAAGCTGGTGTCTCCCAATAAGGT 422
Db 363 TGGGAAGCCAGAAATTTGTAGATTCTGCTCTGAACTCAAGCTGGTGTCTCCCAATAAGGT 422
QY 423 GGGGACATGTGTGTCAGAGGAGGAGTACCTCGAGGAGTCTTAGCTGGCACTTGGATGG 482
Db 423 GGGGACATGTGTGTCAGAGGAGGAGTACCTCGAGGAGTCTTAGCTGGCACTTGGATGG 482
QY 483 GAAGCCCTCTGGTGCCTAATGAGAGGAGGAGTATCTGTGAAGGAAACAGACACAGGAGACCC 542
Db 483 GAAGCCCTCTGGTGCCTAATGAGAGGAGGAGTATCTGTGAAGGAAACAGACACAGGAGACCC 542
QY 543 TGAGACAGGCTCTTCACTGAGTGGAGCTAATGGTGAACCCAGCCCGGGAGGAGA 602
Db 543 TGAGACAGGCTCTTCACTGAGTGGAGCTAATGGTGAACCCAGCCCGGGAGGAGA 602
QY 603 TCCCGTCCCACTCTCTGAGTTCAGCCAGGCTTCCCGGACACCGGGCCCTTGGC 662
Db 603 TCCCGTCCCACTCTCTGAGTTCAGCCAGGCTTCCCGGACACCGGGCCCTTGGC 662
QY 663 CACAGCCCCATCCAGCCCGGTGTCTGGAGGCTGTGCTCTGGAGAGGTCCAATTGGT 722
Db 663 CACAGCCCCATCCAGCCCGGTGTCTGGAGGCTGTGCTCTGGAGAGGTCCAATTGGT 722
QY 723 GGTGGAGCCAGAAAGGTGGAGCAGTAGTCTCTGGTGAACCGTAACCCCTGACCTGTGAAGT 782
Db 723 GGTGGAGCCAGAAAGGTGGAGCAGTAGTCTCTGGTGAACCGTAACCCCTGACCTGTGAAGT 782
QY 783 CCTGCGCAGCCCTCTCTCAATCCACTGGATGAAGATGGTGTGCCCTTGGCCCTTCC 842
Db 783 CCTGCGCAGCCCTCTCTCAATCCACTGGATGAAGATGGTGTGCCCTTGGCCCTTCC 842
QY 843 CCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGGCTCAGGACACAGGAAACCTACAGCTG 902
Db 843 CCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGGCTCAGGACACAGGAAACCTACAGCTG 902
QY 903 TGTGGCCACCAATTCAGCCACGGGCCCCAGGAAAGCCGTGTGTGAGCATCAGCATCAT 962
Db 903 TGTGGCCACCAATTCAGCCACGGGCCCCAGGAAAGCCGTGTGTGAGCATCAGCATCAT 962
QY 963 CGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1022
Db 963 CGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1022

Result No.	Score	Query Match	Length	DB	ID	Description
1	1391	100.0	1391	16	US-10-091-019-1	Sequence 1, Appli
2	1389	99.9	1415	18	US-10-115-635-351	Sequence 351, Appli
3	1162	83.5	1217	17	US-10-309-290-95	Sequence 95, Appli
4	1044	75.1	1226	17	US-10-309-290-97	Sequence 97, Appli
5	1015	73.0	1173	17	US-10-309-290-99	Sequence 99, Appli
6	1013	72.8	1020	16	US-10-091-019-2	Sequence 2, Appli
7	990	71.2	1223	19	US-10-473-507A-1	Sequence 1, Appli
8	973	69.9	1463	18	US-10-115-635-352	Sequence 352, Appli
9	873	62.8	1405	8	US-08-903-709-3	Sequence 3, Appli
10	873	62.8	1405	8	US-08-755-235-3	Sequence 3, Appli
11	873	62.8	1405	8	US-10-850-861-3	Sequence 3, Appli

QY 121 GCCCCCAAGAAACCAACCCAGAGGCTGGAAATGGAACCTGAACACAGCCCGGACAGAACT 180
DB 121 GCCCCCAAGAAACCAACCCAGAGGCTGGAAATGGAACCTGAACACAGCCCGGACAGAACT 180
QY 181 TGAAGGTCTGTCTCCCAAGGAGAGGCCCTGGGAAGTGTGGCTGTGTCTTCCC 240
DB 181 TGAAGGTCTGTCTCCCAAGGAGAGGCCCTGGGAAGTGTGGCTGTGTCTTCCC 240
QY 241 AACGGCTCCCTCTTCCCTCCGGCTGCGGATCCAGGATGAGGGATTTTCGGTCCAG 300
DB 241 AACGGCTCCCTCTTCCCTCCGGCTGCGGATCCAGGATGAGGGATTTTCGGTCCAG 300
QY 301 GCAATCAACAGGAATGGAAGAGAGCAAGTCCAACTACCGAGTCCAGTCCAGATT 360
DB 301 GCAATCAACAGGAATGGAAGAGAGCAAGTCCAACTACCGAGTCCAGTCCAGATT 360
QY 361 CTTGGGAAGCCAGAAATTTAGATTCTGCTCTGAATCTACCGCTGGTGTTCCTAATAG 420
DB 361 CTTGGGAAGCCAGAAATTTAGATTCTGCTCTGAATCTACCGCTGGTGTTCCTAATAG 420
QY 421 GTGGGACATGTGTGTCAGAGGAAGCTACCTGACAGGACTCTTAGCTGGCACTTGGAT 480
DB 421 GTGGGACATGTGTGTCAGAGGAAGCTACCTGACAGGACTCTTAGCTGGCACTTGGAT 480
QY 481 GGAAGCCCTGTGCTTAATGAGAGGAGTATCTGTGAAGGAACAGACCAGGACAC 540
DB 481 GGAAGCCCTGTGCTTAATGAGAGGAGTATCTGTGAAGGAACAGACCAGGACAC 540
QY 541 CTTGAGACAGGCTCTTCACTGCACTGAGTGGAGCTAATGTGACCCAGCCCGGGAGGA 600
DB 541 CTTGAGACAGGCTCTTCACTGCACTGAGTGGAGCTAATGTGACCCAGCCCGGGAGGA 600
QY 601 GATCCCGTCCCACTCTCTGCTAGCTTACAGCCAGGCTTCCCGACACCGGGCTTG 660
DB 601 GATCCCGTCCCACTCTCTGCTAGCTTACAGCCAGGCTTCCCGACACCGGGCTTG 660
QY 661 CGCACAGCCCTCTGCTAGCTTACAGCCAGGCTTCCCGACACCGGGCTTG 720
DB 661 CGCACAGCCCTCTGCTAGCTTACAGCCAGGCTTCCCGACACCGGGCTTG 720
QY 721 GTGGTGGAGCAGAGGTGAGCAGTAGCTCTGTGGTGGAAACCTGACCTGTGAA 780
DB 721 GTGGTGGAGCAGAGGTGAGCAGTAGCTCTGTGGTGGAAACCTGACCTGTGAA 780
QY 781 GTCCCTGCCAGCCCTCTCTCAATCTCAATCTGATGAAGATGTGTGCCCTTGCCCTT 840
DB 781 GTCCCTGCCAGCCCTCTCTCAATCTCAATCTGATGAAGATGTGTGCCCTTGCCCTT 840
QY 841 CCCCCAGCCCTGTGTGATCTCTCCCTGATAGGGCTCAGGACAGGGAACTTACAGC 900
DB 841 CCCCCAGCCCTGTGTGATCTCTCCCTGATAGGGCTCAGGACAGGGAACTTACAGC 900
QY 901 TGTGTGGCCACCAATTCAGCCAGGCCCCAGGAAGCGTGTGTGACATCAGCATC 960
DB 901 TGTGTGGCCACCAATTCAGCCAGGCCCCAGGAAGCGTGTGTGACATCAGCATC 960
QY 961 ATCGAACCGCAGGAGGGGCAACTGTGAGGAGTCTGTGGAGATCAGGGCTGGAACT 1020
DB 961 ATCGAACCGCAGGAGGGGCAACTGTGAGGAGTCTGTGGAGATCAGGGCTGGAACT 1020
QY 1021 CTAGCCCTGGCCCTGGGGATCTTGGAGGCTGGGAACAGCCCGCTGTCTATTTGGGTC 1080
DB 1021 CTAGCCCTGGCCCTGGGGATCTTGGAGGCTGGGAACAGCCCGCTGTCTATTTGGGTC 1080
QY 1081 ATCTTGTGGCAAGCGGCAACCGCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
DB 1081 ATCTTGTGGCAAGCGGCAACCGCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY 1141 GAAGGAGGAGGCTGTGAGAACTGAATCAGTGGAGGAACTGAGGAGGAGGAGTAGT 1200
DB 1141 GAAGGAGGAGGCTGTGAGAACTGAATCAGTGGAGGAACTGAGGAGGAGGAGTAGT 1200
QY 1201 ACTGAGGGCTTGAGGGGCCCAACAGACAGATCCATCCATCCATCTTTTTC 1260

RESULT 2

US-10-115-635-351
; Sequence 351, Application US/10115635
; Publication No. US20040137434A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Bing
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aodong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 797CON
; CURRENT APPLICATION NUMBER: US/10/115,635
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/714,936
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 362
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 351
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(1239)
US-10-115-635-351

Query Match 99.9%; Score 1389; DB 18; Length 1415;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAGCCGGAACAGCAGTTGGAGCCCTGGGTGTGTCTCAGTCTGTGGGGGCACTAGT 62
DB 27 GGAGCCGGAACAGCAGTTGGAGCCCTGGGTGTGTCTCAGTCTGTGGGGGCACTAGT 86
QY 63 AGTGTCTCAAAACATCACAGCCGGATTGGCGAGCCACTGGTGTCTGAAGTGAAGGGGC 122
DB 87 AGTGTCTCAAAACATCACAGCCGGATTGGCGAGCCACTGGTGTCTGAAGTGAAGGGGC 146
QY 123 CCCCAGAAACCAACCCAGCGCTGGAATGGAACCTGAACACAGGCCGACAGAACTTG 182
DB 147 CCCCAGAAACCAACCCAGCGCTGGAATGGAACCTGAACACAGGCCGACAGAACTTG 206
QY 183 GAAGGTCTGTCTTCCCAGGAGGAGGCCCTGGGACAGTGTGGCTGTCTTCCCAA 242
DB 207 GAAGGTCTGTCTTCCCAGGAGGAGGCCCTGGGACAGTGTGGCTGTCTTCCCAA 266
QY 243 CGGCTCCCTCTTCCGCTCTCGGATCCAGGATGAGGGGATTTTCCGTCGCCAGGC 302

Db 267 CGGCTCCCTCTCTCCGCTGTGCGGATCCAGATGAGGGGATTTTCCGGTGCCAGGC 326
QY 303 AATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTC 362
Db 327 AATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTC 386
QY 363 TGGGAAGCAGAAATTTGTAGATTCTGCCCTCTGAACTCAGGGCTGGTGTTCCTCAATAAGT 422
Db 387 TGGGAAGCAGAAATTTGTAGATTCTGCCCTCTGAACTCAGGGCTGGTGTTCCTCAATAAGT 446
QY 423 GGGGACATGTGTGTCAGAGGAGCTACCTGCAGGACTCTTAGCTGGCACTTGGATGG 482
Db 447 GGGGACATGTGTGTCAGAGGAGCTACCTGCAGGACTCTTAGCTGGCACTTGGATGG 506
QY 483 GAAGCCCTGGTGCCTTAATGAGAAGGAGTATCTGTGAAGGAACAGACAGAGACACCC 542
Db 507 GAAGCCCTGGTGCCTTAATGAGAAGGAGTATCTGTGAAGGAACAGACAGAGACACCC 566
QY 543 TGAGACAGGGCTCTTACACTGAGTCGAGCTAATGTGACCCAGCCGCGGGAGGAGA 602
Db 567 TGAGACAGGGCTCTTACACTGAGTCGAGCTAATGTGACCCAGCCGCGGGAGGAGA 626
QY 603 TCCCGTCCCACTCTCTCTGTAGCTTACGCCAGGCCCTTCCCGACACCGGCCCTTGG 662
Db 627 TCCCGTCCCACTCTCTCTGTAGCTTACGCCAGGCCCTTCCCGACACCGGCCCTTGG 686
QY 663 CACAGCCCCATCCAGCCCCGTGTCTGGAGCGCTGTGCCCTCTGGAGAGGTCCAATTGT 722
Db 687 CACAGCCCCATCCAGCCCCGTGTCTGGAGCGCTGTGCCCTCTGGAGAGGTCCAATTGT 746
QY 723 GGTGGAGCAGAAAGTGGAGCTAGTCTCTGTGGTGAACCGTAACCCCTGACCTGTGAAGT 782
Db 747 GGTGGAGCAGAAAGTGGAGCTAGTCTCTGTGGTGAACCGTAACCCCTGACCTGTGAAGT 806
QY 783 CCTGCGCCAGCCCTCTCTCAATCACTGATGAGGATGTGTGCCCTTCCGCCCTTCC 842
Db 807 CCTGCGCCAGCCCTCTCTCAATCACTGATGAGGATGTGTGCCCTTCCGCCCTTCC 866
QY 843 CCCCAGCCCTGTGCTGATCTCTCCAGATAGGGCTCAGGACCCAGGAACTCAGAGTG 902
Db 867 CCCCAGCCCTGTGCTGATCTCTCCAGATAGGGCTCAGGACCCAGGAACTCAGAGTG 926
QY 903 TGTGGCCACCATTCAGCCACGGGCCCCAGGAAGCCGTGTGTGAGCATCAGCATAT 962
Db 927 TGTGGCCACCATTCAGCCACGGGCCCCAGGAAGCCGTGTGTGAGCATCAGCATAT 986
QY 963 CGAACCAGGCGAGGGGCCCAACTGCAGGCTCTGTGGAGGATCAGGCTGGGAACCT 1022
Db 987 CGAACCAGGCGAGGGGCCCAACTGCAGGCTCTGTGGAGGATCAGGCTGGGAACCT 1046
QY 1023 AGCCCTGGCCCTGGGGATCTTGGAGGCTTGGGACAGCGGCCCTGCTCATTTGGGGTAT 1082
Db 1047 AGCCCTGGCCCTGGGGATCTTGGAGGCTTGGGACAGCGGCCCTGCTCATTTGGGGTAT 1106
QY 1083 CTTTGTGGAAAGCGCGCAACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1142
Db 1107 CTTTGTGGAAAGCGCGCAACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1166
QY 1143 AGAGGAGGAGCGTGCAGAGTGAATCAGTCGAGGAACCTGAGGCGAGGCGAGGTAGTAC 1202
Db 1167 AGAGGAGGAGCGTGCAGAGTGAATCAGTCGAGGAACCTGAGGCGAGGCGAGGTAGTAC 1226
QY 1203 TGGAGGGCTTGGGGGCCACAGACAGATCCCATCAGCTCCCTTTCTTTTTCCTCC 1262
Db 1227 TGGAGGGCTTGGGGGCCACAGACAGATCCCATCAGCTCCCTTTCTTTTTCCTCC 1286
QY 1263 TTGAATCTTGTGGCTCAGACCAACTCTCTCTGTATATCTCTCTCTGTATTAACCCC 1322
Db 1287 TTGAATCTTGTGGCTCAGACCAACTCTCTCTGTATATCTCTCTCTGTATTAACCCC 1346
QY 1323 ACCTTCCCAAGCTTTCTTACACAGAGCCCCCAGATGATGATTAACACCTGACA 1382
Db 1347 ACCTTCCCAAGCTTTCTTACACAGAGCCCCCAGATGATGATTAACACCTGACA 1406

RESULT 3

US-10-309-290-95
; Sequence 95, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphy, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenn
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Hailong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 95
; LENGTH: 1217
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(1214)
US-10-309-290-95

Query Match		83.5%;	Score 1162;	DB 17;	Length 1217;		
Best Local Similarity		99.9%;	Pred. No. 0;				
Matches 1212;		Conservative	0;	Mismatches	1;	Indels	0; Gaps 0;
QY	3	GGCAGCCGGAACACAGCAGTGTGAGCCTGGTGTGCTGCTCCTCAGTCTGTGGGGGAGTGT	62				
DB	5	GGCAGCCGGAACACAGCAGTGTGAGCCTGGTGTGCTCCTCAGTCTGTGGGGGAGTGT	64				
QY	63	AGGTGCTCAAAACATACAGCCGATTTGGCGAGCCACTGGTCTGAGTGTAAAGGGGC	122				
DB	65	AGGTGCTCAAAACATACAGCTCGATTGGCGAGCCACTGGTCTGAGTGTAAAGGGGC	124				
QY	123	CCCCAAGAAACCCACCCAGCGGCTTGGAACTGAAACACAGGCCGACAGAAAGCTTG	182				
DB	125	CCCCAAGAAACCCACCCAGCGGCTTGGAACTGAAACACAGGCCGACAGAAAGCTTG	184				
QY	183	GAAGTCTGTCTCCCGCAGGAGAGGCCCTCGTGGACAGTGTGGCTGTCTTCCCAA	242				
DB	185	GAAGTCTGTCTCCCGCAGGAGAGGCCCTCGTGGACAGTGTGGCTGTCTTCCCAA	244				
QY	243	CGGCTCCCTCTCTCTCCGCTGTCCGATTCAGGATGAGGGATTTTCGGTCCAGGC	302				
DB	245	CGGCTCCCTCTCTCTCCGCTGTCCGATTCAGGATGAGGGATTTTCGGTCCAGGC	304				
QY	303	AATGAACAGAAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC	362				
DB	305	AATGAACAGAAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC	364				
QY	363	TGGGAGCCAGAAATGTAGATTTCCTCTGACTCAAGTCCAGGCTGGTGTCCCAATAGGT	422				
DB	365	TGGGAGCCAGAAATGTAGATTTCCTCTGACTCAAGTCCAGGCTGGTGTCCCAATAGGT	424				
QY	423	GGGGACATGTGTGTACAGGGAAGTACCTCGCAGGACTCTTAGCTGGCATTGTGATGG	482				
DB	425	GGGGACATGTGTGTACAGGGAAGTACCTCGCAGGACTCTTAGCTGGCATTGTGATGG	484				
QY	483	GAAGCCCTGGTGCCTAATGAAAGGAGTATCTGTGAAGGAACAGACAGGAGACACC	542				
DB	485	GAAGCCCTGGTGCCTAATGAAAGGAGTATCTGTGAAGGAACAGACAGGAGACACC	544				
QY	543	TGAGACAGGCTCTTACACTGAGTCGGAGCTAATGTTGACCCAGCCCGGGAGGAGA	602				
DB	545	TGAGACAGGCTCTTACACTGAGTCGGAGCTAATGTTGACCCAGCCCGGGAGGAGA	604				
QY	603	TCCCGCTCCACCTCTCTCTGTAGTTACGCCAGGCTTCCCGACACCGGGCTTTGG	662				
DB	605	TCCCGCTCCACCTCTCTCTGTAGTTACGCCAGGCTTCCCGACACCGGGCTTTGG	664				
QY	663	CACAGCCCGATCCAGCCCGTGTCTGGAGCTGTGCTCTGGAGAGGTCCAAATTGT	722				
DB	665	CACAGCCCGATCCAGCCCGTGTCTGGAGCTGTGCTCTGGAGAGGTCCAAATTGT	724				
QY	723	GTGGAGCCAGAGGTGGAGCTAGCTCTGTGTGAACCGTAACCTGACCTGTGAAGT	782				
DB	725	GTGGAGCCAGAGGTGGAGCTAGCTCTGTGTGAACCGTAACCTGACCTGTGAAGT	784				
QY	783	CCCTGCCAGCCCTCTCTCAATCCACTGGATGAGTGTGTGCTTGCCTTGCCTTCC	842				
DB	785	CCCTGCCAGCCCTCTCTCAATCCACTGGATGAGTGTGTGCTTGCCTTGCCTTCC	844				
QY	843	CCCCAGCCCTGTGCTGATCTCTCCTAGATAGGCTCTAGGACAGGGAACCTACAGTGT	902				
DB	845	CCCCAGCCCTGTGCTGATCTCTCCTAGATAGGCTCTAGGACAGGGAACCTACAGTGT	904				
QY	903	TGTGGCCACCCATCTCCAGCCACGGGCCCCAGGAAAGCCGTGTGTGATCAGATCAT	962				
DB	905	TGTGGCCACCCATCTCCAGCCACGGGCCCCAGGAAAGCCGTGTGTGATCAGATCAT	964				
QY	963	CGAACCCAGCGAGGAGGGCCAACTGACAGCTCTGTGGAGGATCAGGGCTGGAACTCT	1022				
DB	965	CGAACCCAGCGAGGAGGGCCAACTGACAGCTCTGTGGAGGATCAGGGCTGGAACTCT	1024				

RESULT 4

US-10-309-290-97
; Sequence 97, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphy, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15

Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuroSeqlist version 0.1
; SEQ ID NO 97
; LENGTH: 1226
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (25)..(1194)
US-10-309-290-97

Query Match 75.1%; Score 1044; DB 17; Length 1226;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1044; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 GGGAGAGGCCCTGGGACAGTGTGCTGCTTCCCAACGGCTCCCTCTTCCTCC 260
DB 183 GGGAGAGGCCCTGGGACAGTGTGCTGCTTCCCAACGGCTCCCTCTTCCTCC 242
QY 261 GGCTGTGGGATCCAGGATGAGGGGATTTTCCGGTCCAGGCAATGAACAGGAATGGAAA 320
DB 243 GGCTGTGGGATCCAGGATGAGGGGATTTTCCGGTCCAGGCAATGAACAGGAATGGAAA 302
QY 321 GGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTTCTGGGAAGCCAGAAATTGT 380
DB 303 GGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTTCTGGGAAGCCAGAAATTGT 362
QY 381 AGATTCTGCTCTGAACTACCGCTGGTGTTCCTCAATAGGTGGGACATGTGTGCAGA 440
DB 363 AGATTCTGCTCTGAACTACCGCTGGTGTTCCTCAATAGGTGGGACATGTGTGCAGA 422
QY 441 GGGAACTACCTTCAGGAGACTCTTAGCTGGCACTTGGATGGGAAGCCCTGTGTGCTTAA 500
DB 423 GGGAACTACCTTCAGGAGACTCTTAGCTGGCACTTGGATGGGAAGCCCTGTGTGCTTAA 482
QY 501 TGAGAGGAGATCTGTGAGGAAACAGACAGGAGACACCTTGAGACAGGGCTCTTTCAC 560
DB 483 TGAGAGGAGATCTGTGAGGAAACAGACAGGAGACACCTTGAGACAGGGCTCTTTCAC 542
QY 561 ACTGAGTGGAGCTAATGGTACCCAGCACCGGGCTTTGGCAGACAGCCGCCATCCAGCC 620
DB 543 ACTGAGTGGAGCTAATGGTACCCAGCACCGGGCTTTGGCAGACAGCCGCCATCCAGCC 602
QY 621 CTGTAGCTTCAGCCAGGCTTCCCGACACCGGGCTTTGGCAGACAGCCGCCATCCAGCC 680
DB 603 CTGTAGCTTCAGCCAGGCTTCCCGACACCGGGCTTTGGCAGACAGCCGCCATCCAGCC 662
QY 681 CGGTGTGGGAGCTGTGCTCTGAGGAGGTCCAAATGGTGGTGGAGCCAGAGGTGG 740
DB 663 CGGTGTGGGAGCTGTGCTCTGAGGAGGTCCAAATGGTGGTGGAGCCAGAGGTGG 722
QY 741 AGCAGTAGCTCTGGTGGAACTGACCTGACCTGAGTCCCTGCCAGCCCTCTCC 800
DB 723 AGCAGTAGCTCTGGTGGAACTGACCTGACCTGAGTCCCTGCCAGCCCTCTCC 782
QY 801 TCAATCCACTGATGAAGATGGTGTGCCCTTGGCCCTTCCCGCCAGCCCTGTGTGAT 860
DB 783 TCAATCCACTGATGAAGATGGTGTGCCCTTGGCCCTTCCCGCCAGCCCTGTGTGAT 842
QY 861 CTCTCTGATAGGCTCTCAGGACAGGAACTTACAGTGTGTGGCCACCCATTCAG 920
DB 843 CTCTCTGATAGGCTCTCAGGACAGGAACTTACAGTGTGTGGCCACCCATTCAG 902
QY 921 CCAGGGCCCCAGGAAAGCGTGTCTGACGATCAGCATCATCGAACAGGCGAGAGG 980
DB 903 CCAGGGCCCCAGGAAAGCGTGTCTGACGATCAGCATCATCGAACAGGCGAGAGG 962
QY 981 GCCAATCGAGGCTCTGTGGAGGATCAGGGCTGGAACTCTAGCCTTGCCCTGGGGAT 1040
DB 963 GCCAATCGAGGCTCTGTGGAGGATCAGGGCTGGAACTCTAGCCTTGCCCTGGGGAT 1022
QY 1041 CTGGGAGGCTGGGGACAGCCGCTGCTCATTTGGGGTTCATTTGTGGCAAGGCGGCA 1100

RESULT 5

US-10-309-290-99
; Sequence 99, Application US/10309290
; Publication NO. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malvankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glennda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.

DB 1023 CTGGAGGCCCTGGGACAGCCGCTGCTCATTTGGGGTCATCTTGTGCAAGGCGGCA 1082
QY 1101 AGCCCGAGGAGGAGAGAGAGGCCGCCAGAAAACACAGGAGGAGAGAGGAGGCTCAGA 1160
DB 1083 AGCCCGAGGAGGAGAGAGAGGCCGCCAGAAAACACAGGAGGAGAGAGGAGGCTCAGA 1142
QY 1161 ACTGAATCAGTCGAGAGGAACCTTGAGGAGGCGGAGAGTAGTACTTGAGAGGCTTTGAGGGGC 1220
DB 1143 ACTGAATCAGTCGAGAGGAACCTTGAGGAGGCGGAGAGTAGTACTTGAGAGGCTTTGAGGGGC 1202
QY 1221 CCACAGACAGATCCCATCCATCAG 1244
DB 1203 CCACAGACAGATCCCATCCATCAG 1226

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; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CurationList version 0.1
; SEQ ID NO 99
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1170)
US-10-309-290-99
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 201 GGGAGGAGGCGCTGGGACAGTGTGGCTGCTGCTTCCCAACGGCTCCCTCTTCTTCC 260
Db 159 GGGAGGAGGCGCTGGGACAGTGTGGCTGCTGCTTCCCAACGGCTCCCTCTTCTTCC 218

Qy 261 GGCTGTCCGGATCCAGATCAGGGGATTTCCGGTCCAGGCAATGAACAGGAATGAAA 320
Db 219 GGCTGTCCGGATCCAGATCAGGGGATTTCCGGTCCAGGCAATGAACAGGAATGAAA 278

Qy 321 GGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCCTGGGAAGCCAGAAATGT 390
Db 279 GGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCCTGGGAAGCCAGAAATGT 338

Qy 381 AGATTCTGCTCTGAACTCACGGCTGGTGTTCCTCAATAAGTGGGACATGTGTGTCAGA 440
Db 339 AGATTCTGCTCTGAACTCACGGCTGGTGTTCCTCAATAAGTGGGACATGTGTGTCAGA 398

Qy 441 GGGAAAGTACCTGCGAGGACTCTTAGTGGCACTTTGGATGGGAAGCCCTGTGTGCTAA 500
Db 399 GGGAAAGTACCTGCGAGGACTCTTAGTGGCACTTTGGATGGGAAGCCCTGTGTGCTAA 458

Qy 501 TGAGAGGGAGTATCTGTGAAGAACAGACACAGGACACCCCTGAGACAGGGCTCTTAC 560
Db 459 TGAGAGGGAGTATCTGTGAAGAACAGACACAGGACACCCCTGAGACAGGGCTCTTAC 518

Qy 561 ACTGCAATCGAGCTAATGTGATGCCACCCAGCCGGGAGGAGATCCCGCTCCACCTTTC 620
Db 519 ACTGCAATCGAGCTAATGTGATGCCACCCAGCCGGGAGGAGATCCCGCTCCACCTTTC 578

Qy 621 CTGTAGCTTACGCGAGGCTTCCCGACACCGGGCTTGGCAGACAGCCGCCATCCAGCC 680
Db 579 CTGTAGCTTACGCGAGGCTTCCCGACACCGGGCTTGGCAGACAGCCGCCATCCAGCC 638

Qy 681 CCGTGTCTGGAGCTGTGCTCTGGAGGAGTCCAAATGGTGGTGGAGCCAGAGGTGG 740
Db 639 CCGTGTCTGGAGCTGTGCTCTGGAGGAGTCCAAATGGTGGTGGAGCCAGAGGTGG 698

Qy 741 AGCAGTAGCTTCTGTGGAAACCGTAACTGTGAAGTCCCTGCGCCAGCCCTCTCC 800
Db 699 AGCAGTAGCTTCTGTGGAAACCGTAACTGTGAAGTCCCTGCGCCAGCCCTCTCC 758

Qy 801 TCAATTCATGATGAAGATGGTGTGCTGCTGCTTCCCGCCAGCCCTGTGTGTAT 860
Db 759 TCAATTCATGATGAAGATGGTGTGCTGCTGCTTCCCGCCAGCCCTGTGTGTAT 818

Qy 861 CTTCTCTGATAGGCGCTCAGGACAGGGAACCTACAGTGTGTGGCCACCATTTCCAG 920
Db 819 CTTCTCTGATAGGCGCTCAGGACAGGGAACCTACAGTGTGTGGCCACCATTTCCAG 878

Qy 921 CCAAGGGCCCCAGGAAAGCGTGTCTGACGATCAGCATCATCGAATCAGGAGGAGGG 980
Db 879 CCAAGGGCCCCAGGAAAGCGTGTCTGACGATCAGCATCATCGAATCAGGAGGAGGG 938

Qy 981 GCCAATGAGGCTCTGTGGAGGATCAGGCTGGGAATCTAGCCCTGGCCCTGGGGAT 1040
Db 939 GCCAATGAGGCTCTGTGGAGGATCAGGCTGGGAATCTAGCCCTGGCCCTGGGGAT 998

Qy 1041 CTTGGAGGCTGGGACAGCCGCTCTCATTTGGGGTCACTTGTGGCAAGGCGGCA 1100
Db 1041 CTTGGAGGCTGGGACAGCCGCTCTCATTTGGGGTCACTTGTGGCAAGGCGGCA 1100
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RESULT 6
US-10-091-019-2
; Sequence 2, Application US/10091019
; Publication No. US20030166063A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Shen, Jane M.
; APPLICANT: Shabazz, Manouchehr M.
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins
; FILE REFERENCE: 41305-270555
; CURRENT APPLICATION NUMBER: US/10/091,019
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/273,418
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1020)
; OTHER INFORMATION:
US-10-091-019-2

Query Match 72.8%; Score 1013; DB 16; Length 1020;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1013; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 GGCAGCGGAAACAGCAGTGTGGAGCCCTGGGTGCTGCTCAGTCTGTGGGGGCAAGTAGT 62

Qy 63 AGGTCTCAAAACATCACAGCCCGGATTTGGCGAGCCACTGGTGTGCTGAAGTGAAGGGGC 122
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Qy 123 CCCCAGAAACACACCCCGGCTGGATGGAATGGAACCTGAACACAGCCCGGACAGAAAGTTG 182
Db 123 CCCCAGAAACACACCCCGGCTGGATGGAATGGAACCTGAACACAGCCCGGACAGAAAGTTG 182

Qy 183 GAAAGTCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCGTGTCTTCCCA 242
Db 183 GAAAGTCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCGTGTCTTCCCA 242

Qy 243 CCGCTCCCTCTTCCCTTCCGGATCCAGGATCAGGGGATTTTCCGGTGGCAGGC 302
Db 243 CCGCTCCCTCTTCCCTTCCGGATCCAGGATCAGGGGATTTTCCGGTGGCAGGC 302

Qy 303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGTTCC 362
Db 303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACCAAGTTCC 362

Qy 363 TGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCAGGCTGTGTGTTCCCAATAGGT 422
Db 363 TGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCAGGCTGTGTGTTCCCAATAGGT 422

Qy 423 GGGGACATGTGTGTCAGAGGGAAGCTACCCCTGCAAGGAGTCTTAGCTGGCACTTTGATGG 482
Db 423 GGGGACATGTGTGTCAGAGGGAAGCTACCCCTGCAAGGAGTCTTAGCTGGCACTTTGATGG 482
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; Publication No. US20040137434A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 797CON
; CURRENT APPLICATION NUMBER: US/10/115,635
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/714,936
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 362
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 352
; LENGTH: 1463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(1287)
; US-10-115-635-352

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Query Match 69.9%; Score 973; DB 18; Length 1463;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 973; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 419 AGTGGGACATGTGTGACAGGAGAGTACCTGCAGGAGACTTGTAGTGGCACTTGG 478
Db 491 AGTGGGACATGTGTGACAGGAGAGTACCTGCAGGAGACTTGTAGTGGCACTTGG 550
QY 479 ATGGGAGCCCTGGTGGCTTAATGAGAGGAGTACTGTGAGGAGAACAGACAGAGAC 538
Db 551 ATGGGAGCCCTGGTGGCTTAATGAGAGGAGTACTGTGAGGAGAACAGACAGAGAC 610
QY 539 ACCCTGAGACAGGCTCTTCCACTGCGAGCTAATGTGACCCCGAGCCCGGGGAG 598
Db 611 ACCCTGAGACAGGCTCTTCCACTGCGAGCTAATGTGACCCCGAGCCCGGGGAG 670
QY 599 GAGATCCCGTCCACTTCTCTGTAGCTTACGCCAGGCTTCCCGAGACCGGGCT 658
Db 671 GAGATCCCGTCCACTTCTCTGTAGCTTACGCCAGGCTTCCCGAGACCGGGCT 730
QY 659 TGCGCAGCCCGATCCAGCCCGGTCTGGGAGCTGTGCTCTGGAGGAGTCCAAT 718
Db 731 TGCGCAGCCCGATCCAGCCCGGTCTGGGAGCTGTGCTCTGGAGGAGTCCAAT 790
QY 719 TGGTGTGGAGCCAGAGGTGGAGCAGTAGCTCTCTGGTGAACCGTAACCTCTGACTGTG 778
Db 791 TGGTGTGGAGCCAGAGGTGGAGCAGTAGCTCTCTGGTGAACCGTAACCTCTGACTGTG 850
QY 779 AGTCTCTGCGAGCCCTCTCTCAATCCACTGAGTGAAGATGTGTGCTTCCCTTCCGCC 838
Db 851 AGTCTCTGCGAGCCCTCTCTCAATCCACTGAGTGAAGATGTGTGCTTCCCTTCCGCC 910
QY 839 TTCCCGCCAGCCCTGTGCTGATCTCTCTGAGATAGGCTCAGGACAGGGAACCTACA 898
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QY 899 GCTGTGTGGCCACCCATTCAGCCAGGCGCCAGGAAAGCCGTGTGTGATCAGCA 958
Db 971 GCTGTGTGGCCACCCATTCAGCCAGGCGCCAGGAAAGCCGTGTGTGATCAGCA 1030
QY 959 TCATCGAACCGGAGGAGGGGCCAACTGCAGGCTCTGTGGAGGATCAGGGCTGGAA 1018

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RESULT 9
US-08-905-709-3
; Sequence 3, Application US/08905709
; Publication No. US2001003256A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David
; APPLICANT: Schmidt, Ann M.
; TITLE OF INVENTION: A METHOD TO PREVENT ACCELERATED
; TITLE OF INVENTION: ATHEROSCLEROSIS USING (sRAGE) SOLUBLE RECEPTOR FOR
; TITLE OF INVENTION: ADVANCED GLYCATION ENDPRODUCTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Cooper & Dunham LLP
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,709
; FILING DATE: 05-AUG-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/52876
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 22:34:24 ; Search time 4945 Seconds
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST.*

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7: gb_est6:*
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9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	644	46.3	841	4 BI771266	BI771266 603054610
5	604	43.4	729	4 BG545652	BG545652 602572917
6	602	43.3	1163	9 AY421474	AY421474 Pan trogl
7	597	42.9	777	4 BG545464	BG545464 602572696
8	586	42.1	715	5 BG529831	BG529831 602558918
9	584	42.0	1194	5 BQ067161	BQ067161 AGENCOURT
10	562	40.4	724	4 BG536369	BG536369 602564760
11	549	39.5	553	4 BI772105	BI772105 603059188
12	540	38.8	750	4 BG548202	BG548202 602575359
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C 14	529	38.0	608	5 BM970294	BM970294 UI-CF-EC1
15	525	37.7	595	6 CD610810	CD610810 56069688J
16	508	36.5	508	7 CN431428	CN431428 170005999
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18	451	32.4	774	4 BG506672	BG506672 601861271
19	442	31.8	567	5 BX105560	BX105560 602558957
20	439	31.6	755	4 BG529866	BG529866 602591356
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C 22	413	29.7	513	2 AW105655	AW105655 xds0105.x
23	411	29.5	730	4 BG539104	BG539104 602568478
24	402	28.9	653	4 BG535354	BG535354 602563012

25	402	28.9	736	4 BG540452	BG540452 602568768
26	400	28.8	569	5 BU949326	BU949326 in65e12.y
C 27	399	28.7	468	5 BM992910	BM992910 UI-H-DT-O
28	379	27.2	832	4 BG548148	BG548148 602575303
29	378	27.2	894	4 BG538911	BG538911 602568563
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39	317	22.8	822	4 BG540530	BG540530 602569259
40	314	22.6	399	4 BM721731	BM721731 UI-E-EO1-
C 41	308	22.1	417	2 BF810418	BF810418 RC1-C1016
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C 44	302	21.7	739	2 BF446696	BF446696 7q90h02.x
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ALIGNMENTS

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LOCUS Homo sapiens AGER gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY421473
VERSION AY421473.1 GI:39748335
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1215)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Perriers,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1215)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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/mol_type="genomic DNA"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 GGCAGCCGGAACAGCAGTGTGGAGCCCTGGTGGTCTCTCAGTCTGTGGGGCAGTAGT 62

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Db 123 CCCAAGAAACACCCCGAGCGGTGGAATGGAACTGAAACACAGGCGGACAGAGCTTG 182
QY 183 GAAGTCTCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGTCTGTCTTCCCAA 242
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QY 243 CGGCTCCCTCTCTCTCCGCTCTCGGATCCAGGATGAGGGATTTTCGGTGCACGCG 302
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QY 303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC 362
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RESULT 2

CB241341/c

LOCUS

DEFINITION

UI-CF-FN0-afy-b-17-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone

UI-CF-FN0-afy-b-17-0-UI 3', mRNA sequence.

CB241341

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 712)

Bonaldo, M.P., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

PUBMED

COMMENT

Contact: McCray, PB

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com) or from Open Biosystems

(www.openbiosystems.com).

Seq primer: M13 FORWARD

POLYA=Yes.

Location/Qualifiers

1..712

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/clone_lib="UI-CF-FN0"

/note="Organ: lung; Vector: pT7T3-Pac (Pharmacia) with a

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UI-CF-FN0 is a subtracted cDNA library derived from two

normalized Human lung epithelial cell libraries (EN1 and

DUL) The library was subtracted according to according to

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. For additional information, contact:

bento-soares@uiowa.edu

TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368

TAG_LIB=UI-CF-FN0

TAG_SEQ=GGCTGTAGGC"

ORIGIN

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Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 697 GTGCTCTGGAGAGGTCCATTGCTGTGGAGCAGAGGTGGAGCTAGCTCTGCT 756

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 18:50:14 ; Search time 4741.31 Seconds
(without alignments)
10424.190 Million cell updates/sec

Title: US-10-091-019-2

Perfect score: 1020

Sequence: 1 atggagcgcggaacagcagct.....gaggatcagggtggtctag 1020

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sta.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1015	99.5	1268	9	AB036432 Homo sapi
2	1015	99.5	1436	9	BC020669 Homo sapi
3	1009.8	99.0	1391	6	AR321600 Sequence
4	1009.8	99.0	1391	9	M91211 Human recep
5	992	97.3	1223	6	BD176670 Soluble R
6	992	97.3	1223	9	AB061668 Homo sapi
7	974.8	95.6	1218	6	CQ730900 Sequence
8	964.6	94.6	1451	9	AB061669 Homo sapi
9	746.4	73.2	1426	4	BOVRAGE
10	746.4	73.2	1426	6	AR321599 Sequence
11	729	71.5	1250	9	HSAL133822
12	696.6	68.3	1348	6	AR321601 Sequence
13	696.6	68.3	1348	10	MUSRECEP
14	691.8	67.8	1399	10	BC061182
15	680.6	66.7	1420	10	RATRECEP
16	477.2	46.8	990	4	AY530943 Canis fam
17	388.8	38.1	511	6	AX795282 Sequence
18	388.8	38.1	511	9	AF536237 Homo sapi
19	384.2	37.7	483	4	AY370908

20	326.2	32.0	698	6	AX795283	AX795283 Sequence
21	326.2	32.0	698	9	AF537303	AF537303 Homo sapi
22	302.6	29.7	653	6	AX795281	AX795281 Sequence
23	302.6	29.7	653	9	AF536236	AF536236 Homo sapi
24	274.6	26.9	358	4	AY382178	AY382178 Canis fam
25	197	19.3	5062	9	HSN808526	BN648378 Homo sapi
26	197	19.3	10108	9	HUMHXRAGE	D28769 Human H0X12
27	197	19.3	56747	9	AL845464	AL845464 Human DNA
28	197	19.3	62944	6	AX334775	AX334775 Sequence
29	197	19.3	62944	6	AX336090	AX336090 Sequence
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31	197	19.3	80063	9	BN284686	BN284686 Human DNA
32	197	19.3	102588	9	BN27239	BN27239 Human DNA
33	197	19.3	103327	9	AL662830	AL662830 Human DNA
34	197	19.3	137935	9	AL662884	AL662884 Human DNA
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36	197	19.3	200685	2	AP001455	AP001455 Homo sapi
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38	176.2	17.3	159822	9	AC148714	AC148714 Macaca mu
39	172.4	16.9	189424	9	AC148664	AC148664 Macaca mu
40	152.6	15.0	127266	4	AL773562	AL773562 Pig DNA s
41	134.2	13.2	266517	2	AC107094	AC107094 Rattus no
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ALIGNMENTS

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LOCUS	AB036432				
DEFINITION	Homo sapiens RAGE mRNA for advanced glycation endproducts receptor, complete cds.				
ACCESSION	AB036432				
VERSION	AB036432.1	GI:6691625			
KEYWORDS	advanced glycation endproducts receptor.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (sites)				
AUTHORS	Abidin,M.J., Yonekura,H., Migita,H., Karasawa,J., Yamamoto,Y. and Yamamoto,H.				
TITLE	Molecular heterogeneity of the receptor for advanced glycation endproducts				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1268)				
AUTHORS	Abidin,M.J., Yonekura,H. and Yamamoto,H.				
TITLE	Direct Submission				
JOURNAL	Submitted (05-JAN-2000) Hideto Yonekura, Kanazawa University School of Medicine, Department of Biochemistry; 13-1 Takara-machi, Kanazawa, Ishikawa 920-8640, Japan				
	(E-mail:hyone@med.kanazawa-u.ac.jp, Tel: +81-76-265-2181, Fax: +81-76-234-4226)				

FEATURES

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ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 3e-246;
 Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAGCCGGAACAGCAGTTGAGCTGGGTCTGCTCAGTCTGTGGGGGGCAGTA 60
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RESULT 2
BC020669
LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

JOURNAL

REMARK

COMMENT

BC020669 1436 bp mRNA linear PRI 29-JUN-2004
 Homo sapiens advanced glycosylation end product-specific receptor,
 transcript variant 1, mRNA (CDNA clone MGC:22357 IMAGE:4718076),
 complete cds.
 BC020669
 BC020669.1 GI:18088362
 Homo sapiens (human)
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1436)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausch, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
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 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Sahney, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S.,
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 1436)
 Strausberg, R.
 Direct Submission
 Submitted (03-JAN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs@mail.nih.gov
 Tissue procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 (Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 37 Row: e Column: 17
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ORIGIN
 Query Match 99.5%; Score 1015; DB 9; Length 1436;
 Best Local Similarity 100.0%; Pred. No. 3e-246;
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QY 1 ATGGCAGCGGAACAGCAGTTGAGCTGGGTCTCTAGTCTGTGGGGGGCAGTA 60
 DB 20 ATGGCAGCGGAACAGCAGTTGAGCTGGGTCTCTAGTCTGTGGGGGGCAGTA 79
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 DB 440 GTGGGACATGTGTGTCAGAGGGAAGCTACCTGCGAGGACTCTTAGCTGGCATTTGGAT 499

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 DEFINITION Sequence 4 from patent US 6563015.
 ACCESSION AR321600
 VERSION AR321600.1 GI:33706929
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1391)
 AUTHORS Stern,D.M., Schmidt,A.M. and Yan,S.D.
 TITLE Transgenic mice over-expressing receptor for advanced glycation endproduct (RAGE) and mutant APP in brain and uses thereof
 JOURNAL Patent: US 6563015-A 4 13-MAY-2003;
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 Matches 1011; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 QY 63 AGGTGCTCAAAACATCAGCCCGGATTCGCGAGCCACTGTGCTGCTGAAAGTGAAGGGGC 122
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QY 483 GAAGCCCTGGTCTTAATGAGAGGGAGTATCTGTGAAGGAACAGACAGAGGACACCC 542
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 QY 663 CACAGCCCCATCCAGCCCGTGTCTGGAGGCTGTGCTCTGGAGAGGTGCAATTTGGT 722
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 QY 843 CCCCAGCCCTGTGCTGATCTCTCTGATATAGGCTCTAGGACAGGGAACCTACAGCTG 902
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RESULT 5
 LOCUS BD176670
 DEFINITION Soluble RAGE protein.
 ACCESSION BD176670
 VERSION BD176670.1 GI:29122380
 KEYWORDS WO 02074805-A/1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 YAMAMOTO, H., YONEKURA, H., YAMAMOTO, Y., SAKURAI, S. and Watanabe, T.
 Soluble RAGE protein
 Patent: WO 02074805-A 1 26-SEP-2002;
 JAPAN AS REPRESENTED BY PRESIDENT OF KANAZAWA UNIVERSITY, HIROSHI YAMAMOTO, HIDETO YONEKURA, YASUHIKO YAMAMOTO, SHIGERU SAKURAI, TAKUO WATANABE
 OS Homo sapiens (human)
 PN WO 02074805-A/1
 PD 26-SEP-2002
 PF 19-MAR-2002 WO 2002/002623
 PR 19-MAR-2001 JP OIP 078409, 10-AUG-2001 JP OIP 243114 PR
 25-FEB-2002 JP OIP 048182
 PI HIROSHI YAMAMOTO, HIDETO YONEKURA, YASUHIKO YAMAMOTO, SHIGERU SAKURAI, TAKUO WATANABE
 PI TAKUO WATANABE
 PC C07K14/47, C12N15/12, C12N1/21, C12N5/10, C12N1/19, A61K39/395, PC A61K45/00,
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Query Match 97.3%; Score 992; DB 6; Length 1223;
 Best Local Similarity 100.0%; Pred. No. 2e-240;
 Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 721 GTGGTGGAGCCAGAGGTGGAGCAGTAGCTCTCTGTGGAAACCGTACCTGACCTGTGAA 780
 DB 745 GTGGTGGAGCCAGAGGTGGAGCAGTAGCTCTCTGTGGAAACCGTAACTGACCTGTGAA 804
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FEATURES

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QY 961 ATCGAACCGAGCGAGGAGGGCCAACTGCAGG 992
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RESULT 6
AB061668 1223 bp mRNA linear PRI 15-MAR-2003
LOCUS Homo sapiens RAGE mRNA for soluble form of receptor for advanced
DEFINITION glycation endproducts, complete cds.
ACCESSION AB061668
VERSION AB061668.1 GI:28971759
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Yonekura,H., Yamamoto,Y., Sakurai,S., Petrova,R.G., Abedin,Md.J.,
Li,H., Yasui,K., Takeuchi,M., Makita,Z., Takasawa,S., Okamoto,H.,
Watanabe,T. and Yamamoto,H.
Novel splice variants of the receptor for advanced glycation
end-products expressed in human vascular endothelial cells and
pericytes, and their putative roles in diabetes-induced vascular
injury
Biochem. J. 370 (Pt 3), 1097-1109 (2003)
JOURNAL 22510265
MEDLINE 12495433
PUBMED
REFERENCE 2 (bases 1 to 1223)
Yonekura,H., Yamamoto,Y., Sakurai,S. and Yamamoto,H.
Direct Submission
TITLE Submitted (11-MAY-2001) Hideto Yonekura, Kanazawa University,
Graduate School of Medical Science; 13-1 Takara-machi, Kanazawa,
Tshikawa 920-8640, Japan (E-mail:hyone@med.kanazawa-u.ac.jp,
Tel:81-76-265-2182, Fax:81-76-234-4226)
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Query Match 97.3%; Score 992; DB 9; Length 1223;
Best Local Similarity 100.0%; Pred. No. 2e-240;
Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS         Sequence 16834 from Patent WO2068579.
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ACCESSION    CQ730900
VERSION      CQ730900.1 GI:42306010
KEYWORDS     Homo sapiens (human)
SOURCE
ORGANISM     Homo sapiens
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              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE        Kits, such as nucleic acid arrays, comprising a majority of
              humanexons or transcripts, for detecting expression and other uses
              thereof
JOURNAL      Patent: WO 02068579-A 16834 06-SEP-2002;
              PE Corporation (NY) (US)
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Best Local Similarity 98.0%; Pred. No. 4.7e-236;
Matches 998; Conservative 0; Mismatches 17; Indels 3; Gaps 1;

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Qy 181 TGGAGGTCCTGTCTCCAGGAGAGAGCCCTCGGACAGTGTGCTGTCTCTCC 240
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Qy 481 GGGAAAGCCCTGTGTCTAATGAGAGGGAGTATCTGTGAAGGAAACAGACCCAGGAGACAC 540
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LOCUS         Homo sapiens RAGE mRNA for N-terminal truncated form of receptor
DEFINITION    for advanced glycation endproducts, complete cds.
ACCESSION    AB061669
VERSION      AB061669.1 GI:28971761
KEYWORDS     Homo sapiens (human)
SOURCE
ORGANISM     Homo sapiens
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              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Yonekura, H., Yamamoto, Y., Sakurai, S., Petrova, R.G., Abedin, Md. J.,
              Li, H., Yasui, K., Takeuchi, M., Makita, Z., Takasawa, S., Okamoto, H.,
              Watanabe, T. and Yamamoto, H.
TITLE        Novel splice variants of the receptor for advanced glycation
              end-products expressed in human vascular endothelial cells and
              pericytes, and their putative roles in diabetes-induced vascular
              injury
JOURNAL      Biochem. J. 370 (Pt 3), 1097-1109 (2003)
MEDLINE      22510265
PUBMED       12495433
AUTHORS      Yonekura, H., Yamamoto, Y., Sakurai, S. and Yamamoto, H.
TITLE        Direct Submission
JOURNAL      Submitted (11-MAY-2001) Hideto Yonekura, Kanazawa University,
              Graduate School of Medical Science, 13-1 Takara-machi, Kanazawa,
              Ishikawa 920-8640, Japan (E-mail:hyone@med.kanazawa-u.ac.jp,
              Tel:81-76-265-2182, Fax:81-76-234-4226)
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Best Local Similarity 99.6%; Pred. No. 1.8e-233;
Matches 967; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 45 TCCTGGGGGGAGTAGTGTCTCAAAACATCACAGCCGCGATTGGCGAGCCACTGTG 104
DB 252 TCCTCCAGGGGAGTAGTGTCTCAAAACATCACAGCCGCGATTGGCGAGCCACTGTG 311
QY 105 GCTGAAGTGTAAAGGGGGCCCCCAAGAAACACACCCAGCGGCTGGAATGGAACCTGAACAC 164
DB 312 GCTGAAGTGTAAAGGGGGCCCCCAAGAAACACACCCAGCGGCTGGAATGGAACCTGAACAC 371
QY 165 AGCCCGGACAGAAGCTTGGAGGTCTGTCTCCCAAGGAGAGGCCCCCTGGGACAGTGT 224
DB 372 AGCCCGGACAGAAGCTTGGAGGTCTGTCTCCCAAGGAGAGGCCCCCTGGGACAGTGT 431
QY 225 GGCTGTGTCTTCCCAAGCGCTCTCTTCTTCCGCGCTGTCCGATCCAGGATCAGGAGG 284
DB 432 GGCTGTGTCTTCCCAAGCGCTCTCTTCTTCCGCGCTGTCCGATCCAGGATCAGGAGG 491
QY 285 GATTTTCCGCTGTCAGGCAATGAACAGGAATGAAGAGGAGACCAAGTCCAACTACCGAGT 344
DB 492 GATTTTCCGCTGTCAGGCAATGAACAGGAATGAAGAGGAGACCAAGTCCAACTACCGAGT 551
QY 345 CCGTGTCTACAGATTCCTGGGAGGACGAAATGTAGATTCGCTCTGAACTCAAGGC 404
DB 552 CCGTGTCTACAGATTCCTGGGAGGACGAAATGTAGATTCGCTCTGAACTCAAGGC 611
QY 405 TGGTGTTCCTCAATAAGGTGGGACATGTGTGTGTCAGAGGAAGTACCTCCGAGGAGTCT 464
DB 612 TGGTGTTCCTCAATAAGGTGGGACATGTGTGTGTCAGAGGAAGTACCTCCGAGGAGTCT 671
QY 465 TAGCTGGCATCTGGATGGGAAGCCCTGTGTCTTAATGAAGGGAGTATCTGTGAAGGA 524
DB 672 TAGCTGGCATCTGGATGGGAAGCCCTGTGTCTTAATGAAGGGAGTATCTGTGAAGGA 731
QY 525 ACAGACGAGGAGACCTTGACAGAGGCTTTCACACTGCAGTGGAGCTAATGCTGAC 584
DB 732 ACAGACGAGGAGACCTTGACAGAGGCTTTCACACTGCAGTGGAGCTAATGCTGAC 791
QY 585 CCAGACCCGGGAGGAGATCCCGTCCCACTTCTCTGTAGCTTCAGCCAGGCTTCC 644
DB 792 CCAGACCCGGGAGGAGATCCCGTCCCACTTCTCTGTAGCTTCAGCCAGGCTTCC 851
QY 645 CCGACACCCGGGCTTCGACACAGCCCCATCCAGCCCGCTGTCTGGAGCCCTGTGCTCT 704
DB 852 CCGACACCCGGGCTTCGACACAGCCCCATCCAGCCCGCTGTCTGGAGCCCTGTGCTCT 911
QY 705 GGAGGAGTCCAAATGGTGTGGAGCCAGAGGTGGAGCAGTGTCTCTGTGGAGCCGT 764
DB 912 GGAGGAGTCCAAATGGTGTGGAGCCAGAGGTGGAGCAGTGTCTCTGTGGAGCCGT 971
QY 765 AACCTTGACCTGTGAAGTCCCTGCCAGGCTCTCTCTCAAAATCCACTGATGAAGGATGG 824
DB 972 AACCTTGACCTGTGAAGTCCCTGCCAGGCTCTCTCTCAAAATCCACTGATGAAGGATGG 1031
QY 825 TGTGCCCTTGGCCCTTCCGCCAGCCCTGTGTGTGATCTCTCTGTGATGAGGCTCAGGA 884
DB 1032 TGTGCCCTTGGCCCTTCCGCCAGCCCTGTGTGTGATCTCTCTGTGATGAGGCTCAGGA 1091
QY 885 CCAGGGAACCTACAGCTGTGTGCGCACCACTTCCAGCCAGGCCCCCAGGAAGCGGTGC 944

DB 1092 CCAGGGAACCTACAGCTGTGTGCCCAACCCATTCACGCCACCGGCCCAAGAACCGGTGC 1151
QY 945 TGTACGATCAGCATCATCGAACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1004
DB 1152 TGTACGATCAGCATCATCGAACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1211
QY 1005 ATCAGGGCTGG 1015
DB 1212 ATCAGGGCTGG 1222
RESULT 9
BOVRAGE
LOCUS
DEFINITION BOVRAGE 1426 bp mRNA linear MAM 09-DEC-1993
Cow receptor for advanced glycosylation end products (RAGE) mRNA,
complete cds.
ACCESSION M91212.1 GI:163650
VERSION RAGE; cell surface receptor.
KEYWORDS Bos taurus (cow)
SOURCE Bos taurus
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 1426)
AUTHORS Neepor M., Schmidt, A.M., Brett, J., Yan, S.D., Wang, F., Pan, Y.C.,
Elliston, K., Stern, D. and Shaw, A.
TITLE Cloning and expression of a cell surface receptor for advanced
glycosylation end products of proteins
JOURNAL J. Biol. Chem. 267 (21), 14998-15004 (1992)
MEDLINE 92340547
PUBMED 1378843
REFERENCE 2 (bases 1 to 1426)
AUTHORS Shaw, A.
TITLE Direct Submission
JOURNAL Submitted (15-APR-1992) A. Shaw, Department of Cellular and
Molecular Biology, Merck Sharp and Dohme Research Laboratories,
West Point, PA 19486 USA
COMMENT Original source text: Bos taurus cDNA to mRNA.
FEATURES
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1..1426
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="lung"
10..1260
/standard_name="RAGE"
/codon_start=1
/product="receptor for advanced glycosylation end
products"
/protein_id="AAA03575.1"
/db_xref="GI:163651"
/translation="MAGAVVGAAMVLVLGGTVDONITARIKPLVNLCKGAPK
PQQLWKLTGRTAEAWKVLSPQDPWDSVARVLPNGSILLPAGVIGDEGFRCRATS
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KTLPLDGGKVSVEETKRPHTLTLSELMTVPARGALHPTFSCFTPLPRRA
LHTAPIQURVMSHRRGEGPNVDAPLVEQVWVEGGAVAGTGTTLTCEAPQPP
POIHWIKDRPLPLPPGPMILLPEVGEDQCTYSCVATHSHSGPQBSRAVSIETG
EECTAGSGEGPGLTALTLGLLGLTALLIGVILWQRQRGRERKRAVPEKQ
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polyA_signal
1406..1411
polyA_site
1426
ORIGIN
Query Match 73.2%; Score 746.4; DB 4; Length 1426;
Best Local Similarity 84.1%; Pred. No. 3.5e-178;
Matches 881; Conservative 0; Mismatches 131; Indels 36; Gaps 2;
QY 1 ATGGCAGCGGGAACAGCAGTGGAGCCCTGGTGTGCTCTCAGTCTGTGGGGGCGCAGTA 60
DB 10 ATGGCAGCGGCGAGTGGTGGAGCCCTGGATGCTAGTCTCAGTCTGGGGGCGCAGTC 69
QY 61 GTAGTGTCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAGTGAAGGG 120

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 17:18:58 ; Search time 643.487 Seconds

(without alignments)
9383.456 Million cell updates/sec

Title: US-10-091-019-2

Perfect score: 1020

Sequence: 1 atggcagccggaacagcagt.....gaggatcagggtggtctag 1020

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1020	100.0	1020	6	Abq79956 Human sol
2	1015	99.5	1023	2	Aav12394 Human sol
3	1015	99.5	1023	2	Aav06517 Human RAG
4	1015	99.5	1268	10	Adg33024 Human DNA
5	1015	99.5	1329	12	Adp19665 Human LP2
6	1015	99.5	1415	6	Abq99597 Human cod
7	1015	99.5	1436	12	Adk00130 Human RAG
8	1013.4	99.4	1217	10	Ad95563 Human NOV
9	1013.4	99.4	1582	4	Aah57444 Human lun
10	1013	99.3	1391	6	Abq79955 Human RAG
11	1010.2	99.0	1146	13	Adsl0302 Human the
12	1010.2	99.0	1761	12	Adk00128 Human RAG
13	1009.8	99.0	1391	6	Abk10856 DNA encod
14	1009.8	99.0	1391	6	Abk84114 Human cdn
15	1009.8	99.0	1391	6	Ad36952 Human rec
16	1009.8	99.0	1391	10	Ad59952 Human RAG
17	1009.8	99.0	1391	10	Adg32021 Human DNA
18	992	97.3	1223	6	Abv73151 Human sol
19	992	97.3	1223	10	Adg37043 Receptor
20	992	97.3	1291	12	Adp19655 Human LP2

21	979	96.0	1323	12	Adp19667	Adp19667 Human LP2
22	957	93.8	1384	12	Adp19659	Adp19659 Human LP2
23	957	93.8	1463	6	Abq99598	Abq99598 Human cod
24	949	93.0	957	2	Aav06518	Aav06518 Human RAG
25	945.8	92.7	957	2	AAV12395	AAV12395 Human mat
26	934	91.6	1339	12	Adp19661	Adp19661 Human LP2
27	933	91.5	1539	9	ACC59920	ACC59920 Human REM
28	921	90.3	1173	10	Ad95567	Ad95567 Human NOV
29	921	90.3	1294	12	Adp19669	Adp19669 Human LP2
30	921	90.3	1678	9	ACC5907	ACC5907 Human REM
31	919.4	90.1	1226	10	Ad95565	Ad95565 Human NOV
32	878	86.1	1239	12	Adp19663	Adp19663 Human LP2
33	863	84.6	1627	9	ACC59921	ACC59921 Human REM
34	822	80.6	1090	12	Adm80824	Adm80824 Human CAD
35	822	80.6	1194	12	Adp19657	Adp19657 Human LP2
36	746.4	73.2	1426	6	Abk10855	Abk10855 DNA encod
37	746.4	73.2	1426	6	Ad36951	Ad36951 Cow recep
38	746.4	73.2	1426	10	Ad59951	Ad59951 Bovine RA
39	746.4	73.2	1426	10	Adg32020	Adg32020 DNA encod
40	696.6	68.3	1347	6	Abk10858	Abk10858 DNA encod
41	696.6	68.3	1348	6	Abk10857	Abk10857 DNA encod
42	696.6	68.3	1348	6	Ad36953	Ad36953 Mouse rec
43	696.6	68.3	1348	10	Ad59953	Ad59953 Murine RA
44	696.6	68.3	2057	12	Adk00123	Adk00123 Murine so
45	388.8	38.1	511	10	ADD40791	ADD40791 Human RAG

ALIGNMENTS

RESULT 1

ABQ79956
ID ABQ79956 standard; DNA; 1020 BP.

XX
AC ABQ79956;

XX
DT 23-DEC-2002 (first entry)

XX
DE Human soluble RAGE (sRAGE) encoding DNA.

XX
KW Receptor for Advanced Glycated end product; RAGE; recombinant; nootropic;
KW antiarteriosclerotic; antidiabetic; cytosolic; nephrotropic; vasotropic;
KW neuroprotective; antiinflammatory; gene therapy; human; gene; ds.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1020
FT /tag= a
FT /product= "sRAGE"
FT /note= "soluble, extracellular portion of RAGE"

XX
PN WO200270667-A2.

XX
PD 12-SEP-2002.

XX
PF 05-MAR-2002; 2002WO-US006881.

XX
PR 05-MAR-2001; 2001US-0273418P.

XX
PA (TRAN-) TRANSTECH PHARMA INC.

XX
PI Harris R, Shen J, Shahbaz M;

XX
DR WPI; 2002-713443/77.

XX
DR P-PSDB; AB82164.

XX
PT High level expression of recombinant Receptors for Advanced Glycated end
PT products (sRAGE) proteins for treating increased levels of advanced
PT glycosylation end products, comprises infecting cells with a high titer
PT recombinant virus.
XX
PS Claim 13; Fig 2B; 5lpp; English.

XX The invention relates to a method for high level expression of
CC recombinant forms of the Receptor for Advanced Glycated end products
CC (RAGE) or its fragments. The method involves (i) subcloning a nucleotide
CC sequence encoding RAGE or its fragment into a virus; (ii) preparing a
CC high titer stock of recombinant virus; and (iii) infecting host cells
CC with the high titer recombinant virus under conditions such that
CC predetermined levels of RAGE or its fragment is produced, where the
CC predetermined levels of RAGE comprises at least 25 mg recombinant protein
CC per liter of culture. The method is useful for high level expression of
CC recombinant RAGE polypeptide or its fragment which may be useful in
CC preventing, treating or ameliorating diseases associated with increased
CC levels of advanced glycosylation end products, such as atherosclerosis,
CC diabetes and its symptoms, amyloidosis, kidney failure, Alzheimer's
CC disease, inflammation, systemic lupus nephritis, inflammatory lupus
CC nephritis, cancer or erectile dysfunction. The present sequence
CC represents the nucleotide sequence of human sRAGE (soluble, extracellular
CC portion of RAGE)
XX
SQ Sequence 1020 BP; 216 A; 299 C; 316 G; 189 T; 0 U; 0 Other

QY	721	GTGTGGAGCCAGAAAGTGGAGCAGTACGTCCTGGTGGAAACCGTAAACCCCTGACCTGTGGAA	780
Db	721	GTGTGGAGCCAGAAAGTGGAGCAGTACGTCCTGGTGGAAACCGTAAACCCCTGACCTGTGGAA	780
QY	781	GTCCCTGCCAGGCCCTCTCTCAAATCCACTGGATGAAGGATGCTGTGCCCTTGGCCCTT	840
Db	781	GTCCCTGCCAGGCCCTCTCTCAAATCCACTGGATGAAGGATGCTGTGCCCTTGGCCCTT	840
QY	841	CCCCCAGCCCTGTGCTGATCTCTCCCTGAGATAGGGCCTCAGGACCAAGGAAACCTACAGC	900
Db	841	CCCCCAGCCCTGTGCTGATCTCTCCCTGAGATAGGGCCTCAGGACCAAGGAAACCTACAGC	900
QY	901	TGTGTGGCCACCCATTCACAGCCAGGGCCCCAGGAAGCCGTCTGTTCAGCATCAGATC	960
Db	901	TGTGTGGCCACCCATTCACAGCCAGGGCCCCAGGAAGCCGTCTGTTCAGCATCAGATC	960
QY	961	ATCGAACCAAGCCAGGAGGGGCCCAACTGCAGGCTCTGTGGAGGATCAGGGCTGGTCTAG	1020
Db	961	ATCGAACCAAGCCAGGAGGGGCCCAACTGCAGGCTCTGTGGAGGATCAGGGCTGGTCTAG	1020
RESULT 2			
AAV12394			
ID	AAV12394	standard; DNA; 1023 BP.	
XX	XX		
AC	AAV12394;		
XX	XX		
DT	14-MAY-1998	(first entry)	
XX	XX	Human soluble receptor to an advanced glycosylation end product DNA.	
DE	XX	Human; soluble receptor; advanced glycosylation end product; RAGE; AGE;	
KW	XX	antibody; vascular permeability; diabetes mellitus; ds.	
KW	XX		
XX	XX	Homo sapiens.	
OS	XX		
FH	Key	Location/Qualifiers	
FT	CDS	1..1023	
FT		/*tag= a	
FT		/product= "soluble RAGE"	
XX	XX		
FN	WO9739125-A1.		
XX	XX		
PD	23-OCT-1997.		
XX	XX		
PF	11-APR-1997; 97WO-EP001834.		
XX	XX		
PR	16-APR-1996; 96US-00633148.		
XX	XX	(SCHD) SCHERING PATENTE AG.	
FA	XX		
XX	XX	Morser MJ, Nagashima M, Hollander DA;	
PI	XX		
XX	XX	WPI: 1997-558580/51.	
DR	XX	P-PSDB; AAW44199.	
PT	XX	Anti-advanced glycosylation end product polypeptide antibody - prevents	
PT	XX	receptor binding and therefore reduces vascular permeability, useful to	
PT	XX	treat diabetes mellitus.	
XX	XX		
PS	XX	Disclosure; Page 39; 90pp; English.	
XX	XX		
CC	XX	The present sequence encodes a soluble human receptor to an advanced	
CC	XX	glycosylation end product (RAGE) polypeptide. The present invention	
CC	XX	describes an isolated antibody (Ab), specifically immunoreactive with	
CC	XX	RAGE. Advanced glycosylation end products (AGE) of proteins are non-	
CC	XX	enzymatically glycosylated proteins, which accumulate in vascular tissue	
CC	XX	in ageing, and at an accelerated rate in individuals with diabetes. The	
CC	XX	Ab, which prevents the interaction between an AGE and it's receptor	
CC	XX	(RAGE), reduces vascular permeability. The Ab can be used to treat	
CC	XX	diabetes mellitus symptoms, e.g. macrovasculopathy, occlusive vascular	
CC	XX	disorders, neuropathy, nephropathy, retinopathy, haemodialysis associated	
CC	XX	amyloidosis or atherosclerosis. The Ab can also be used for the isolation	

CC and purification of human RAGE polypeptide

XX Sequence 1023 BP; 218 A; 299 C; 317 G; 189 T; 0 U; 0 Other;

Query Match 99.5%; Score 1015; DB 2; Length 1023;
Best Local Similarity 100.0%; Pred. No. 7.6e-261; Indels 0; Gaps 0;
Matches 1015; Conservative 0; Mismatches 0;

QY 1 ATGGCAGCGGACACAGCTTGAGCTGGTGTCTGCTCCTCAGTCTGTGGGGGCGAGTA 60
DB 1 ATGGCAGCGGACACAGCTTGAGCTGGTGTCTCAGTCTGTGGGGGCGAGTA 60
QY 61 GTAGGTGCTCAAAACATCAGCCCCGGATTGGGAGCCACTGGTGTGAAGTGTAAAGGG 120
DB 61 GTAGGTGCTCAAAACATCAGCCCCGGATTGGGAGCCACTGGTGTGAAGTGTAAAGGG 120
QY 121 GCCCCCAAGAAACACCCAGCGGCTGGAACTGAACACAGCCCGGACAGAGCT 180
DB 121 GCCCCCAAGAAACACCCAGCGGCTGGAACTGAACACAGCCCGGACAGAGCT 180
QY 181 TGGAGGTCTCTCTCCAGGAGGAGGCCCTTGGGACAGTGTGGCTCTGTCTCTTCC 240
DB 181 TGGAGGTCTCTCTCCAGGAGGAGGCCCTTGGGACAGTGTGGCTCTGTCTCTTCC 240
QY 241 AACGGTCTCTCTCTCCAGGAGGAGGCCCTTGGGACAGTGTGGCTCTGTCTCTTCC 300
DB 241 AACGGTCTCTCTCTCCAGGAGGAGGCCCTTGGGACAGTGTGGCTCTGTCTCTTCC 300
QY 301 GCAATGAACAGGATCGAAGGAGGAGCCAGTCCACTACCGAGTCCGTCTACCAAGT 360
DB 301 GCAATGAACAGGATCGAAGGAGGAGCCAGTCCACTACCGAGTCCGTCTACCAAGT 360
QY 361 CTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
DB 361 CTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
QY 421 GTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
DB 421 GTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY 481 GGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
DB 481 GGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 541 CTTGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
DB 541 CTTGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
QY 601 GATCCCGGTCACCTTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
DB 601 GATCCCGGTCACCTTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 661 GGCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
DB 661 GGCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 721 GTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
DB 721 GTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 781 GTCCCTGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
DB 781 GTCCCTGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 841 CCCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
DB 841 CCCCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 901 TGTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
DB 901 TGTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
QY 961 ATCGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1015

DB 961 ATCGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1015
RESULT 3
AAV06517
ID AAV06517 standard; DNA; 1023 BP.
XX AAV06517;
AC AC
XX DT 08-MAY-1998 (first entry)
XX DE Human RAGE polypeptide (340 amino acid residues) encoding DNA.
XX KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;
XX KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;
XX KW Alzheimer's disease; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 1..1023
FT /tag= a
FT /product= "RAGE polypeptide"
XX W09739121-A1.
XX 23-OCT-1997.
XX 11-APR-1997; 97WO-EP001832.
XX 16-APR-1996; 96US-00633147.
XX (SCHD) SCHERING AG.
XX Morser MJ, Nagashima M;
XX WPI; 1997-526458/48.
XX P-PSDB; AAW33753.
XX New soluble advanced glycosylation end-product receptor polypeptide -
XX used for reducing vascular permeability, complications of diabetes etc.,
XX also for purification and to screen for modulators.
XX Claim 12; Fig 1A; 91pp; English.
XX This genomic DNA encodes a human advanced glycosylation end-product
XX receptor (RAGE) polypeptide (340 amino acid residues). The RAGE
XX polypeptides and its active fragments or their mimetics, inhibit
XX interaction between advanced glycosylation end-products (AGE) and a
XX receptor (specifically RAGE). They are used to treat diseases associated
XX with AGE/RAGE interaction, such as increased vascular permeability,
XX diabetes mellitus (particularly complications such as micro- or macro-
XX vasculopathy or occlusive vascular disorders such as neuropathy,
XX nephropathy, retinopathy or atherosclerosis) or haemodialysis-associated
XX amyloidosis, also activation of microglial cells by beta-amyloid peptides
XX in Alzheimer's disease or age-related disorders such as oxidative stress.
XX These RAGE polypeptides are also used, when immobilised, to purify AGE
XX from a protein mixture and to screen for compounds that are agonists and
XX antagonists of AGE/RAGE interaction. They can also be used diagnostically
XX to detect abnormal levels of AGE. Antibodies against RAGE polypeptides
XX are useful as immunoassay reagents for measurement of RAGE levels, and as
XX inhibitors of interaction between AGE and RAGE or other receptors and for
XX purification and quantification of RAGE polypeptides. The encoding
XX nucleic acids are used to express recombinant RAGE and as probes for
XX isolating related genes
XX Sequence 1023 BP; 218 A; 299 C; 317 G; 189 T; 0 U; 0 Other;

Query Match 99.5%; Score 1015; DB 2; Length 1023;
Best Local Similarity 100.0%; Pred. No. 7.6e-261; Indels 0; Gaps 0;
Matches 1015; Conservative 0; Mismatches 0;

Qy	1	ATGGCAGCCGGAAACAGCAGTGTGGAGCCTGGGTGCTGTGTCCTCAGTCTGTGTGGGGGGCAGTA	60
Db	1	ATGGCAGCCGGAAACAGCAGTGTGGAGCCTGGGTGCTGTGTCCTCAGTCTGTGTGGGGGGCAGTA	60
Qy	61	GTAGGTGCTCAAAACATCACAGCCCGGATGTGGCAGGCACCTGGTGTCTGAAGTGTAAAGGG	120
Db	61	GTAGGTGCTCAAAACATCACAGCCCGGATGTGGCAGGCACCTGGTGTCTGAAGTGTAAAGGG	120
Qy	121	GCCTCCAGAAAAACACCCAGCGGCTGGAAATGGAAACTTGAAACACAGGCCGGACAGAAAGCT	180
Db	121	GCCTCCAGAAAAACACCCAGCGGCTGGAAATGGAAACTTGAAACACAGGCCGGACAGAAAGCT	180
Qy	181	TGGAAGGTCTGTCTCTCCACAGGAGGAGGCCCTCGGACAGTGTGGCTCGTGTCTCTTCCC	240
Db	181	TGGAAGGTCTGTCTCTCCACAGGAGGAGGCCCTCGGACAGTGTGGCTCGTGTCTCTTCCC	240
Qy	241	AACGGTCTCTCTCTCTCTCCGTGTGCGGATTCAGGATGAGGGATTTTCCGGTGCAG	300
Db	241	AACGGTCTCTCTCTCTCTCCGTGTGCGGATTCAGGATGAGGGATTTTCCGGTGCAG	300
Qy	301	GCAATGAACAGGAATGGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCCAGATT	360
Db	301	GCAATGAACAGGAATGGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCCAGATT	360
Qy	361	CTTGGGAAGCCAGAAATCTAGATTCTGCCTCTGAACTCACGGCTGTGTGTCCCAATAAG	420
Db	361	CTTGGGAAGCCAGAAATCTAGATTCTGCCTCTGAACTCACGGCTGTGTGTCCCAATAAG	420
Qy	421	GTGGGACATGTGTGTACAGAGGAAGCTACCTCGCAGGACTCTTACCTGGCACTTTGGAT	480
Db	421	GTGGGACATGTGTGTACAGAGGAAGCTACCTCGCAGGACTCTTACCTGGCACTTTGGAT	480
Qy	481	GGGAAGCCCTGTGTCTTAATCAGAAAGGAGTATCTGTGAAGAACACAGACAGGAGACAC	540
Db	481	GGGAAGCCCTGTGTCTTAATCAGAAAGGAGTATCTGTGAAGAACACAGACAGGAGACAC	540
Qy	541	CTTGAGACAGGGCTCTTACACTGCAGTCTGAGAGTAAATGTGACCCACAGCCCGGGGAGGA	600
Db	541	CTTGAGACAGGGCTCTTACACTGCAGTCTGAGAGTAAATGTGACCCACAGCCCGGGGAGGA	600
Qy	601	GATCCCGTCCCACTTCTCTGTAGTTCAGCCAGCCCTTCCCGACACCCGGGCTTG	660
Db	601	GATCCCGTCCCACTTCTCTGTAGTTCAGCCAGCCCTTCCCGACACCCGGGCTTG	660
Qy	661	CGCACAGCCCCATCAGCCCCGTGTCTGGGAGCTGTGCTCTGAGGAGGTCCCAATTG	720
Db	661	CGCACAGCCCCATCAGCCCCGTGTCTGGGAGCTGTGCTCTGAGGAGGTCCCAATTG	720
Qy	721	GTGGTGGAGCAGAAAGGTGGACAGTACTCTCTGTGGAAACCGTAACCTCGACCTGTGAA	780
Db	721	GTGGTGGAGCAGAAAGGTGGACAGTACTCTCTGTGGAAACCGTAACCTCGACCTGTGAA	780
Qy	781	GTCCCTGCCAGCCCTCTCTCAATCCACTGGATGAGGATGTGTGTCCTTGGCCCTT	840
Db	781	GTCCCTGCCAGCCCTCTCTCAATCCACTGGATGAGGATGTGTGTCCTTGGCCCTT	840
Qy	841	CCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGGCTCAGGACACAGGAACTACAGC	900
Db	841	CCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGGCTCAGGACACAGGAACTACAGC	900
Qy	901	TGTGTGGCCACCATCTCCAGCCACCGGGCCCCAGGAAAGCCGTGTGTGTCAGCATCAGATC	960
Db	901	TGTGTGGCCACCATCTCCAGCCACCGGGCCCCAGGAAAGCCGTGTGTGTCAGCATCAGATC	960
Qy	961	ATCGAACACAGGCGAGGAGGGCCAACTCAGGCTCTGTGGGAGGATCAGGGCTGG	1015
Db	961	ATCGAACACAGGCGAGGAGGGCCAACTCAGGCTCTGTGGGAGGATCAGGGCTGG	1015

RESULT 4
ADG33024
ID ADG33024 standard; DNA: 1268 BP.

AC	ADG33024;
XX	
DT	26-FEB-2004 (first entry)
XX	
DE	Human DNA differentially expressed in patients with SLE SeqID348.
XX	
KW	human; ds; autoimmune; chronic inflammatory disease; SLE;
KW	systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;
KW	Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;
KW	ulcerative colitis; primary sclerosing cholangitis; appendicitis;
KW	diverticulitis; primary biliary sclerosis.
XX	
OS	Homo sapiens.
XX	
PN	WO2003090694-A2.
XX	
PD	06-NOV-2003.
XX	
PF	24-APR-2003; 2003WO-US013015.
XX	
PR	24-APR-2002; 2002US-00131827.
XX	
PA	(EXPR-) EXPRESSION DIAGNOSTICS INC.
XX	
PI	Wohlgemuth J, Fry K, Woodward R, Ly N;
XX	
DR	WPI; 2003-877243/81.
XX	
PT	Diagnosing or monitoring autoimmune and chronic inflammatory diseases,
PT	such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative
PT	colitis, psoriasis and asthma by detecting the expression level of one or
PT	more genes.
XX	
PS	Claim 18; SEQ ID NO 348; 877pp; English.
XX	
CC	This invention relates to novel methods for diagnosing and monitoring
CC	autoimmune and chronic inflammatory diseases. Specifically, it refers to
CC	the identification of genes that have a clinical utility as diagnostic
CC	tools for the management of, in particular, patients with systemic lupus
CC	erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the
CC	present invention describes a method for determining the levels of
CC	multiple differentially expressed genes of a patient, in a concerted
CC	manner, in order to achieve an improved diagnostic assay with sensitivity
CC	and specificity for the disease in question. As such, these genes are
CC	useful for the diagnosis of various other inflammatory disorders
CC	including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,
CC	ankylosing spondylitis, ulcerative colitis, primary sclerosing
CC	cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.
CC	This polynucleotide is a DNA sequence representing human mRNA that is
CC	differentially expressed in patients with SLE, used in an exemplification
CC	of the invention.
XX	
SQ	Sequence 1268 BP; 280 A; 361 C; 410 G; 217 T; 0 U; 0 Other;

RESULT 4
ADG33024
ID ADG
XX

```
QY 241 AACGGCTCCCTCTCTCTCCGCTGTCGGATCCAGGATGAGGGGATTTTCGGTCCAG 300
DB 265 AACGGCTCCCTCTCTCTCCGCTGTCGGATCCAGGATGAGGGGATTTTCGGTCCAG 324
QY 301 GCATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCGCTGTACCAAGATT 360
DB 325 GCATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCGCTGTACCAAGATT 384
QY 361 CTTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCAGGCTGCTGTTCCTCAATAG 420
DB 385 CTTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCAGGCTGCTGTTCCTCAATAG 444
QY 421 GTGGGACATGTGTGTGAGAGGAAGTACCTCTGAGGGACTCTTAGCTGGCACTTTGGAT 480
DB 445 GTGGGACATGTGTGTGAGAGGAAGTACCTCTGAGGGACTCTTAGCTGGCACTTTGGAT 504
QY 481 GGGAAAGCCCTGTGCTTAATGAGAGGGAGTATCTGTGAAGAAACAGACAGGAGACAC 540
DB 505 GGGAAAGCCCTGTGCTTAATGAGAGGGAGTATCTGTGAAGAAACAGACAGGAGACAC 564
QY 541 CTTGAGACAGGGCTCTTCACTGACGTGAGCTAATGTGACCCAGCCGCGGGAGGA 600
DB 565 CTTGAGACAGGGCTCTTCACTGACGTGAGCTAATGTGACCCAGCCGCGGGAGGA 624
QY 601 GATCCCGTCCCACTTCTCTGTAGCTTTCAGCCAGGCTTCCCGGACACCGGGCTTG 660
DB 625 GATCCCGTCCCACTTCTCTGTAGCTTTCAGCCAGGCTTCCCGGACACCGGGCTTG 684
QY 661 CGCAGAGCCCTCATCAGCCCGTGTCTGGAGCCTGTGCTGTGAGGAGTCCAAATGG 720
DB 685 CGCAGAGCCCTCATCAGCCCGTGTCTGGAGCCTGTGCTGTGAGGAGTCCAAATGG 744
QY 721 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTGTGTGGAACCTGACCTGTGTGAA 780
DB 745 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTGTGTGGAACCTGACCTGTGTGAA 804
QY 781 GTCCCTGCCAGCCCTCTCTCTCAATCCACTGGATGAAGGATGGTGTGCCCTTGCCCTT 840
DB 805 GTCCCTGCCAGCCCTCTCTCTCAATCCACTGGATGAAGGATGGTGTGCCCTTGCCCTT 864
QY 841 CCCCCAGCCCTGTGTGTATCTCTCTGATAGATAGGCTTCAGACAGGAACTTACAGC 900
DB 865 CCCCCAGCCCTGTGTGTATCTCTCTGATAGATAGGCTTCAGACAGGAACTTACAGC 924
QY 901 TGTGTGGCCACCCATTCCAGCCAGCGGCCCCAGGAAGCGTGTCTCAGCATCAGCATC 960
DB 925 TGTGTGGCCACCCATTCCAGCCAGCGGCCCCAGGAAGCGTGTCTCAGCATCAGCATC 984
QY 961 ATCGAACCCAGGAGGAGGGGCCAACTGAGGCTCTGTGGGAGGATCAGGGCTGG 1015
DB 985 ATCGAACCCAGGAGGAGGGGCCAACTGAGGCTCTGTGGGAGGATCAGGGCTGG 1039

RESULT 5
ADP19665
ID ADP19665 standard; cDNA; 1329 BP.
XX AC ADP19665;
XX DT 12-AUG-2004 (first entry)
XX DE Human LP2005 encoding cDNA SEQ ID NO:11.
XX KW human; LP2005; antidiabetic; neuroprotective; nontropic;
KW antinflammatory; antirheumatic; antiarthritic; vulnery; cytosstatic;
KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;
KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;
KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;
XX systemic lupus erythematosus; gene; ss.
OS Homo sapiens.
XX
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FH Key Location/Qualifiers
FT CDS 46..1206
FT /tag= b
FT /product= "LP2005"
FT /note= "the present sequence only seems to encodes amino
FT acids 1 to 386 of the LP2005 protein"
FT sig_peptide 46..114
FT mat_peptide 115..1203
FT /tag= a
FT /tag= c
XX WO2004044126-A2.
XX 27-MAY-2004.
XX 05-NOV-2003; 2003WO-US032734.
XX 14-NOV-2002; 2002US-0426253P.
XX (ELIL ) LILLY & CO EMI.
XX Na S, Perkins DR;
XX WPI; 2004-411705/38.
XX P-PSDB; ADP19666.
XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or
XX LP2003) for diagnosing or treating disorders associated with aberrant
XX levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome
XX identification.
XX Claim 1; SEQ ID NO 11; lllpp; English.
XX The present sequence encodes human LP2005, which is used in the
XX exemplification of the present invention. The present invention
XX describes: (1) an isolated nucleic acid (1) comprising DNA having at
XX least 95% sequence identity to a polynucleotide selected from the group
XX consisting of: (a) a polynucleotide having a nucleotide sequence as shown
XX in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a
XX polypeptide or mature form of a polypeptide having the amino acid
XX sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide
XX fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide
XX having a nucleotide sequence which is complementary to the nucleotide
XX sequence of a polynucleotide as in (a), (b) or (c); (2) a vector
XX comprising (1); (3) a host cell comprising the vector; (4) producing an
XX LP polypeptide; (5) an isolated polypeptide produced by the above method
XX and comprising an amino acid sequence comprising about 95% sequence
XX identity to a sequence of amino acid residues comprising LP2001, LP2003,
XX LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric
XX molecule comprising an LP polypeptide fused to a heterologous amino acid
XX sequence; (7) an antibody which specifically binds to an LP polypeptide
XX described above; (8) a composition (C) comprising a therapeutic amount of
XX an active agent selected from an LP polypeptide, an agonist to an LP
XX polypeptide, an antagonist to an LP polypeptide, an LP polypeptide
XX antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a
XX polynucleotide in combination with a pharmaceutical carrier; and (9)
XX diagnosing or treating a mammal suffering from a disease, condition or
XX disorder associated with aberrant levels of an LP-polypeptide. (C) has
XX antidiabetic, neuroprotective, nontropic, antiinflammatory,
XX antirheumatic, antiarthritic, vulnery, cytosstatic, immunosuppressive,
XX nephrotropic and dermatological activities, and can be used in gene
XX therapy. The compositions (C) and methods are useful for diagnosing or
XX treating disorders associated with aberrant levels of an LP polypeptide,
XX such as diabetes and its complications, Alzheimer's disease,
XX inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple
XX sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They
XX may also be used for chromosome identification. The LP polypeptide can
XX also be used in manufacturing a medicament for the treatment of the above
XX mentioned diseases, conditions or disorders associated with aberrant
XX levels of the LP polypeptide.
XX Sequence 1329 BP; 289 A; 379 C; 424 G; 235 T; 0 U; 2 Other;
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Query Match		99.5%;	Score 1015;	DB 12;	Length 1329;
Best Local Similarity		100.0%;	Pred. No. 8.3e-261;		
Matches 1015;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGCAGCCGGAACAGCAGTTGAGCCTCGGTGCTGCTCCTCAGTCTGTGGGGGAGTA	60		
Db	46	ATGCAGCCGGAACAGCAGTTGAGCCTCGGTGCTGCTCCTCAGTCTGTGGGGGAGTA	105		
Qy	61	GTAGGTGCTCAAAACATCAGCCCGATTGGGAGCCACTGCTGAAGTTAAGGG	120		
Db	106	GTAGGTGCTCAAAACATCAGCCCGATTGGGAGCCACTGCTGAAGTTAAGGG	165		
Qy	121	GCCCCAAGAAACACACCCAGCGCTGGAATGAAACTGAACACAGGCCGACAGAAGCT	180		
Db	166	GCCCCAAGAAACACACCCAGCGCTGGAATGAAACTGAACACAGGCCGACAGAAGCT	225		
Qy	181	TGAAAGTCTGTCTCCCAAGGAGGAGGCCCTCGGACAGTGTGGTCTGTCTCTCC	240		
Db	226	TGAAAGTCTGTCTCCCAAGGAGGAGGCCCTCGGACAGTGTGGTCTGTCTCTCC	285		
Qy	241	AACGGCTCCCTCTCTCCCTCCGGCTGTCCGGATCCAGATGAGGGGATTTCCGGTCCAG	300		
Db	286	AACGGCTCCCTCTCTCCCTCCGGCTGTCCGGATCCAGATGAGGGGATTTCCGGTCCAG	345		
Qy	301	GCAATGAACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATT	360		
Db	346	GCAATGAACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATT	405		
Qy	361	CTTGGGAGCCAGAAATTGAGATTCTGCTCTGAACTACGGCTGGTGTCCCAATAG	420		
Db	406	CTTGGGAGCCAGAAATTGAGATTCTGCTCTGAACTACGGCTGGTGTCCCAATAG	465		
Qy	421	GTGGGACATGTGTGTCAGAGGAAGCTACCCCTGACGGAGCTCTTAGCTGGCACTTGGAT	480		
Db	466	GTGGGACATGTGTGTCAGAGGAAGCTACCCCTGACGGAGCTCTTAGCTGGCACTTGGAT	525		
Qy	481	GGAAAGCCCTGTGTCTTAATGAGAGGGAGTATCTGTGAAGAAACAGACAGGAGACAC	540		
Db	526	GGAAAGCCCTGTGTCTTAATGAGAGGGAGTATCTGTGAAGAAACAGACAGGAGACAC	585		
Qy	541	CTTGAGACAGGCTCTTACACTGACGTGGAGCTAATGGTGACCCAGCCCGGGAGGA	600		
Db	586	CTTGAGACAGGCTCTTACACTGACGTGGAGCTAATGGTGACCCAGCCCGGGAGGA	645		
Qy	601	GATCCCGCTCCCACTTCTCTGTAGCTTCAGCCAGGCTTCCCGACACCGGGCTTG	660		
Db	646	GATCCCGCTCCCACTTCTCTGTAGCTTCAGCCAGGCTTCCCGACACCGGGCTTG	705		
Qy	661	CGACAGCCCCATCCAGCCCGCTGTCTGGAGCCTGTGCTCTGGAGAGTCCAAATTG	720		
Db	706	CGACAGCCCCATCCAGCCCGCTGTCTGGAGCCTGTGCTCTGGAGAGTCCAAATTG	765		
Qy	721	GTGGTGGAGCCAGAGTGGAGCAGTAGCTCTCTGGTGGAACTTACCTGACCTGTGAA	780		
Db	766	GTGGTGGAGCCAGAGTGGAGCAGTAGCTCTCTGGTGGAACTTACCTGACCTGTGAA	825		
Qy	781	GTCCCTGCCAGCCCTCTCTCTCAATCCACTGTGATGAAGGATGGTGTGCCCTT	840		
Db	826	GTCCCTGCCAGCCCTCTCTCTCAATCCACTGTGATGAAGGATGGTGTGCCCTT	885		
Qy	841	CCCCCAGCCCTGTGTGATCTCTCTGATAGATAGGCCCTCAGAACAGGAACTTACAG	900		
Db	886	CCCCCAGCCCTGTGTGATCTCTCTGATAGATAGGCCCTCAGAACAGGAACTTACAG	945		
Qy	901	TGTGTGGCCACCATTCAGCCACGGGCCCGAGGAAGCCGTCTGTGAGCATCAGCATC	960		
Db	946	TGTGTGGCCACCATTCAGCCACGGGCCCGAGGAAGCCGTCTGTGAGCATCAGCATC	1005		
Qy	961	ATCGAACCCAGGCGAGGAGGGGCCAACTGCAGGCTCTGTGGGAGGATCAGGGCTGG	1015		
Db	1006	ATCGAACCCAGGCGAGGAGGGGCCAACTGCAGGCTCTGTGGGAGGATCAGGGCTGG	1060		

RESULT 6	
ID	ABQ99597
XX	ABQ99597 standard; cDNA; 1415 BP.
XX	ABQ99597;
XX	
DT	25-FEB-2003 (first entry)
XX	
DE	Human coding sequence SEQ ID 330.
XX	
KW	Human; expressed sequence tag; EST; chromosome 6p21.3;
KW	haematopoietic disorder; central nervous system disease; viral infection;
KW	peripheral nervous system disease; non-healing wound; infectious disease;
KW	immune deficiency; immune disorder; bacterial infection; allergy; cancer;
KW	fungal infection; autoimmune disorder; coagulation disorder; neutropenic;
KW	antiallergic; antitumour; immunosuppressive; neuroprotective;
KW	cytostatic; haemostatic; virucide; antibacterial; fungicide;
KW	immunostimulant; cerebroprotective; gene therapy; gene; ss.
OS	Homo sapiens.
XX	
PN	WO200259260-A2.
XX	
PD	01-AUG-2002.
XX	
PP	16-NOV-2001; 2001WO-US042950.
XX	
PR	17-NOV-2000; 2000US-00714936.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;
PI	Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX	
DR	WPI; 2002-590824/63.
DR	N-PSDB; ABP65011.
XX	
PT	New isolated polynucleotide, useful in research, diagnostic or
PT	therapeutic methods, e.g. preventing or treating disorders involving
PT	aberrant protein expression or biological activity.
XX	
PS	Claim 1; SEQ ID NO 330; 394pp; English.
XX	
CC	The present invention relates to novel human coding sequences (ABQ99268-
CC	ABQ99608) and proteins (ABP64682-ABP65022). The sequences are useful in
CC	therapeutic, diagnostic and research methods. The polynucleotides may be
CC	used in the field of molecular biology as hybridisation probes, primers
CC	for PCR, for chromosome and gene mapping, for the recombinant production
CC	of protein, or in generation of anti-sense DNA or RNA. The
CC	polynucleotides are useful in diagnostics as expressed sequence tags
CC	(ESTs) for identifying expressed genes or for physical mapping of the
CC	human genome. The proteins may be used as molecular weight markers, or as
CC	nutritional sources or supplements. The proteins may be used to maintain
CC	and expand cell population in a totipotent or pluripotential state
CC	useful for re-engineering damaged or diseased tissues, transplantation,
CC	manufacture of bio-pharmaceuticals or the development of bio-sensors. The
CC	polynucleotides and proteins are useful for preventing, treating or
CC	ameliorating disorders involving aberrant protein expression or
CC	biological activity, e.g. haematopoietic disorders, central/peripheral
CC	nervous system diseases, mechanical and traumatic disorders, non-healing
CC	wounds, immune deficiencies and disorders, infectious diseases caused by
CC	viral, bacterial or fungal infection, autoimmune disorders, allergic
CC	reactions and conditions, coagulation disorders, or cancer. The
CC	polynucleotide sequences of the invention were assembled from ESTs
CC	isolated mainly by sequencing by hybridisation, and in some cases,
CC	sequences obtained from one or more public databases. Note: The sequence
CC	data for this patent did not form part of the printed specification, but
CC	was obtained in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 1415 BP; 313 A; 414 C; 425 G; 263 T; 0 U; 0 Other;

Query Match 99.5%; Score 1015; DB 6; Length 1415;

Best Local Similarity 100.0%; Pred. No. 8.4e-261; Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGGCAGCCGGAACAGCAGTTGGAGCTGGCTGCTGCTCCTCAGTCTGTGGGGGCGAGTA	60
DB	25	ATGGCAGCCGGAACAGCAGTTGGAGCTGGCTGCTCCTCAGTCTGTGGGGGCGAGTA	84
QY	61	GTAGGTGCTCAAAACATCAAGCCCGGATTTGGGAGCCACTGGTGTGAAGTGAAGGG	120
DB	85	GTAGGTGCTCAAAACATCAAGCCCGGATTTGGGAGCCACTGGTGTGAAGTGAAGGG	144
QY	121	GCCCCCAAGAAACACCCAGCGCTGGATGAACTGAACACAGCCGGAAGAAGCT	180
DB	145	GCCCCCAAGAAACACCCAGCGCTGGATGAACTGAACACAGCCGGAAGAAGCT	204
QY	181	TGGAAGTCTCTGCTCTCCCAAGGAGAGGCCCTGGGACAGTGTGGCTGTGCTCTTCCC	240
DB	205	TGGAAGTCTCTGCTCTCCCAAGGAGAGGCCCTGGGACAGTGTGGCTGTGCTCTTCCC	264
QY	241	AACGGTCTCTCTCTCTCCGCTGTGCGGATCCAGATGAGGGATTTTCGGTGCAG	300
DB	265	AACGGTCTCTCTCTCTCCGCTGTGCGGATCCAGATGAGGGATTTTCGGTGCAG	324
QY	301	GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTCTACCAAGTT	360
DB	325	GCAATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTCTACCAAGTT	384
QY	361	CTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTACCGCTGGTGTTCCTCAATAAG	420
DB	385	CTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTACCGCTGGTGTTCCTCAATAAG	444
QY	421	GTGGGACATGTGTGTGAGAGGAAGTACCTGCGAGGACTCTTAGCTGGCACTTGGAT	480
DB	445	GTGGGACATGTGTGTGAGAGGAAGTACCTGCGAGGACTCTTAGCTGGCACTTGGAT	504
QY	481	GGGAAGCCCTGTGCTTAATGAGAGGAGTATCTGTGAGAAACAGACCAGGACAC	540
DB	505	GGGAAGCCCTGTGCTTAATGAGAGGAGTATCTGTGAGAAACAGACCAGGACAC	564
QY	541	CTTGAGACAGGGCTCTTCACTGTCAGTCCGAGCTAATGTGACCCAGCCCGGGGAGGA	600
DB	565	CTTGAGACAGGGCTCTTCACTGTCAGTCCGAGCTAATGTGACCCAGCCCGGGGAGGA	624
QY	601	GATCCCGTCCACCTCTCTGCTAGCTTCCAGCCAGGCTTCCCGACACCGGGCTTG	660
DB	625	GATCCCGTCCACCTCTCTGCTAGCTTCCAGCCAGGCTTCCCGACACCGGGCTTG	684
QY	661	CGCAGACCCCATCCAGCCCTGTCTGGAGCCTGTGCTCTGGAGAGTCCCAATTG	720
DB	685	CGCAGACCCCATCCAGCCCTGTCTGGAGCCTGTGCTCTGGAGAGTCCCAATTG	744
QY	721	GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTGCTGGTGAACCTGAACCTGACCTGTGAA	780
DB	745	GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTGCTGGTGAACCTGAACCTGACCTGTGAA	804
QY	781	GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAAGATGGTGTGCCCTTGCCCTTT	840
DB	805	GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAAGATGGTGTGCCCTTGCCCTTT	864
QY	841	CCCCCAGCCCTGTGCTGATCTCTCTGATGATAGGGCTCAGGACAGGGAACCTACAGC	900
DB	865	CCCCCAGCCCTGTGCTGATCTCTCTGATGATAGGGCTCAGGACAGGGAACCTACAGC	924
QY	901	TGTGTGGCCACCATTCAGCCAGGGCCCCAGGAAAGCGTCTGTGACATCAGCATC	960
DB	925	TGTGTGGCCACCATTCAGCCAGGGCCCCAGGAAAGCGTCTGTGACATCAGCATC	984
QY	961	ATCGAACCAGGCGGAGGGGGCCAACTGCAAGCTCTGTGGGAGGATCAGGGCTGG	1015
DB	985	ATCGAACCAGGCGGAGGGGGCCAACTGCAAGCTCTGTGGGAGGATCAGGGCTGG	1039

ADK00130	ADK00130 standard; cDNA; 1436 BP.
XX	
AC	ADK00130;
XX	
DT	20-MAY-2004 (first entry)
XX	
DE	Human RAGE encoding sequence.
XX	
KW	Advanced Glycation End Product Ligand Binding Element; RAGE-LBE;
KW	Cytostatic; Antidiabetic; Nootropic; Antiarthritic; Osteopathic;
KW	Neuroprotective; Antiinflammatory; Dermatological; Immunosuppressive;
KW	Vasotropic; Antipsoriatic; Antibacterial; Antiarteriosclerotic;
KW	amyloidosis; cancer; Crohn's disease; diabetes; Alzheimer's disease;
KW	chronic inflammatory disease; osteoarthritis; irritable bowel disease;
KW	multiple sclerosis; psoriasis; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
Key	Location/Qualifiers
FT	1..1436
CDS	/*tag= a
FT	/product= "RAGE"
XX	
XX	WO2004016229-A2.
XX	
PD	26-FEB-2004.
XX	
PF	18-AUG-2003; 2003WO-US025996.
XX	
PR	16-AUG-2002; 2002US-0404205P.
XX	
PA	(AMHP) WYETH.
XX	
PI	Pittman DD, Clancy B, Larsen G, Trepicchio WL, Brennan FM;
PI	Feldmann M, Foxwell BJM, Feldman JL;
XX	
DR	WPI; 2004-192067/18.
XX	P-PSDB; ADK00129.
XX	
PT	New fusion protein comprising a Receptor for Advanced Glycation End
PT	Product Ligand Binding Element (RAGE-LBE) and an immunoglobulin element,
PT	useful for preparing a composition for treating e.g., Alzheimer's
PT	disease.
XX	
PS	Disclosure; SEQ ID NO 44; 100pp; English.
XX	
CC	The present invention relates to a new fusion protein comprises a
CC	Receptor for Advanced Glycation End Product Ligand Binding Element (RAGE-
CC	LBE) and an immunoglobulin element. The fusion protein is useful for
CC	preparing a composition for treating RAGE-associated disorders such as
CC	amyloidosis, cancer, Crohn's disease, diabetes, complications of
CC	diabetes, prion-related disorders, vasculitis, nephropathies,
CC	retinopathies and/or neuropathies; Alzheimer's disease, chronic
CC	inflammatory disease e.g., rheumatoid arthritis, osteoarthritis,
CC	irritable bowel disease, multiple sclerosis, psoriasis or lupus, acute
CC	inflammatory disease e.g., sepsis, or cardiovascular disease, e.g.,
CC	atherosclerosis or restenosis. The present sequence represents human RAGE
CC	protein encoding sequence.
XX	
SQ	Sequence 1436 BP; 340 A; 411 C; 422 G; 263 T; 0 U; 0 Other;
Query Match 99.5%; Score 1015; DB 12; Length 1436;	
Best Local Similarity 100.0%; Pred. No. 8.5e-261;	
Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ATGGCAGCCGGAACAGCAGTTGGAGCTGGCTGCTCCTCAGTCTGTGGGGGCGAGTA 60
DB	20 ATGGCAGCCGGAACAGCAGTTGGAGCTGGCTGCTCCTCAGTCTGTGGGGGCGAGTA 79
QY	61 GTAGGTGCTCAAAACATCAAGCCCGGATTTGGGAGCCACTGGTGTGAAGTGAAGGG 120

Db 80 GTAGTGTCTCAAAACATCATCAGCCCGGATTGGGAGCCACTGGTGTCTGAAGTGTAAAGGG 139
QY 121 GCCCCCAAGAAACACACCCAGCGCTGGAATGAACTGAACACAGCCGCGACAGAGCT 180
Db 140 GCCCCCAAGAAACACACCCAGCGCTGGAATGAACTGAACACAGCCGCGACAGAGCT 199
QY 181 TGAAGGTCTGTCTCTCCCAAGGAGGAGGCCCTCGGACAGTGTGGCTGTGTCTTCCC 240
Db 200 TGAAGGTCTGTCTCTCCCAAGGAGGAGGCCCTCGGACAGTGTGGCTGTGTCTTCCC 259
QY 241 AACGGTCTCTCTCTCTCCCGCTGTGGATCCAGATGAGGGGATTTTCGGTCCGAG 300
Db 260 AACGGTCTCTCTCTCTCCCGCTGTGGATCCAGATGAGGGGATTTTCGGTCCGAG 319
QY 301 GCAATGAACAGGAATGGAAGAGAGACCAAGTCAACTACCGAGTCCGTGTCTACCAAGT 360
Db 320 GCAATGAACAGGAATGGAAGAGAGACCAAGTCAACTACCGAGTCCGTGTCTACCAAGT 379
QY 361 CTTGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCACGGCTGGTGTCTCCCAATAAG 420
Db 380 CTTGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCACGGCTGGTGTCTCCCAATAAG 439
QY 421 GTGGGACATGTGTCTCAGAGGAAAGTACCTTCGAGGAGCTCTTAGCTGGCACTTGGAT 480
Db 440 GTGGGACATGTGTCTCAGAGGAAAGTACCTTCGAGGAGCTCTTAGCTGGCACTTGGAT 499
QY 481 GGAAGCCCTGTGTCTTAATGAGAGGAGTATCTGTGAAGAAACAGACACAGAGACAC 540
Db 500 GGAAGCCCTGTGTCTTAATGAGAGGAGTATCTGTGAAGAAACAGACACAGAGACAC 559
QY 541 CTTGAGACAGGGCTCTTCACTGCACTGAGTGGAGCTAATGTGACCCAGCCCGGGAGGA 600
Db 560 CTTGAGACAGGGCTCTTCACTGCACTGAGTGGAGCTAATGTGACCCAGCCCGGGAGGA 619
QY 601 GATCCCGTCCCACTTCTCTGTAGTTCAGCCCGAGGCTTCCCGACACACCGGCTTG 660
Db 620 GATCCCGTCCCACTTCTCTGTAGTTCAGCCCGAGGCTTCCCGACACACCGGCTTG 679
QY 661 CGCACAGCCCCCATCCAGCCCCCTGTCTGGAGCCTGTGCTCTGGAGAGGTCCCAATTG 720
Db 680 CGCACAGCCCCCATCCAGCCCCCTGTCTGGAGCCTGTGCTCTGGAGAGGTCCCAATTG 739
QY 721 GTGGTGGAGCAGAGGTGGAGCAGTAGTCTCTGTGGAAACCGTAACCTGTACCTGTGAA 780
Db 740 GTGGTGGAGCAGAGGTGGAGCAGTAGTCTCTGTGGAAACCGTAACCTGTACCTGTGAA 799
QY 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAAGATGGTGTGCCCTTGCCCTT 840
Db 800 GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAAGATGGTGTGCCCTTGCCCTT 859
QY 841 CCCCCAGCCCTGTGTCTGATCTCTCCCTGAGATAGGCGCTCAGACACAGGAACCTACAGC 900
Db 860 CCCCCAGCCCTGTGTCTGATCTCTCCCTGAGATAGGCGCTCAGACACAGGAACCTACAGC 919
QY 901 TGTGTGGCCACCCATTCCAGCCACAGGCCCCAGGAAAGCGTGTCTCAGCATCAGCATC 960
Db 920 TGTGTGGCCACCCATTCCAGCCACAGGCCCCAGGAAAGCGTGTCTCAGCATCAGCATC 979
QY 961 ATCGAACCCAGGCGAGGAGGCGCAACTGCAAGCTCTGTGGAGGATCAGGGCTGG 1015
Db 980 ATCGAACCCAGGCGAGGAGGCGCAACTGCAAGCTCTGTGGAGGATCAGGGCTGG 1034

RESULT 8
ADE95563
ID ADE95563 standard; cDNA; 1217 BP.
AC ADE95563;
XX
XX
DT 12-FEB-2004 (first entry)
XX
DE Human NOVX16c protein cDNA sequence.
XX

KW NOVX protein; biochemical stimulation; physiological stimulation;
KW cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
KW antirheumatic; antiarthritic; antidiabetic; nephrotropic; dermatological;
KW immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;
KW nootropic; antipsoriatic; antiparkinsonian; antiaschmatic; neuroleptic;
KW antidepressant; antiallergic; gynaecological; gene therapy; vaccine;
KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;
KW cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;
KW psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;
KW Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;
KW depression; allergy; fertility disorder; gene; ss; NOVX16c.
XX
OS Homo sapiens.
XX WO2003050245-A2.
PN 19-JUN-2003.
XX
PD 03-DEC-2002; 2002WO-US038594.
XX
PF 05-DEC-2001; 2001US-0336600P.
XX
PR 07-DEC-2001; 2001US-0338285P.
PR 12-DEC-2001; 2001US-0341346P.
PR 17-DEC-2001; 2001US-0341477P.
PR 20-DEC-2001; 2001US-0341540P.
PR 27-DEC-2001; 2001US-0342592P.
PR 31-DEC-2001; 2001US-0344297P.
PR 31-DEC-2001; 2001US-0344903P.
PR 17-APR-2002; 2002US-0373288P.
PR 15-MAY-2002; 2002US-0380981P.
PR 17-MAY-2002; 2002US-0381495P.
PR 28-MAY-2002; 2002US-0383534P.
PR 28-MAY-2002; 2002US-0383744P.
PR 29-MAY-2002; 2002US-0383829P.
PR 29-MAY-2002; 2002US-0384024P.
PR 07-AUG-2002; 2002US-0401788P.
PR 26-AUG-2002; 2002US-0406353P.
PR 31-OCT-2002; 2002US-00401788.
PR 02-DEC-2002; 2002US-00406353.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru RA,
PI Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X;
PI Jeffers ME, Ji W, Li L, Malyankar UM, Miller CE, Murphy R;
PI Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG,
PI Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;
XX WPI; 2003-513974/48.
DR P-PSDB; ADE95564.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 20; SEQ ID NO 95; 211pp; English.
XX
XX This invention relates to novel NOVX proteins, and the DNA sequence which
CC encode them, having properties related to stimulation of biochemical or
CC physiological responses in a cell, a tissue, an organ or an organism.
CC Compounds which modulate the proteins of the invention may have cardiant,
CC antiarteriosclerotic, hypotensive, cytostatic, anorectic, antirheumatic,
CC antiarthritic, antidiabetic, nephrotropic, dermatological,
CC immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,
CC antipsoriatic, antiparkinsonian, antiaschmatic, neuroleptic,
CC antidepressant, antiallergic or gynaecological activities. The DNA
CC sequences of the invention may be useful for gene therapy whilst the
CC protein sequences may allow the development of a vaccine. The protein is
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease. The invention may be useful in
CC diagnosing, treating or preventing NOVX-associated disorders, for example
CC cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,

CC rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin
CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
CC Parkinson's disease, asthma, schizophrenia, depression, allergies or
CC fertility disorders. The nucleic acids may further be used as
CC hybridisation probes, in chromosome mapping, tissue typing, preventive
CC medicine, and pharmacogenomics. The present sequence is the cDNA sequence
XX which encodes the human NOV16c protein of the invention.

QY Sequence 1217 BP; 265 A; 343 C; 393 G; 216 T; 0 U; 0 Other;
Query Match 99.4%; Score 1013.4; DB 10; Length 1217;
Best Local Similarity 99.9%; Pred. No. 2.1e-260;
Matches 1014; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCAGCGGACACAGCAGTTGGAGCTGGGTCTGCTGCTCTCAGTCTGTGGGGGCGAGTA 60
DB 3 ATGGCAGCGGACACAGCAGTTGGAGCTGGGTCTGCTGCTCTCAGTCTGTGGGGGCGAGTA 62

QY 61 GTAGTGTCTCAAAACATCAGCCCGATTTGGGAGCCACTGGTGTGAAGTGTAAAGGG 120
DB 63 GTAGTGTCTCAAAACATCAGCTCGGATTTGGGAGCCACTGGTGTGAAGTGTAAAGGG 122

QY 121 GCCCCCAAGAAACACCCAGCGGCTGGATGGAATGAACTGAACACAGCCGACAGAGCT 180
DB 123 GCCCCCAAGAAACACCCAGCGGCTGGATGGAATGGAATGAACTGAACACAGCCGACAGAGCT 182

QY 181 TGAAGTCTCTGTCTCCCGAGGAGGAGGCCCTCGGACAGTGTGCTGTCTTCCC 240
DB 183 TGAAGTCTCTGTCTCCCGAGGAGGAGGCCCTCGGACAGTGTGCTGTCTTCCC 242

QY 241 AACGGTCTCTTCTTCTCCGCTGTGCGGATCCAGGATGAGGGGATTTTCGGTCCAG 300
DB 243 AACGGTCTCTTCTTCTCCGCTGTGCGGATCCAGGATGAGGGGATTTTCGGTCCAG 302

QY 301 GCAATGAACAGGAATGGAAGGAGCAAGTCCAACTACCGTCCGTCTACCAAGATT 360
DB 303 GCAATGAACAGGAATGGAAGGAGCAAGTCCAACTACCGTCCGTCTACCAAGATT 362

QY 361 CTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCACGGCTGGTGTCCCAATAAG 420
DB 363 CTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCACGGCTGGTGTCCCAATAAG 422

QY 421 GTGGGACATGTGTGTGACAGGAACTACCTGTGACGAGACTTTAGCTGGCACTTGGAT 480
DB 423 GTGGGACATGTGTGTGACAGGAACTACCTGTGACGAGACTTTAGCTGGCACTTGGAT 482

QY 481 GGGAGCCCTGTGTGCTTAATGAGAGGAGTATCTGTGAAGGAGGATATCTGTGAAGGAGGAGGAGAC 540
DB 483 GGGAGCCCTGTGTGCTTAATGAGAGGAGGATATCTGTGAAGGAGGAGGAGGAGAC 542

QY 541 CCTGAGACAGGGCTCTTTCACACTGCACTCGGAGCTAATGTGACCCAGCCCGGGGAGGA 600
DB 543 CCTGAGACAGGGCTCTTTCACACTGCACTCGGAGCTAATGTGACCCAGCCCGGGGAGGA 602

QY 601 GATCCCGTCCCACTTCTCTGTAGCTTCAAGCCAGGCTTCCCGACACCGGGGCTTG 660
DB 603 GATCCCGTCCCACTTCTCTGTAGCTTCAAGCCAGGCTTCCCGACACCGGGGCTTG 662

QY 661 CGCAGAGCCCATCCAGCCCGTGTCTGGAGCCTGTGCTGTGAGAGGCTTCAATTTG 720
DB 663 CGCAGAGCCCATCCAGCCCGTGTCTGGAGCCTGTGCTGTGAGAGGCTTCAATTTG 722

QY 721 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTGTGGTGAACCTGACCTGTGTAA 780
DB 723 GTGGTGGAGCCAGAGGTGAGCAGTAGCTCTGTGGTGAACCTGACCTGTGTAA 782

QY 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGGATGAAGATGGTGTGCCCTTGCCCTTT 840
DB 783 GTCCCTGCCAGCCCTCTCTCAATCCACTGGATGAAGATGGTGTGCCCTTGCCCTTT 842

QY 841 CCCCCAGCCCTGTGTGTATCTCTCCCTGAGATAGGCGCTCAGGACAGGGAACCTACAGC 900
DB 843 CCCCCAGCCCTGTGTGTATCTCTCCCTGAGATAGGCGCTCAGGACAGGGAACCTACAGC 902

QY 901 TGTGTGGCCACCCATTCCAGCCACGGGCCCCAGGAAAGCCGTGTGTCTCAGCATCAGCATC 960
DB 903 TGTGTGGCCACCCATTCCAGCCACGGGCCCCAGGAAAGCCGTGTGTCTCAGCATCAGCATC 962

QY 961 ATCGAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1015
DB 963 ATCGAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1017

RESULT 9
AAH57444
ID AAH57444 standard; cDNA; 1582 BP.
XX
AC AAH57444;
DT 10-SEP-2001 (first entry)
XX
DE Human lung cell specific cDNA sequence SEQ ID NO:284.
XX
KW Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;
KW liver; uterus; ovary; stomach; intestine; kidney; pancreas; es;
KW metabolic disease; developmental disease; cytostatic; immunomodulatory;
KW neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
XX
OS Homo sapiens.
XX
PN WO200132927-A2.
XX
PD 10-MAY-2001.
XX
PF 02-NOV-2000; 2000WO-US030396.
XX
PR 04-NOV-1999; 99US-0163508P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Sornasse T, Seilhamer JJ, Watson GA;
WPI; 2001-291057/30.
XX
PT New cell and tissue specific polynucleotides useful for diagnosis,
PT prognosis or monitoring of treatments for disorders where the gene is
PT associated with a cancer, immunopathology or neuropathology.
XX
PS Claim 1: Page 210; 327pp; English.
XX
CC AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
CC sequences (I). (I) can have cytostatic, immunomodulatory and
CC neuroprotective activities, and can be used in gene therapy. (I) and
CC proteins (II) encoded by then are used in high throughput screening
CC assays to select DNA molecules, RNA molecules, peptide nucleic acids,
CC mimetics, peptides, proteins, agonists, antagonists, antibodies or their
CC fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical
CC agents. Expression of (I) in a sample indicates the differentiation of
CC embryonic stem cells into a tissue selected from brain, heart, kidney,
CC liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used
CC to produce an expression profile that defines a metabolic or
CC developmental process, treatment, condition, disease or disorder. The
CC gene profile can be used for diagnosis, prognosis or monitoring of
CC treatments and for investigating a predisposition to a disorder where the
CC gene is associated with a cancer, immunopathology or neuropathology
XX
SQ Sequence 1582 BP; 355 A; 448 C; 486 G; 293 T; 0 U; 0 Other;

Query Match 99.4%; Score 1013.4; DB 4; Length 1582;
Best Local Similarity 99.9%; Pred. No. 2.3e-260;
Matches 1014; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCAGCGGACACAGCAGTTGGAGCTGGGTCTGCTGCTCTCAGTCTGTGGGGGCGAGTA 60
DB 201 ATGGCAGCGGACACAGCAGTTGGAGCTGGGTCTGCTGCTCTCAGTCTGTGGGGGCGAGTA 260

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QY 61 GTAGTGTCTCAAAACATCAAGCCCGGATTGGAGCCACTGTGTCTGAAGTGTAAAGGG 120
D 61 |
D 261 GTAGTGTCTCAAAACATCAAGCCCGGATTGGAGCCACTGTGTCTGAAGTGTAAAGGG 320
QY 121 GCCCCCAAGAAACACCCAGCGGTGGAAATGAAACTGAACACAGCCCGGACAGAAGCT 180
D 121 |
D 321 GCCCCCAAGAAACACCCAGCGGTGGAAATGAAACTGAACACAGCCCGGACAGAAGCT 380
QY 181 TGAAGGTCTGTCTCTCCAGGAGGAGGCCCTCTGGACAGTGTGTCTGTCTCTTCC 240
D 181 |
D 381 TGAAGGTCTGTCTCTCCAGGAGGAGGCCCTCTGGACAGTGTGTCTGTCTCTTCC 440
QY 241 AACGGTCCCTCTCTCTCCGCTGTGGGATCCAGATCCAGATGAGGGGATTTTCGGTCCAG 300
D 241 |
D 441 AACGGTCCCTCTCTCTCCGCTGTGGGATCCAGATCCAGATGAGGGGATTTTCGGTCCAG 500
QY 301 GCAATGACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATT 360
D 301 |
D 501 GCAATGACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATT 560
QY 361 CTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACTCAAGGCTGTGTCTCCCAATAAG 420
D 361 |
D 561 CTGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACTCAAGGCTGTGTCTCCCAATAAG 620
QY 421 GTGGGACATGTGTGTGACAGGGAAGCTACCTGACAGGACTCTTAGCTGGCACTTGGAT 480
D 421 |
D 621 GTGGGACATGTGTGTGACAGGGAAGCTACCTGACAGGACTCTTAGCTGGCACTTGGAT 680
QY 481 GGGAAAGCCCTGTGTCTTAATGAGAGGGAGTATCTGTGAAGAAACAGACCCAGGAGAC 540
D 481 |
D 681 GGGAAAGCCCTGTGTCTTAATGAGAGGGAGTATCTGTGAAGAAACAGACCCAGGAGAC 740
QY 541 CTTGACAGAGGCTCTTCACTACAGTGTGAGTCAATGTGACCCAGCCAGCGGGAGGA 600
D 541 |
D 741 CTTGACAGAGGCTCTTCACTACAGTGTGAGTCAATGTGACCCAGCCAGCGGGAGGA 800
QY 601 GATCCCGTCCCACTCTCTCTGTAGCTTCTGAGCCAGGCTTCCCGACACCGGCGCTTG 660
D 601 |
D 801 GATCCCGTCCCACTCTCTCTGTAGCTTCTGAGCCAGGCTTCCCGACACCGGCGCTTG 860
QY 661 CGCAGAGCCCATCCAGCCCGTGTCTGGAGCTGTGCTCTGAGAGAGTCCCAATTG 720
D 661 |
D 861 CGCAGAGCCCATCCAGCCCGTGTCTGGAGCTGTGCTCTGAGAGAGTCCCAATTG 920
QY 721 GTGGTGGAGCCAGAGGTGGAGCAGTAGCTCTGTGGTGAACCGTAACTGACCTGTGAA 780
D 721 |
D 921 GTGGTGGAGCCAGAGGTGGAGCAGTAGCTCTGTGGTGAACCGTAACTGACCTGTGAA 980
QY 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGGATGAAGATGGTGTGCCCTTGCCCTTT 840
D 781 |
D 981 GTCCCTGCCAGCCCTCTCTCAATCCACTGGATGAAGATGGTGTGCCCTTGCCCTTT 1040
QY 841 CCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGCTTCAAGACAGGGAACCTTACAGC 900
D 841 |
D 1041 CCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGCTTCAAGACAGGGAACCTTACAGC 1100
QY 901 TGTGTGGCCACCAATTCAGACCAAGCCCGCCAGGAAAGCCGTGTGTGACATCAGCATC 960
D 901 |
D 1101 TGTGTGGCCACCAATTCAGACCAAGCCCGCCAGGAAAGCCGTGTGTGACATCAGCATC 1160
QY 961 ATCGAACAGGAGAGAGGGGGCAACTGAGGCTCTGTGGAGGATTCAGGGCTGG 1015
D 961 |
D 1161 ATCGAACAGGAGAGAGGGGGCAACTGAGGCTCTGTGGAGGATTCAGGGCTGG 1215
```

RESULT 10

ABQ79955

ID ABQ79955 standard; DNA; 1391 BP.

XX

AC ABQ79955;

XX

DT 23-DEC-2002 (first entry)

XX

DE Human RAGE nucleotide sequence.

XX Receptor for Advanced Glycated end product; RAGE; recombinant; nootropic;
KW antiarteriosclerotic; antidiabetic; cytostatic; nephrotropic; vasotropic;
KW neuroprotective; antiinflammatory; gene therapy; human; db.
XX Homo sapiens.
XX OS
XX WO200270667-A2.
XX PN
XX PD 12-SEP-2002.
XX PF
XX 05-MAR-2002; 2002WO-US006881.
XX PR
XX 05-MAR-2001; 2001US-0273418P.
XX (TRAN-) TRANSTECH PHARMA INC.
XX PA
XX Harris R, Shen J, Shahbaz M;
XX PI
XX WPI; 2002-713443/77.
XX DR
XX

PT High level expression of recombinant Receptors for Advanced Glycated end

PT products (RAGE) proteins for treating increased levels of advanced
PT glycosylation end products, comprises infecting cells with a high titer
PT recombinant virus.
XX
XX Claim 12; Fig 2A; 51pp; English.
XX
XX The invention relates to a method for high level expression of
CC recombinant forms of the Receptor for Advanced Glycated end products
CC (RAGE) or its fragments. The method involves (i) subcloning a nucleotide
CC sequence encoding RAGE or its fragment into a virus; (ii) preparing a
CC high titer stock of recombinant virus; and (iii) infecting host cells
CC with the high titer recombinant virus under conditions such that
CC predetermined levels of RAGE or its fragment is produced, where the
CC predetermined levels of RAGE comprises at least 25 mg recombinant protein
CC per liter of culture. The method is useful for high level expression of
CC recombinant RAGE polypeptide or its fragment which may be useful in
CC preventing, treating or ameliorating diseases associated with increased
CC levels of advanced glycosylation end products, such as atherosclerosis,
CC diabetes and its symptoms, amyloidosis, kidney failure, Alzheimer's
CC disease, inflammation, systemic lupus nephritis, inflammatory lupus
CC nephritis, cancer or erectile dysfunction. The present sequence
CC represents the nucleotide sequence of human RAGE as reported in GenBank
CC /EMBL Accession no. XM004205
XX

PS Sequence 1391 BP; 305 A; 408 C; 417 G; 261 T; 0 U; 0 Other;

XX Query Match 99.3%; Score 1013; DB 6; Length 1391;
XX Best Local Similarity 100.0%; Pred. No. 2.9e-260;
XX Matches 1013; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GCGAGCCGGAACAGCAGTGTGGAGCCTGGGTCTGTCTCTCAGTCTGTGGGGGAGTAGT 62
D 3 |
D 3 GCGAGCCGGAACAGCAGTGTGGAGCCTGGGTCTGTCTCTCAGTCTGTGGGGGAGTAGT 62
QY 63 AGGTCTCAAAACATCAAGCCCGGATTGGAGCCACTGTGTGAAGTGTAAAGGGGC 122
D 63 |
D 63 AGGTCTCAAAACATCAAGCCCGGATTGGAGCCACTGTGTGAAGTGTAAAGGGGC 122
QY 123 CCCCAGAAAAACACCCAGCGGCTGGAATGGAACCTGAACACAGGCCCGGACAGAGCTTG 182
D 123 |
D 123 CCCCAGAAAAACACCCAGCGGCTGGAATGGAACCTGAACACAGGCCCGGACAGAGCTTG 182
QY 183 GAAGTCTCTGTCTCCCGAGGAGAGGCCCTCTGGGACAGTGTGGCTCTGTCTTCCAA 242
D 183 |
D 183 GAAGTCTCTGTCTCCCGAGGAGAGGCCCTCTGGGACAGTGTGGCTCTGTCTTCCAA 242
QY 243 CGGCTCCCTCTTCTTCCGCTGTGCGGATCCAGATCAGGGGATTTTCCGCTGCAGGC 302
D 243 |
D 243 CGGCTCCCTCTTCTTCCGCTGTGCGGATCCAGATCAGGGGATTTTCCGCTGCAGGC 302

QY	303	AATGAACAGGAATGGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC	362
Db	303	AATGAACAGGAATGGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC	362
QY	363	TGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACCTACGGCTGGTGTCCCAATAGGT	422
Db	363	TGGGAAGCCAGAAATTGTAGATTCTGCTCTGAACCTACGGCTGGTGTCCCAATAGGT	422
QY	423	GGGGACATGTGTCTGAGAGGAAGCTACCTCGAGGAGCTCTTAGCTGGCACTTGGATGG	482
Db	423	GGGGACATGTGTCTGAGAGGAAGCTACCTCGAGGAGCTCTTAGCTGGCACTTGGATGG	482
QY	483	GAAGCCCTGGTGCCTAATGAGAAGGGAGTATCTGTGAAGGAACAGACCGAGACACC	542
Db	483	GAAGCCCTGGTGCCTAATGAGAAGGGAGTATCTGTGAAGGAACAGACCGAGACACC	542
QY	543	TGAGACAGGGCTCTTACACCTGAGTCGGAGCTAATGTTGACCCAGCCGGGGAGGAGA	602
Db	543	TGAGACAGGGCTCTTACACCTGAGTCGGAGCTAATGTTGACCCAGCCGGGGAGGAGA	602
QY	603	TCCCGTCCACCTTCTCTGTAGCTTACGCCAGGCTTTCCCGACACCGGGCTTGGG	662
Db	603	TCCCGTCCACCTTCTCTGTAGCTTACGCCAGGCTTTCCCGACACCGGGCTTGGG	662
QY	663	CACAGCCCCCATCAGCCCGCTGTCTGGAGCTGTGCTCTCTGGAGAGGTCCAATTGGT	722
Db	663	CACAGCCCCCATCAGCCCGCTGTCTGGAGCTGTGCTCTCTGGAGAGGTCCAATTGGT	722
QY	723	GGTGGAGCCAGAGGTGGAGCTAGCTCTCTGTGGAAACCGTAACCTTGACCTGTGAAGT	782
Db	723	GGTGGAGCCAGAGGTGGAGCTAGCTCTCTGTGGAAACCGTAACCTTGACCTGTGAAGT	782
QY	783	CCCTGCCAGCCCTCTCTCAATCCACTGGAATGAGTGTGCTTGCCTTGCCTTCC	842
Db	783	CCCTGCCAGCCCTCTCTCAATCCACTGGAATGAGTGTGCTTGCCTTGCCTTCC	842
QY	843	CCCGAGCTGTGCTGATCTCTCTGAGATAGGGCTCTGAGACAGGGAACTTACAGCTG	902
Db	843	CCCGAGCTGTGCTGATCTCTCTGAGATAGGGCTCTGAGACAGGGAACTTACAGCTG	902
QY	903	TGTGGCCACCATTCAGCCACCGGCCCCAGGAAGCCGTGTCTGAGCATCAGCATCAT	962
Db	903	TGTGGCCACCATTCAGCCACCGGCCCCAGGAAGCCGTGTCTGAGCATCAGCATCAT	962
QY	963	CGAACAGGCGAGGAGGGCCAACTGCGAGCTCTGTGGAGGATCAGGGCTGG	1015
Db	963	CGAACAGGCGAGGAGGGCCAACTGCGAGCTCTGTGGAGGATCAGGGCTGG	1015

RESULT 11

ADSI0302

ID ADSI0302 standard; DNA; 1146 BP.

XX AC ADSI0302;

XX DT 16-DEC-2004 (first entry)

XX DE Human therapeutic DNA - SEQ ID 539.

XX XX antiinflammatory; neuroprotective; antianemic; cytostatic; vulnery;

XX XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;

XX XX aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.

XX OS Homo sapiens.

XX XX WO2004080148-A2.

XX PD 23-SEP-2004.

XX XX 30-SEP-2003; 2003WO-US030720.

XX XX 02-OCT-2002; 2002US-0416186P.

XX XX

PA (NUVE-) NUVELO INC.

XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;

PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Wang G, Zhou P;

XX WPI; 2004-568857/65.

DR P-PSDB; ADSI0986.

XX New polynucleotide, useful in preparing a composition for diagnosing or

PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,

PT aplastic anemia or cancer for promoting wound healing.

XX Claim 1; SEQ ID NO 539; 718pp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded

CC polypeptide. The molecules of the invention demonstrate antiinflammatory,

CC neuroprotective, antianemic, cytostatic and vulnerary activities and may

CC be useful in preparing a composition for diagnosing or treating

CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell

CC disorders, such as aplastic anaemia or cancer, as well as for promoting

CC wound healing. The molecules may also be utilised during gene therapy

CC procedures. The current sequence is that of a human therapeutic DNA of

CC the invention. The current sequence is not shown explicitly within the

CC specification but can be accessed from the WIPO web-site.

XX SQ Sequence 1146 BP; 248 A; 332 C; 362 G; 204 T; 0 U; 0 Other;

Query Match 99.0%; Score 1010.2; DB 13; Length 1146;

Best Local Similarity 99.7%; Pred. No. 1.5e-259;

Matches 1012; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGCAGCCGGAACAGCAGTTCGGCTCGGTCTCTCAGTCTGTGGGGGCGAGTA 60

Db 1 ATGGCAGCCGGAACAGCAGTTCGGCTCGGTCTCTCAGTCTGTGGGGGCGAGTA 60

QY 61 GTAGTGTCTCAAAACATCAAGCCCGGATTCGGAGCCACTGGTGTGAAGTGAAGG 120

Db 61 GTAGTGTCTCAAAACATCAAGCCCGGATTCGGAGCCACTGGTGTGAAGTGAAGG 120

QY 121 GCGCCCAAGAAACACCCAGCGGCTGGAAATGMAACTGAACACAGCCGCGACAGAAGCT 180

Db 121 GCGCCCAAGAAACACCCAGCGGCTGGAAATGMAACTGAACACAGCCGCGACAGAAGCT 180

QY 181 TGAAGGTCTCTGTCTCCAGGAGAGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCC 240

Db 181 TGAAGGTCTCTGTCTCCAGGAGAGAGCCCTCGGACAGTGTGGCTCGTGTCTTCCC 240

QY 241 AACGGCTCCCTCTTCTTCCGCTGTCCGGATTCAGGATTCAGGGGATTTCCGGTCCAG 300

Db 241 AACGGCTCCCTCTTCTTCCGCTGTCCGGATTCAGGATTCAGGGGATTTCCGGTCCAG 300

QY 301 GCAATGAACAGGAATGGAAAGGAGACCAAGTCCAAGTCCAGTCCGTGTCTACCAAGATT 360

Db 301 GCAATGAACAGGAATGGAAAGGAGACCAAGTCCAAGTCCAGTCCGTGTCTACCAAGATT 360

QY 361 CTGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCACGGCTGGTGTTCCTCAATAAG 420

Db 361 CTGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCACGGCTGGTGTTCCTCAATAAG 420

QY 421 GTGGGACATGTGTCTCAGAGGAGTACCTTCCAGGAGCTCTTAGCTGGCACTTGGAT 480

Db 421 GTGGGACATGTGTCTCAGAGGAGTACCTTCCAGGAGCTCTTAGCTGGCACTTGGAT 480

QY 481 GGGAGCCCTCTGTGCTTAATGAGAGGAGTATCTGTGAAGAAACAGACCGAGGACAC 540

Db 481 GGGAGCCCTCTGTGCTTAATGAGAGGAGTATCTGTGAAGAAACAGACCGAGGACAC 540

QY 541 CCTGAGACAGGGCTCTTTCACACTGCACTCGGAGCTAATGGTGAACCCAGCCGGGGAGGA 600

Db 541 CCTGAGACAGGGCTCTTTCACACTGCACTCGGAGCTAATGGTGAACCCAGCCGGGGAGGA 600

QY 601 GATCCCGTCCACCTTCTCTGTAGCTTTCAGCCAGGCTTCCCGCGACACCGGGCTTGG 660

Db 601 GATCCCGTCCACCTTCTCTGTAGCTTTCAGCCAGGCTTCCCGCGACACCGGGCTTGG 660

D	b		601	GATCCCGTCCCACCTTCCTCTGTAGCTTCAGCCACAGGCTTCCCCGACACCGGGCCTTG	660
Q	y		661	CGCACAGCCCCCATCAGCCCCCGTGTCTGTGGAGGCTGTGCCTCTGGAGGAGGTCCAATTG	720
D	b		661	CGCACAGCCCCCATCAACCCCGTGTCTGGGAGCTGTGTCCCTCTGGAGGAGTCCAATTG	720
Q	y		721	GTGGTGGAGCGCAGAGGTGGAGCAGTAGCTCTGTGTGAACCGTAACCCTGACCTGTGAA	780
D	b		721	GTGGTGGAGCGCAGAAGGTGGAGCAGTAGCTCTCTAGTGGAACCGTAACCTGACCTGTGAA	780
Q	y		781	GTCCCTGTGCCAGCCCTCTCCTCAAATCCACTGGATGAAGGATGGTGTGCCCTTTGCCCCCTT	840
D	b		781	GTCCCTGTGCCAGCCCTCTCCTCAATCCACTGGATGAAGGATGGTGTGCCCTTTGCCCCCTT	840
Q	y		841	CCCCCAGCCCTGTGTGTATCTCCCTGAGATAGGGCTCTAGGACAGGGAACCTACAGC	900
D	b		841	CCCCCAGCCCTGTGTGTATCTCCCTGAGATAGGGCTCTAGGACAGGGAACCTACAGC	900
Q	y		901	TGTGTGGCCACCCATTCCAGGCCAGAGGGCCCCCAGGAAAAGCCGTGTGTGACATCAGCATC	960
D	b		901	TGTGTGGCCACCCATTCCAGGCCAGAGGGCCCCCAGGAAAAGCCGTGTGTGACATCAGCATC	960
Q	y		961	ATCGAACCAGGCGAGAGGGGCCAACTCAGGCTCTGTGGAGGATCAGGGCTGG	1015
D	b		961	ATCGAACCAGGCGAGAGGGGCCAACTCAGGCTCTGTGGAGGATCAGGGCTGG	1015
RESULT 12					
A	D	K00128			
I	D		ADK00128 standard; DNA; 1761 BP.		
X	X				
A	C		ADK00128;		
X	X				
D	T		20-MAY-2004 (first entry)		
X	X				
D	E		Human RAGE-LBE fused to Pc element DNA sequence.		
X	X				
K	W		Advanced Glycation End Product Ligand Binding Element; RAGE-LBE;		
K	W		Cytostatic; Antidiabetic; Nootropic; Antiarthritic; Osteopathic;		
K	W		Neuroprotective; Antiinflammatory; Dermatological; Immunosuppressive;		
K	W		Vasotropic; Antiparasitic; Antibacterial; Antiarteriosclerotic;		
K	W		amyloidosis; cancer; Crohn's disease; diabetes; Alzheimer's disease;		
K	W		chronic inflammatory disease; osteoarthritis; irritable bowel disease;		
K	W		multiple sclerosis; psoriasis; ds.		
O	S		Homo sapiens.		
O	S		Synthetic.		
P	H				
F	T		Key Location/Qualifiers		
F	T		i . .1761		
F	T		/tag= a		
F	T		/product= "RAGE-LBE"		
X	X				
P	N		WO2004016229-A2.		
X	X				
D	D		26-FEB-2004.		
X	X				
P	F		19-AUG-2003; 2003WO-US025996.		
X	X				
P	R		16-AUG-2002; 2002US-0404205P.		
X	X		(AMHP) WYETH.		
P	A				
P	I		Pittman DD, Clancy B, Larsen G, Trepicchio WL, Brennan FM;		
P	I		Feldmann M, Foxwell BJM, Feidman JL;		
X	X		WPI; 2004-192067/18.		
D	R		P-PSDB; ADK00127.		
X	X				
P	T		New fusion protein comprising a Receptor for Advanced Glycation End		
P	T		Product Ligand Binding Element (RAGE-LBE) and an immunoglobulin element,		
P	T		useful for preparing a composition for treating e.g., Alzheimer's		
P	T		disease.		

QY 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAGATGGTGTGCGCCCTT 840
D 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGATGAGATGGTGTGCGCCCTT 840
QY 841 CCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGCGCTCAGACAGGAACTACAGC 900
D 841 CCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGCGCTCAGACAGGAACTACAGC 900
QY 901 TGTGTGGCCACCCATTCAGCCACGCGCGCCCGCCAGGAAAGCGTCTGTGACGATCAGCATC 960
D 901 TGTGTGGCCACCCATTCAGCCACGCGCGCCCGCCAGGAAAGCGTCTGTGACGATCAGCATC 960
QY 961 ATGAAACAGGCGAGAGGCGCCCACTGACAGGCTCTGTGGAGGATCAGGCGTGG 1015
D 961 ATGAAACAGGCGAGAGGCGCCCACTGACAGGCTCTGTGGAGGATCAGGCGTGG 1015

RESULT 13
ABK10856
ID ABK10856 standard; cDNA; 1391 BP.
AC ABK10856;
DT 05-JUN-2002 (first entry)
XX
DE DNA encoding human receptor for advanced glycosylation end product.
KW Receptor for advanced glycation end product; RAGE; receptor;
KW amyloid beta peptide; blood-brain barrier; neurovascular stress;
KW cerebral vasoconstriction suppressor; cerebral blood flow enhancer;
KW cerebral amyloid angiopathy; transgenic animal; amyloid beta precursor;
KW Alzheimer's disease; Down's syndrome; head trauma; stroke; human; gene;
KW ss.
OS Homo sapiens.
XX

Key Location/Qualifiers
FH 1.1215
FT CDS
FT /*tag= a
FT /product= "RAGE"
FT /note= "Receptor for advanced glycation end product"
FT /partial
FT /note= "No start codon given"
XX

W0200214519-A1.
PN
XX
PD 21-FEB-2002.
XX
PF 14-AUG-2001; 2001WO-US025416.
XX
PR 14-AUG-2000; 2000US-00638648.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Stern DM, Schmidt AM, Yan SD, Zlokovic B;
XX
XX WPI: 2002-257610/30.
DR P-PSDB; AAU77543.
DR
XX Ameliorating neurovascular stress and decreasing cerebral
PT vasoconstriction in subject suffering from chronic/acute cerebral amyloid
PT angiopathy, by administering inhibitor of receptor for advanced glycation
PT endproduct.
XX
PS Disclosure; Page 16-17; 68pp; English.
XX
CC The invention describes a method of ameliorating neurovascular stress,
CC and decreasing cerebral vasoconstriction in subject suffering from
CC chronic or acute cerebral amyloid angiopathy, comprising administering an
CC inhibitor (I) of receptor for advanced glycation end product (RAGE). (I)
CC inhibits transcytosis of amyloid beta peptides across blood-brain
CC barrier, thus decreasing cerebral vasoconstriction and increasing

CC cerebral blood flow. (I) is useful for treating amyloid angiopathy in a
CC subject, decreasing cerebral vasoconstriction in a transgenic non-human
CC animal (preferably, transgenic mouse overexpressing mutant human amyloid
CC beta precursor protein) or a human, suffering from chronic or acute
CC cerebral amyloid angiopathy, preferably, Alzheimer's disease, and for
CC ameliorating neurovascular stress comprising cerebral amyloid angiopathy
CC in a subject, where the neurovascular stress is caused by Alzheimer's
CC disease, aging, Down's syndrome, head trauma or stroke. This sequence
CC encodes the human receptor for advanced glycation end product (RAGE)
CC described in the invention
XX
SQ Sequence 1391 BP; 305 A; 407 C; 418 G; 261 T; 0 U; 0 Other;

Query Match 99.0%; Score 1009.8; DB 6; Length 1391;
Best Local Similarity 99.8%; Pred. No. 2.1e-259;
Matches 1011; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCAGCCGGAACAGCAGCTTGGAGCCCTGGGTGCTGGTCTCAGTCTGTGGGGGCGCAGTAGT 62
D 3 GGCAGCCGGAACAGCAGCTTGGAGCCCTGGGTGCTGGTCTCAGTCTGTGGGGGCGCAGTAGT 62
QY 63 AGGTGCTCAAAACATCACAGCCCGGATTTGGCGAGCCACTGGTGTGAAGTAAAGGGGCG 122
D 63 AGGTGCTCAAAACATCACAGCCCGGATTTGGCGAGCCACTGGTGTGAAGTAAAGGGGCG 122
QY 123 CCCCAGAAACCAACCCAGCGCTGGAATGGAACCTGAACACAGGCCCGACAGAACCTTG 182
D 123 CCCCAGAAACCAACCCAGCGCTGGAATGGAACCTGAACACAGGCCCGACAGAACCTTG 182
QY 183 GAAGTCTCTCTCCCGAGGAGGCGCCCTGGGACAGTGGTCTGCTTCCCTCCCAA 242
D 183 GAAGTCTCTCTCTCCCGAGGAGGCGCCCTGGGACAGTGGTCTGCTTCCCTCCCAA 242
QY 243 CGGCTCCCTCTTCTTCCGCTGTGGGATCCAGATGAGGGGATTTTCCGGTCCAGGC 302
D 243 CGGCTCCCTCTTCTTCCGCTGTGGGATCCAGATGAGGGGATTTTCCGGTCCAGGC 302
QY 303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACAGATTCC 362
D 303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACAGATTCC 362
QY 363 TGGGAGCCAGAAATTTGATGTTCTGCTCTGAACTCAGGCTGGTGTCCCAATAGGT 422
D 363 TGGGAGCCAGAAATTTGATGTTCTGCTCTGAACTCAGGCTGGTGTCCCAATAGGT 422
QY 423 GGGGACATGTGTGTCAGAGGAGTACCTCTGAGGAGTCTTAGCTGCGACTTGGATGG 482
D 423 GGGGACATGTGTGTCAGAGGAGTACCTCTGAGGAGTCTTAGCTGCGACTTGGATGG 482
QY 483 GAAGCCCTGTGCTTAATGAGAGGAGTATCTGTGAAGGAAACAGACAGGAGACACCC 542
D 483 GAAGCCCTGTGCTTAATGAGAGGAGTATCTGTGAAGGAAACAGACAGGAGACACCC 542
QY 543 TGAGACAGGGCTCTTACACTCGAGTAAATGTTGACCCAGCCCGGGGAGGAGA 602
D 543 TGAGACAGGGCTCTTACACTCGAGTAAATGTTGACCCAGCCCGGGGAGGAGA 602
QY 603 TCCCGTCCCACTCTCTCTGTAGTTCAGCCCGAGCCCTTCCCGACACCGGGCTTGG 662
D 603 TCCCGTCCCACTCTCTCTGTAGTTCAGCCCGAGCCCTTCCCGACACCGGGCTTGG 662
QY 663 CACAGCCCCCATCCAGCCCCCGTGTCTGGAGGCTGTGCTCTGGAGAGGTCCAATTGGT 722
D 663 CACAGCCCCCATCCAGCCCCCGTGTCTGGAGGCTGTGCTCTGGAGAGGTCCAATTGGT 722
QY 723 GGTGAGCCAGAAAGGTGGAGCAGTAGTCTCTGGTGAACCGTAACCTGACCTGTGAAGT 782
D 723 GGTGAGCCAGAAAGGTGGAGCAGTAGTCTCTGGTGAACCGTAACCTGACCTGTGAAGT 782
QY 783 CCTGCGCCAGCCCTCTCTCAATCCACTGGAATGAGGATGGTGTGCTCTGCGCCCTTCC 842
D 783 CCTGCGCCAGCCCTCTCTCAATCCACTGGAATGAGGATGGTGTGCTCTGCGCCCTTCC 842

QY 843 CCCAGCCCTGTGCTGATCCTCCCTGAGATAGGSCCTCAGGACCAGGGAACCTACAGCTG 902
Db 843 CCCAGCCCTGTGCTGATCCTCCCTGAGATAGGSCCTCAGGACCAGGGAACCTACAGCTG 902
QY 903 TGTGGCCACCCATTCCAGCCACGGGCCCCAGGAAAGCCGTGCTGTCAGCATCAGCATCAT 962
Db 903 TGTGGCCACCCATTCCAGCCACGGGCCCCAGGAAAGCCGTGCTGTCAGCATCAGCATCAT 962
QY 963 CGAACACAGGCGAGGAGGGGCAACTGCAGGCTCTGTGGGAGGATCAGGGCTGG 1015
Db 963 CGAACACAGGCGAGGAGGGGCAACTGCAGGCTCTGTGGGAGGATCAGGGCTGG 1015
RESULT 14
ABK84114
ID ABK84114 standard; cDNA; 1391 BP.
XX AC ABK84114;
XX DT 14-AUG-2002 (first entry)
XX DE Human cDNA differentially expressed in granulocytic cells #685.
XX KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX OS Homo sapiens.
XX PN WO200228999-A2.
XX PD 11-APR-2002.
XX PF 03-OCT-2001; 2001WO-US030821.
XX PR 03-OCT-2000; 2000US-0237189P.
XX PA (GENE-) GENE LOGIC INC.
XX PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX DR WPI; 2002-435328/46.
XX PT Detecting granulocyte activation by detecting differential expression of
PT genes associated with granulocyte activation, which serves as diagnostic
PT markers that is useful for monitoring disease states and drug toxicity.
XX PS Claim 1; SEQ ID NO 685; 114pp; English.
XX CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing the
CC expression level to an expression level in an unactivated GC, where
CC differential expression of Gs is indicative of GCA. Also included are
CC modulating (M2) GA by contacting GC with an agent that alters the
CC expression of at least one gene in Gs; (2) screening (M3) for an agent
CC capable of modulating GCA or an inflammation (especially chronic) in a
CC tissue, an allergic response or an inflammation (especially chronic) in a
CC pathogen or sterile inflammatory disease using the gene expression
CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease, by detecting the level of
CC expression in a sample of the tissue of gene(s) from Gs, where the level
CC of expression of the gene is indicative of inflammation; (4) treating
CC (M5) an inflammation (especially chronic) or in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease, by contacting a tissue having inflammation with an
CC agent that modulates the expression of gene(s) from Gs in the tissue. M1

CC is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful
CC for screening an agent capable of modulating GCA preferably in an
CC inflammation in a tissue; M4 is useful for detecting an inflammation
CC (especially chronic) in a tissue, an allergic response in a subject,
CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
CC disease, ulcerative colitis, periodontal disease; also bacterial
CC infection, viral infection, parasitic infection, protozoal infection,
CC fungal infection and M5 is useful for treating one of the above
CC conditions. The present sequence represents a gene differentially
CC expressed in granulocytes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1391 BP; 305 A; 407 C; 418 G; 261 T; 0 U; 0 Other;

Query Match 99.0%; Score 1009.8; DB 6; Length 1391;
Best Local Similarity 99.8%; Pred. No. 2.1e-259;
Matches 1011; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 GGCAGCCGGAACAGCAGTTGGAGCTGGGTGCTGCTCTCAGTCTGTGGGGGCGAGTAGT 62
Db 3 GGCAGCCGGAACAGCAGTTGGAGCTGGGTGCTGCTCTCAGTCTGTGGGGGCGAGTAGT 62
QY 63 AGGTCTCTAAACATCAGCCCCGATTTGGGAGCCACTGGTCTGAAGTCTAAAGGGGCG 122
Db 63 AGGTCTCTAAACATCAGCCCCGATTTGGGAGCCACTGGTCTGAAGTCTAAAGGGGCG 122
QY 123 CCCCAAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGGCCGAGACAGAGCTTG 182
Db 123 CCCCAAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGGCCGAGACAGAGCTTG 182
QY 183 GAAGTCTCTGCTCTCCCAAGGAGGAGGCCCTTGGACAGTGTGGTCTGTCTTTCCAA 242
Db 183 GAAGTCTCTGCTCTCCCAAGGAGGAGGCCCTTGGACAGTGTGGTCTGTCTTTCCAA 242
QY 243 CGGCTCCCTCTCTTCCGCTGTCGGGATCCAGATCAGGGGATTTTCGGTCCGAGCG 302
Db 243 CGGCTCCCTCTCTTCCGCTGTCGGGATCCAGATCAGGGGATTTTCGGTCCGAGCG 302
QY 303 AATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCCTGTCTACAGATTCC 362
Db 303 AATGAACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCCTGTCTACAGATTCC 362
QY 363 TGGGAAGCCAGAAATTTAGATTCTGCTGAACTCAAGTCTGCTGTGTTCCCAATAAGGT 422
Db 363 TGGGAAGCCAGAAATTTAGATTCTGCTGAACTCAAGTCTGCTGTGTTCCCAATAAGGT 422
QY 423 GGGGACATGTGTTCAGAGGGAAGCTACCTCCAGGGGACTCTTAGCTGCACTTGGATGG 482
Db 423 GGGGACATGTGTTCAGAGGGAAGCTACCTCCAGGGGACTCTTAGCTGCACTTGGATGG 482
QY 483 GAAAGCCCTGCTGCTTAATGAGAGGGAGATCTCTGAAGGAACAGACAGGAGACACCC 542
Db 483 GAAAGCCCTGCTGCTTAATGAGAGGGAGATCTCTGAAGGAACAGACAGGAGACACCC 542
QY 543 TGAGACAGGGCTTTTCACTGTCAGTCCGAGCTAATGTGACCCCGAGCCGGGAGGAGA 602
Db 543 TGAGACAGGGCTTTTCACTGTCAGTCCGAGCTAATGTGACCCCGAGCCGGGAGGAGA 602
QY 603 TCCCGTCCCACTTCTCTCTAGCTTCCAGCCGAGGCTTCCCGACACCGGGCTTGG 662
Db 603 TCCCGTCCCACTTCTCTCTAGCTTCCAGCCGAGGCTTCCCGACACCGGGCTTGG 662
QY 663 CACAGCCCCATCCAGCCCCGCTGTCTGGAGGCTCTGTGGAGAGGTCCTAATTGGT 722
Db 663 CACAGCCCCATCCAGCCCCGCTGTCTGGAGGCTCTGTGGAGAGGTCCTAATTGGT 722
QY 723 GGTGAGCCAGAGGTGAGCAGTAGCTCTGTGGTGGAAACCGGTAAACCTGTGAGT 782
Db 723 GGTGAGCCAGAGGTGAGCAGTAGCTCTGTGGTGGAAACCGGTAAACCTGTGAGT 782


```
Db 723 GGTGGAGCCAGAGGTGGAGCAGTAGCTCTGTGTGAACCGTAAACCCCTGACCTGTGAAGT 782
Qy CCTGCCCCAGCCCTCTCTCAAAATCCACTGGATGAAGAGTGTGTGCCCTTGCCCTTCC 842
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Qy CCCCAGCCCTGTGCTGATCTCTCTAGATAGGGCTTCAGGACCAGGGAACCTACAGCTG 902
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Qy TGTGGCCACCCATTCACAGCCACGGGCCCCAGGAAAGCCGTGCTGTCAGCATCAGCATCAT 962
Db TGTGGCCACCCATTCACAGCCACGGGCCCCAGGAAAGCCGTGCTGTCAGCATCAGCATCAT 962
Qy CGAACAGCGGAGGAGGGGCCAACTCAGAGCTCTGTGGAGGATCAGGCTGG 1015
Db CGAACAGCGGAGGAGGGGCCAACTCAGAGCTCTGTGGAGGATCAGGCTGG 1015

RESULT 15
AAD36952
ID AAD36952 standard; cDNA; 1391 BP.
XX
AC AAD36952;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human receptor for advanced glycosylation end product (RAGE) cDNA.
XX
KW Human; Receptor for advanced glycosylation end product; RAGE; cardiant;
KW tissue growth; neointimal formation; blood vessel; restenosis; diabetes;
KW myocardial infarction; angioplasty; peripheral vascular surgery; angina;
KW transgenic animal; acute thrombotic stroke; venous thrombosis; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1215
FT FT /*tag= a
FT FT /product= "Human RAGE protein"
FT FT /notes= "CDS does not include start codon"
FT FT /partial
FT FT polyA_signal 1368..1373
FT FT /*tag= b
FT FT polyA_site 1391
FT FT /*tag= c
XX
PN WO200230889-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032036.
XX
PR 13-OCT-2000; 2000US-00687528.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI Stern DM, Schmidt A, Marso S, Topol E, Lincoff AM;
XX
XX WPI; 2002-426260/45.
XX
DR P-PSDB; AAE23219.
XX
PT Inhibiting new tissue growth or neointimal formation in blood vessels of
PT subject suffering from diabetes, stroke and preventing restenosis,
PT comprises administering inhibitor of receptor for advance glycation end
PT product.
XX
PS Disclosure; Page 16-17; 43pp; English.
XX
CC The invention relates to a method for inhibiting new tissue growth or
CC neointimal formation in blood vessels in a subject that has experienced
CC blood vessel injury and preventing exaggerated restenosis in a diabetic
CC subject. The method comprises administering an inhibitor of receptor
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CC advanced glycation/glycosylation end product (RAGE), so as to inhibit new
CC tissue growth or neointimal formation in subject's blood vessels and
CC preventing restenosis in the subject. The method is useful for inhibiting
CC new tissue growth or neointimal formation in blood vessels in a subject
CC like non-human animal, a transgenic non-human animal or a human suffering
CC from diabetes, acute thrombotic stroke, venous thrombosis, unstable
CC angina, myocardial infarction, abrupt closure following angioplasty or
CC stent placement, or thrombosis as a result of peripheral vascular surgery
CC The method is also useful for preventing restenosis and for determining
CC whether a compound inhibits new tissue growth in a blood vessel in a
CC subject. The present sequence is human receptor for advanced
CC glycosylation end product (RAGE) cDNA
XX
SQ Sequence 1391 BP; 305 A; 407 C; 418 G; 261 T; 0 U; 0 Other;

Query Match 99.0%; Score 1009.8; DB 6; Length 1391;
Best Local Similarity 99.8%; Pred. No. 2.1e-259;
Matches 1011; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGCCGGAACAGCAGTTGGAGCCTGTGGTGTCTCTCAGTCTCTGTGGGGGCGCAGTAGT 62
Db 3 GGAGCCGGAACAGCAGTTGGAGCCTGTGGTGTCTCTCAGTCTCTGTGGGGGCGCAGTAGT 62
Qy 63 AGGTGCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTCTGAAGTGAAGGGGC 122
Db 63 AGGTGCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTCTGAAGTGAAGGGGC 122
Qy 123 CCCCAGAAACCAACCCAGCGCTGGAATGGAACCTGAAACACAGGCGCGACAGAACTTG 182
Db 123 CCCCAGAAACCAACCCAGCGCTGGAATGGAACCTGAAACACAGGCGCGACAGAACTTG 182
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Db 183 GAAGTCTCTGTCTCTCCAGGAGGAGGCCCTTGGGACAGTGTGGTCTGTCTTCCCAA 242
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Db 243 CGGCTCCCTTCTCTTCCGGCTGTGGGATCAGGATGAGGGGATTTCCGGTGCCAGGC 302
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Db 303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCC 362
Qy 363 TGGGAAGCCAGAAATTTAGATTCTGCCCTCTGAACTCACGGCTGTGTCTCCCAATAGGT 422
Db 363 TGGGAAGCCAGAAATTTAGATTCTGCCCTCTGAACTCACGGCTGTGTCTCCCAATAGGT 422
Qy 423 GGGGACATGTGTCTCAGAGGGAAGCTACCTTCAGGGAGCTTAGCTGGCACTTGGATGG 482
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Qy 483 GAAAGCCCTGTGTCTTAATGAGAAGGAGTATCTGTGAAGGAACACAGCCAGGAGACCCC 542
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Qy 543 TGAGACAGGGCTCTTTCACACTGCGAGTAAATGTTGACCCCGCCGCGGGAGAGAGA 602
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Qy 603 TCCCGTCCCACTTCTCTGTAGTTTCAGCCAGGCTTCCCGACACCGGGCCCTTGG 662
Db 603 TCCCGTCCCACTTCTCTGTAGTTTCAGCCAGGCTTCCCGACACCGGGCCCTTGG 662
Qy 663 CACAGCCCCCATCCAGCCCCCGTGTGGGAGCTGTGCCCTCTGGAGAGGTCCAATTGGT 722
Db 663 CACAGCCCCCATCCAGCCCCCGTGTGGGAGCTGTGCCCTCTGGAGAGGTCCAATTGGT 722
Qy 723 GGTGGAGCCAGAGGTGGAGCAGTAGCTCTCTGTGGAACCGTAACCCCTGACCTGTAAGT 782
Db 723 GGTGGAGCCAGAGGTGGAGCAGTAGCTCTCTGTGGAACCGTAACCCCTGACCTGTAAGT 782
Qy 783 CCTGCGCAGCCCTCTCTCAAAATCAGTCGATGAAGGATGGTGTGCCCTTGCCTTCC 842
Db 783 CCTGCGCAGCCCTCTCTCTCAAAATCAGTCGATGAAGGATGGTGTGCCCTTGCCTTCC 842
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Db	783	CCCTGCCAGCCCTCTCTCAATCCACTGGATGAAGGATGGTGTGCCCTTGCCCTTCC	842
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Db	843	CCCAGCCCTGTGTGATCCTCCTGAGATAGGGCTTCAGGACCAAGGAACCTACAGCTG	902
Qy	903	TGTGGCCACCCATTCCAGCCACGGGCCCACTGCGGCTCTGTGGAGGATCAGGCTGG	962
Db	903	TGTGGCCACCCATTCCAGCCACGGGCCCACTGCGGCTCTGTGGAGGATCAGGCTGG	962
Qy	963	CGAACCAGGCGAGGGGCCAATGCGAGCTCTGTGGAGGATCAGGCTGG	1015
Db	963	CGAACCAGGCGAGGGGCCAATGCGAGCTCTGTGGAGGATCAGGCTGG	1015

Search completed: March 14, 2005, 18:41:03
Job time : 646.487 secs

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3	1013.4	99.4	1217	17	US-10-309-290-95	Sequence 1
4	1013	99.3	1391	16	US-10-091-019-1	Sequence 1
5	992	97.3	1223	19	US-10-472-507A-1	Sequence 1
6	986.8	96.7	1405	8	US-08-905-709-3	Sequence 3
7	986.8	96.7	1405	8	US-08-755-235-3	Sequence 3
8	986.8	96.7	1405	18	US-10-850-861-3	Sequence 1
9	957	93.8	1463	18	US-10-115-635-352	Sequence 1
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QY 121 GCGCCCAAGAAACACACCCAGCGGCTGGAATGGAATCTGAACACAGCCCGGACAGAAGCT 180
Db 121 GCGCCCAAGAAACACACCCAGCGGCTGGAATGGAATCTGAACACAGCCCGGACAGAAGCT 180
QY 181 TGAAGGTCTGTCTCTCCAGGAGGAGGCGCCCTGGGACAGTGTGGCTCGTGTCTTCCC 240
Db 181 TGAAGGTCTGTCTCTCCAGGAGGAGGCGCCCTGGGACAGTGTGGCTCGTGTCTTCCC 240
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QY 361 CCTGGGAAGCCAGAAATGTAGATTCTGCTCTGAACTCACGGCTGGTGTCTCCCAATAG 420
Db 361 CCTGGGAAGCCAGAAATGTAGATTCTGCTCTGAACTCACGGCTGGTGTCTCCCAATAG 420
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Db 421 GTGGGACATGTGTGTCTGAGAGGAGGAGTACCTCTGAGGAGTCTTAGCTGGCACTTGGAT 480
QY 481 GGGAGCCCTGTGCTCTAATGAGAGGAGTATCTGTGAGGAAACAGACAGGAGACAC 540
Db 481 GGGAGCCCTGTGCTCTAATGAGAGGAGTATCTGTGAGGAAACAGACAGGAGACAC 540
QY 541 CCTGAGACAGGGCTCTTCACTGCACTCGAGTCCGAGCTAATGGTGAACCCCGGGAGGA 600
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QY 601 GATCCCGTCCCACTTCTCTGTAGTTCAGCCCGGCTTCCCGGACACCGGGGCTTG 660
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QY 661 CGCACAGCCCACTCAGCCCGGCTGTGGAGCTGTGGAGCTTCCCGGACACCGGGGCTTG 720
Db 661 CGCACAGCCCACTCAGCCCGGCTGTGGAGCTGTGGAGCTTCCCGGACACCGGGGCTTG 720
QY 721 GTGGTGGAGCAGAGGTGGAGCAGTGTCTCTGTGGAGCAGTGTCTGTGGAGCAGTGTGAA 780
Db 721 GTGGTGGAGCAGAGGTGGAGCAGTGTCTCTGTGGAGCAGTGTCTGTGGAGCAGTGTGAA 780
QY 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGTGATGAAGATGTGTGCTTGCCTTGCCTTT 840
Db 781 GTCCCTGCCAGCCCTCTCTCAATCCACTGTGATGAAGATGTGTGCTTGCCTTGCCTTT 840
QY 841 CCCCCCAGCCCTGTGTGTCTCTCTCTGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Db 841 CCCCCCAGCCCTGTGTGTCTCTCTCTGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 901 TGTGTGGCACCACATTCAGCCACCGGGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Db 901 TGTGTGGCACCACATTCAGCCACCGGGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
QY 961 ATCGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
Db 961 ATCGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
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RESULT 2

US-10-115-635-351

; Sequence 351, Application US/10115635

; Publication No. US2004013743A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Zhou, Ping

; APPLICANT: Goodrich, Ryle

```
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 797CON
; CURRENT APPLICATION NUMBER: US/10/115,635
; CURRENT FILING DATE: 2002-04-03
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 362
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 351
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(1239)
; US-10-115-635-351
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Query Match 99.5%; Score 1015; DB 18; Length 1415;

Best Local Similarity 100.0%; Pred. No. 9.5e-285;

Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCAGCCGGAACAGCAGTGTGGAGCCCTGGTGTCTGCTCCTCAGTCTGTGGGGGGCAGTA 60
Db 25 ATGGCAGCCGGAACAGCAGTGTGGAGCCCTGGTGTCTGCTCCTCAGTCTGTGGGGGGCAGTA 84
QY 61 GTAGTGTCTCAAAACATCACAGCCCGGATTGGCGACCACTGGTGTCTGAAGTGTAAAGGG 120
Db 85 GTAGTGTCTCAAAACATCACAGCCCGGATTGGCGACCACTGGTGTCTGAAGTGTAAAGGG 144
QY 121 GCGCCCAAGAAACACACCCAGCGGCTGGAATGGAATCTGAACACAGCCCGGACAGAAGCT 180
Db 145 GCGCCCAAGAAACACACCCAGCGGCTGGAATGGAATCTGAACACAGCCCGGACAGAAGCT 204
QY 181 TGAAGGTCTGTCTCTCCAGGAGGAGGCGCCCTGGGACAGTGTGGCTCGTGTCTTCCC 240
Db 205 TGAAGGTCTGTCTCTCCAGGAGGAGGCGCCCTGGGACAGTGTGGCTCGTGTCTTCCC 264
QY 241 AACGGCTCCCTCTCTTCCGCTGTCTGGGATCCAGGATCAGGGGATTTTCCGGTGCAG 300
Db 265 AACGGCTCCCTCTCTTCCGCTGTCTGGGATCCAGGATCAGGGGATTTTCCGGTGCAG 324
QY 301 GCATGACAGGAATGAAGAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGT 360
Db 325 GCATGACAGGAATGAAGAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGT 384
QY 361 CTTGGGAGCCAGAAATTTAGATTCTGCTCTGAACTCACCGGCTGGTGTCTCCCAATAG 420
Db 385 CTTGGGAGCCAGAAATTTAGATTCTGCTCTGAACTCACCGGCTGGTGTCTCCCAATAG 444
QY 421 GTGGGACATGTGTGTCTCAGAGGAGGAGTACCTTGCAGGAGTCTTTAGCTGGCACTTGGAT 480
Db 445 GTGGGACATGTGTGTCTCAGAGGAGGAGTACCTTGCAGGAGTCTTTAGCTGGCACTTGGAT 504
QY 481 GGGAGGCCCTGTGTCTAATGAGAGGAGTATCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Db 505 GGGAGGCCCTGTGTCTAATGAGAGGAGTATCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 564
QY 541 CTTGAGACAGGGCTCTTCACTGCACTCGAGTCCGAGTATATGTGTGACCCCGGAGGAGGA 600
Db 565 CTTGAGACAGGGCTCTTCACTGCACTCGAGTCCGAGTATATGTGTGACCCCGGAGGAGGA 624
QY 601 GATCCCGTCCCACTTCTCTGTAGTTCAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
```

Db 625 GATCCCGGTCACACCTTCTCTGTAGCTTACGCCACAGGCTTCCCGGACACACCGGGCTTG 684
Qy 661 CGCACAGCCCCCATCCAGCCCGCTGTCTGGAGCCTGTGCTCTGGAGAGGTCCAAATG 720
Db 685 CGCACAGCCCCCATCCAGCCCGCTGTCTGGAGCCTGTGCTCTGGAGAGGTCCAAATG 744
Qy 721 GTGGTGAGCCAGAGGTGAGAGTGTAGTCTCTGTGTGAACCGTAACCTGACCTGTGAA 780
Db 745 GTGGTGAGCCAGAGGTGAGAGTGTAGTCTCTGTGTGAACCGTAACCTGACCTGTGAA 804
Qy 781 GTCCTGCCCCAGCCTCTCTCAATCCACTGATGAAGGATGTGCTGCTGCCCCCTT 840
Db 805 GTCCTGCCCCAGCCTCTCTCAATCCACTGATGAAGGATGTGCTGCTGCCCCCTT 864
Qy 841 CCCCCAGCCTGTGTGTATCTCTCTGATAGAGGCTCTCAGGACCCAGGAACTACAGC 900
Db 865 CCCCCAGCCTGTGTGTATCTCTCTGATAGAGGCTCTCAGGACCCAGGAACTACAGC 924
Qy 901 TGTGTGGCCACCATTCAGGCCACCGGCCCCAGGAAAGCGTGTGTAGCATCAGCATC 960
Db 925 TGTGTGGCCACCATTCAGGCCACCGGCCCCAGGAAAGCGTGTGTAGCATCAGCATC 984
Qy 961 ATCGAACAGGCGAGAGGGGCCCACTGAGGCTCTGTGGAGGATCAGGGCTGG 1015
Db 985 ATCGAACAGGCGAGAGGGGCCCACTGAGGCTCTGTGGAGGATCAGGGCTGG 1039

RESULT 3

US-10-309-290-95
; Sequence 95, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malvankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glennda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17

; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 95
; LENGTH: 1217
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(1214)
US-10-309-290-95

Query Match 99.4%; Score 1013.4; DB 17; Length 1217;
Best Local Similarity 99.9%; Pred. No. 2.7e-284;
Matches 1014; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGCAGCGGAAACAGCAGTTGGAGCCTGGGCTCTCAGTCTGTGGGGGGCAGTA 60
Db |||||
Qy 3 ATGGCAGCGGAAACAGCAGTTGGAGCCTGGGCTCTCAGTCTGTGGGGGGCAGTA 62
Db |||||
Qy 61 GTAGTGTCTCAAAACATCAGCAGCCCGGATTTGGCGAGCCACTGGTGTGAAGTGTAAAGGG 120
Db |||||
Qy 63 GTAGTGTCTCAAAACATCAGCAGCTCGATTTGGCGAGCCACTGGTGTGAAGTGTAAAGGG 122
Db |||||
Qy 121 GCGCCCAAGAAACACACCCCGGCTGGAATGGAACCTGAACACAGCCCGGACAGAGCT 180
Db |||||
Qy 123 GCGCCCAAGAAACACACCCCGGCTGGAATGGAACCTGAACACAGCCCGGACAGAGCT 182
Db |||||
Qy 181 TGGAAAGTCTCTCTCTCCCGAGGAGGAGCCCTCGGACAGTGTGGTGTCTCTCTCTCC 240
Db |||||
Qy 183 TGGAAAGTCTCTCTCTCCCGAGGAGGAGCCCTCGGACAGTGTGGTGTCTCTCTCTCC 242
Db |||||
Qy 241 AACGGCTCTCTCTCTCTCCCGAGTTCAGGATTCAGGAGGAGGATTTTCGGTGGCCAG 300
Db |||||
Qy 243 AACGGCTCTCTCTCTCTCCCGAGTTCAGGATTCAGGAGGAGGATTTTCGGTGGCCAG 302
Db |||||
Qy 301 GCAATGAACAGAAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGTT 360
Db |||||
Qy 303 GCAATGAACAGAAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGTT 362
Db |||||
Qy 361 CCTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCACGGCTGGTGTCTCCCAATAG 420
Db |||||
Qy 363 CCTGGGAAGCCAGAAATTTAGATTCTGCTCTGAACTCACGGCTGGTGTCTCCCAATAG 422
Db |||||
Qy 421 GTGGGACATGTGTCTCAGAGGAAAGTACCTCTGAGGAGCTCTTAGTGTGGACATTTGGAT 480
Db |||||
Qy 423 GTGGGACATGTGTCTCAGAGGAAAGTACCTCTGAGGAGCTCTTAGTGTGGACATTTGGAT 482
Db |||||
Qy 481 GGGAGCCCTCTGCTCTCAATCAGAGGAGTATCTGTGAAGGAACAGACACAGGAGACAC 540
Db |||||
Qy 483 GGGAGCCCTCTGCTCTCAATCAGAGGAGTATCTGTGAAGGAACAGACACAGGAGACAC 542
Db |||||
Qy 541 CTGTAGACAGGCTCTTTCACACTGCAGTCCGAGCTAAATGGTCAACCCAGCCGGGAGGA 600
Db |||||
Qy 543 CTGTAGACAGGCTCTTTCACACTGCAGTCCGAGCTAAATGGTCAACCCAGCCGGGAGGA 602
Db |||||
Qy 601 GATCCCGTCCACTTCTCTGTAGTTCAGCCAGGCTTCCCGACACACCGGGCTTTG 660
Db |||||
Qy 603 GATCCCGTCCACTTCTCTGTAGTTCAGCCAGGCTTCCCGACACACCGGGCTTTG 662
Db |||||
Qy 661 CGCAGAGCCCTCTCAGGCCCCGTGTCTGGGAGCTGTGCTCTGGAGAGGTCCTCAATTG 720
Db |||||
Qy 663 CGCAGAGCCCTCTCAGGCCCCGTGTCTGGGAGCTGTGCTCTGGAGAGGTCCTCAATTG 722
Db |||||

QY 721 GTGTGAGCAGAGAGGTGAGCAGTAGTCTCTGTGGAAACCGTAACCTGACCTGTGAA 780
Db 723 GTGTGAGCAGAGAGGTGAGCAGTAGTCTCTGTGGAAACCGTAACCTGACCTGTGAA 782
QY 781 GTCCCTGCCAGCCCTCTCTCAATCCATGATGAAGATGGTGTGCCCTT 840
Db 783 GTCCCTGCCAGCCCTCTCTCAATCCATGATGAAGATGGTGTGCCCTT 842
QY 841 CCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGGCTCAGACAGGGAACCTACAGC 900
Db 843 CCCCCAGCCCTGTGTGATCTCTCCCTGAGATAGGGCTCAGACAGGGAACCTACAGC 902
QY 901 TGTGTGCGCACCCATTCCAGCCACGGGCCCCAGGAAAGCGTCTGTGACGATCAGCATC 960
Db 903 TGTGTGCGCACCCATTCCAGCCACGGGCCCCAGGAAAGCGTCTGTGACGATCAGCATC 962
QY 961 ATCGAACCGAGGAGGGGGCCCACTGACGGCTCTGTGGAGGATCAGGGCTGG 1015
Db 963 ATCGAACCGAGGAGGGGGCCCACTGACGGCTCTGTGGAGGATCAGGGCTGG 1017
RESULT 4
US-10-091-019-1
; Sequence 1, Application US/10091019
; Publication No. US20030166063A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Shen, Jane M.
; APPLICANT: Shahbaz, Manouchehr M.
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins
; FILE REFERENCE: 41305-270555
; CURRENT APPLICATION NUMBER: US/10/091,019
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/273,418
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1391
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-091-019-1
Query Match 99.3%; Score 1013; DB 16; Length 1391;
Best Local Similarity 100.0%; Pred. No. 3.6e-284;
Matches 1013; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GGCAGCGGAAACAGCAGTGTGGAGCCTGGTGTGGTCTCTCAGTCTGTGGGGGCGAGTAGT 62
Db 3 GGCAGCGGAAACAGCAGTGTGGAGCCTGGTGTGGTCTCTCAGTCTGTGGGGGCGAGTAGT 62
QY 63 AGGTGCTCAAAACATCACAGCCCGGATTCGGAGCCACTGTGTGCTGAAGTGAAGGGGC 122
Db 63 AGGTGCTCAAAACATCACAGCCCGGATTCGGAGCCACTGTGTGCTGAAGTGAAGGGGC 122
QY 123 CCCCAGAAACACCCAGCGGTGGAATGGAACCTGAACACAGGCGGACAGAGCTTG 182
Db 123 CCCCAGAAACACCCAGCGGTGGAATGGAACCTGAACACAGGCGGACAGAGCTTG 182
QY 183 GAAGTCTCTCTCCCGAGGAGGCGCCCTGGGACAGTGTGGTCTGTCTTCCCAA 242
Db 183 GAAGTCTCTCTCCCGAGGAGGCGCCCTGGGACAGTGTGGTCTGTCTTCCCAA 242
QY 243 CGGCTCCCTCTTCTCCCGGTGTGGGATCAGGATGAGGGGATTTTCGGTGCCAGGC 302
Db 243 CGGCTCCCTCTTCTCCCGGTGTGGGATCAGGATGAGGGGATTTTCGGTGCCAGGC 302
QY 303 AATGAACAGGATGGAAGGAGACCAAGTCCAACTACGAGTCTGTGTACCAAGTTC 362
Db 303 AATGAACAGGATGGAAGGAGACCAAGTCCAACTACGAGTCTGTGTACCAAGTTC 362
QY 363 TGGGAAGCAGAAATTTGTAGATTCTTCCTCTGAACTCAGCGCTGTGTTCCTCAATAAGGT 422

Db 363 TGGGAAGCAGAAATTTGTAGATTCTTCCTCTGAACTCAGCGCTGTGTTCCTCAATAAGGT 422
QY 423 GGGGACATGTGTCTCAGAGGAGCTACCTTCAGGGACTCTTAGCTGGCACTTGGATGG 482
Db 423 GGGGACATGTGTCTCAGAGGAGCTACCTTCAGGGACTCTTAGCTGGCACTTGGATGG 482
QY 483 GAAAGCCCTGTGTCTTAATGAGAGGAGTATCTGTGAAGGAAACAGACAGGAGACACCC 542
Db 483 GAAAGCCCTGTGTCTTAATGAGAGGAGTATCTGTGAAGGAAACAGACAGGAGACACCC 542
QY 543 TGAGACAGGCTCTTCACTGACGTCGAGCTAATGTGACCCAGCCCGGGAGGAGA 602
Db 543 TGAGACAGGCTCTTCACTGACGTCGAGCTAATGTGACCCAGCCCGGGAGGAGA 602
QY 603 TCCCGCTCCCACTCTCTCTGTAGCTCAGCCAGCCCTTCCCGACACCGGGCCCTTGGG 662
Db 603 TCCCGCTCCCACTCTCTCTGTAGCTCAGCCAGCCCTTCCCGACACCGGGCCCTTGGG 662
QY 663 CACAGCCCTCCATCCAGCCCTGTGTCTGGAGCCTGTGCTCTGGAGGAGGTCCTAATTGGT 722
Db 663 CACAGCCCTCCATCCAGCCCTGTGTCTGGAGCCTGTGCTCTGGAGGAGGTCCTAATTGGT 722
QY 723 GGTGAGCCAGAAAGGTGAGCAGTAGTCTCTGTGGAAACCGTAACCTGACCTGTGAAAGT 782
Db 723 GGTGAGCCAGAAAGGTGAGCAGTAGTCTCTGTGGAAACCGTAACCTGACCTGTGAAAGT 782
QY 783 CCGTCCCGCAGCCCTCTCTCAATCCACTGGATGAAGATGGTGTGCCCTTGGCCCTTCC 842
Db 783 CCGTCCCGCAGCCCTCTCTCAATCCACTGGATGAAGATGGTGTGCCCTTGGCCCTTCC 842
QY 843 CCCCAGCCCTGTGTGTGATCTCTCCCTGAGATAGGGCTCAGACACAGGGAACCTACAGCTG 902
Db 843 CCCCAGCCCTGTGTGTGATCTCTCCCTGAGATAGGGCTCAGACACAGGGAACCTACAGCTG 902
QY 903 TGTGCGCACCCATTCCAGCCACGGGCCCCAGGAAAGCGTCTGTGACGATCAGCATCAT 962
Db 903 TGTGCGCACCCATTCCAGCCACGGGCCCCAGGAAAGCGTCTGTGACGATCAGCATCAT 962
QY 963 CGAACCGAGGAGGAGGGGGCCCACTGACGGCTCTGTGGAGGATCAGGGCTGG 1015
Db 963 CGAACCGAGGAGGAGGGGGCCCACTGACGGCTCTGTGGAGGATCAGGGCTGG 1015
RESULT 5
US-10-472-507A-1
; Sequence 1, Application US/10472507A
; Publication No. US2005003017A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, Hiroshi
; APPLICANT: Yonekura, Hideto
; APPLICANT: Yamamoto, Yasuhiko
; APPLICANT: Sakurai, Shigeru
; APPLICANT: Watanabe, Takuo
; TITLE OF INVENTION: Soluble RAGE Protein
; FILE REFERENCE: 026350-089
; CURRENT APPLICATION NUMBER: US/10/472,507A
; CURRENT FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: PCT/JP02,02623
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: JP 2001-78409
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: JP 2001-243114
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: JP 2002-48182
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1223
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

NAME/KEY: CDS
LOCATION: (25) ... (1068)
US-10-472-507A-1

Query Match 97.3%; Score 992; DB 19; Length 1223;
Best Local Similarity 100.0%; Pred. No. 4.5e-278; Indels 0; Gaps 0;
Matches 992; Conservative 0; Mismatches 0;

QY 1 ATGGCAGCGGAAACAGCAGTTGGAGCTGGTCTGCTGCTCAGTCTGTGGGGGCGAGTA 60
DB 25 ATGGCAGCGGAAACAGCAGTTGGAGCTGGTCTGCTCAGTCTGTGGGGGCGAGTA 84
QY 61 GTAGTGTCTAAAACATCAAGCCCGGATTTGGAGCCACTGGTGTGAAGTGTAAAGGG 120
DB 85 GTAGTGTCTAAAACATCAAGCCCGGATTTGGAGCCACTGGTGTGAAGTGTAAAGGG 144
QY 121 GCCCCCAAGAAACACCCAGCGGCTGGAACTGAACTGAACACAGCCGCGACAGAGCT 180
DB 145 GCCCCCAAGAAACACCCAGCGGCTGGAACTGAACTGAACACAGCCGCGACAGAGCT 204
QY 181 TGAAGGTCTCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTGTCTCTTCCC 240
DB 205 TGAAGGTCTCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTGTCTCTTCCC 264
QY 241 AAGCGTCTCTCTCTCTCCCGATTCAGGATCAGGAGATTTTCGGTGGCCAG 300
DB 265 AAGCGTCTCTCTCTCTCCCGATTCAGGATCAGGAGATTTTCGGTGGCCAG 324
QY 301 GCAATGAACAGGAATGGAAGGAGCAAGTCCAACTACCGATCCGTCCTACCAAGTT 360
DB 325 GCAATGAACAGGAATGGAAGGAGCAAGTCCAACTACCGATCCGTCCTACCAAGTT 384
QY 361 CTGGGAAGCCAGAAATTTAGATTTCTGCTCTGAACTCAGCGCTGGTGTCCCAATAAG 420
DB 385 CTGGGAAGCCAGAAATTTAGATTTCTGCTCTGAACTCAGCGCTGGTGTCCCAATAAG 444
QY 421 GTGGGACATGTGTTCAGAGGAAAGTACCTTCAGGAGACTTTAGCTGGCACTTGGAT 480
DB 445 GTGGGACATGTGTTCAGAGGAAAGTACCTTCAGGAGACTTTAGCTGGCACTTGGAT 504
QY 481 GGGAGCCCTGGTGTCTAATGAGGAGGATCTGTGAAGGACAGACACAGGAGACAC 540
DB 505 GGGAGCCCTGGTGTCTAATGAGGAGGATCTGTGAAGGACAGACACAGGAGACAC 564
QY 541 CTGAGACAGGGCTCTTCACTGTCAGTGGAGCTAATGTGACCCAGCCAGCGGGAGGA 600
DB 565 CTGAGACAGGGCTCTTCACTGTCAGTGGAGCTAATGTGACCCAGCGGGAGGA 624
QY 601 GATCCCGTCCCACTTCTCTGTAGCTTCAAGCCAGGCTTCCCGACACCGGGCTTTG 660
DB 625 GATCCCGTCCCACTTCTCTGTAGCTTCAAGCCAGGCTTCCCGACACCGGGCTTTG 684
QY 661 CGCAGACCCCATCCAGCCCGTGTCTGGAGCTGTGCTGTGGAGAGTCCCAATTG 720
DB 685 CGCAGACCCCATCCAGCCCGTGTCTGGAGCTGTGCTGTGGAGAGTCCCAATTG 744
QY 721 GTGGTGGAGCCAGAAAGGTGGAGCAGTAGCTCTGTGGTGAACCGTAACCTGTGTGAA 780
DB 745 GTGGTGGAGCCAGAAAGGTGGAGCAGTAGCTCTGTGGTGAACCGTAACCTGTGTGAA 804
QY 781 GTCCCTGCCAGCCCTCTCTCAATCACTGATGAAGATGGTGTGCCCTTGCCTT 840
DB 805 GTCCCTGCCAGCCCTCTCTCAATCACTGATGAAGATGGTGTGCCCTTGCCTT 864
QY 841 CCCCCCAGCCCTGTGTGATCTCTCTCTGATAGAGGCTTCAGGACAGGAACTTACAGC 900
DB 865 CCCCCCAGCCCTGTGTGATCTCTCTCTGATAGAGGCTTCAGGACAGGAACTTACAGC 924
QY 901 TGTGTGGCCACCATTTCCAGCCAGCGGCCCCAGGAAAGCGTGTCTCAGCATCAGCATC 960
DB 925 TGTGTGGCCACCATTTCCAGCCAGCGGCCCCAGGAAAGCGTGTCTCAGCATCAGCATC 984
QY 961 ATCGAACCGGAGGAGGGGCCAACTGCAGG 992

DB 985 ATCGAACCGGAGGAGGGGCCAACTGCAGG 1016

RESULT 6

US-08-905-709-3
; Sequence 3, Application US/08905709
; Publication NO. US20010039256A1
; GENERAL INFORMATION:
; APPLICANT: Steirn, David
; APPLICANT: Schmidt, Ann M.
; TITLE OF INVENTION: A METHOD TO PREVENT ACCELERATED
; TITLE OF INVENTION: ATHEROSCLEROSIS USING (SRAGE) SOLUBLE RECEPTOR FOR
; TITLE OF INVENTION: ADVANCED GLYCATION ENDPRODUCTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,709
; FILING DATE: 05-AUG-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/52876
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-905-709-3

Query Match 96.7%; Score 986.8; DB 8; Length 1405;
Best Local Similarity 99.6%; Pred. No. 1.5e-276;
Matches 1010; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 3 GGCAGCCGGAACAGCAGTTGGAGCCTGGGTCTGTGGTCTCAGTCTGTGGGGGCGAGTAGT 62
DB 3 GGCAGCCGGAACAGCAGTTGGAGCCTGGGTCTGTGGTCTCAGTCTGTGGGGGCGAGTAGT 62
QY 63 AGGTGCTCAAAACATCACAGCCCGAATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGC 122
DB 63 AGGTGCTCAAAACATCACAGCCCGAATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGC 122
QY 123 CCCCAGAAACACCCAGCCGCTGGAACTGGAACACAGCCGCGGACAGAGCTTG 182
DB 123 CCCCAGAAACACCCAGCCGCTGGAACTGGAACACAGCCGCGGACAGAGCTTG 182
QY 183 GAAAGTCTGTCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTGTCTTCCCAA 242
DB 183 GAAAGTCTGTCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTGTCTTCCCAA 242
QY 243 CGGCTCCCTCTTCTTCCGGCTGTCCGGATCAGGATGAGGGGATTTTCGGTGCAGGC 302
DB 243 CGGCTCCCTCTTCTTCCGGCTGTCCGGATCAGGATGAGGGGATTTTCGGTGCAGGC 302
QY 303 AATGAACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCC 362

APPLICANT: Schmidt, Ann Marie	
APPLICANT: Wu, Jun	
TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES	
FILE REFERENCE: 0575/50159	
CURRENT APPLICATION NUMBER: US/10/850,861	
CURRENT FILING DATE: 2004-05-20	
PRIOR APPLICATION NUMBER: US/08/755,235	
PRIOR FILING DATE: 1996-11-22	
NUMBER OF SEQ ID NOS: 4	
SOFTWARE: PatentIn version 3.1	
SEQ ID NO 3	
LENGTH: 1405	
TYPE: DNA	
ORGANISM: Human	
US-10-850-861-3	

Query Match	96.7%;	Score 986.8;	DB 18;	Length 1405;
Best Local Similarity	99.6%;	Pred. No. 1.5e-276;		
Matches 1010;	Conservative 0;	Mismatches 2;	Indels 2;	Gaps 2;

Qy	3	GGCAGCGGAACAGCAGTGTGGAGCCCTGGGTGCTGCTCTCAGTCTGTGTGGGGGCGAGTAGT	62
Db	3	GGCAGCGGAACAGCAGTGTGGAGCCCTGGGTGCTGCTCTCAGTCTGTGTGGGGGCGAGTAGT	62
Qy	63	AGTGCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGTGTCTGAAGTGTAAAGGGGC	122
Db	63	AGTGCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGTGTCTGAAGTGTAAAGGGGC	122
Qy	123	CCCCAAGAACACACCCAGCGGCTGGATGGAAATCTGAACACAGCCCGGACAGAGCTTG	182
Db	123	CCCCAAGAACACACCCAGCGGCTGGATGGAAATCTGAACACAGCCCGGACAGAGCTTG	182
Qy	183	GAAGGTCCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTGTCTTCCCAA	242
Db	183	GAAGGTCCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTGTCTTCCCAA	242
Qy	243	CGGCTCCCTCTTCTTCCCGGCTGTGGGATCCAGATGAGGGATTTCCGGTCCAGGC	302
Db	243	CGGCTCCCTCTTCTTCCCGGCTGTGGGATCCAGATGAGGGATTTCCGGTCCAGGC	302
Qy	303	AATGAACAGAAATGGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCC	362
Db	303	AATGAACAGAAATGGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCC	362
Qy	363	TGGGAAGCCAGAAATTTAGATTCTGCCTCTGAATCTCACGGCTGGTGTCCCAATAAGGT	422
Db	363	TGGGAAGCCAGAAATTTAGATTCTGCCTCTGAATCTCACGGCTGGTGTCCCAATAAGGT	422
Qy	423	GGGGAATGTGTGTACAGGGGAAGTACCTCGAGGACTCTTTAGCTGGGACTTTGGATGG	482
Db	423	GGGGAATGTGTGTACAGGGGAAGTACCTCGAGGACTCTTTAGCTGGGACTTTGGATGG	482
Qy	483	GRAGCCCTCGTCCCTAAATGAAGGGAGTATCTGTGAAGGACAGACAGACGACACCC	542
Db	483	GRAGCCCTCGTCCCTAAATGAAGGGAGTATCTGTGAAGGACAGACAGACGACACCC	542
Qy	543	TGAGACAGGGCTCTTCACTCTGAGTGGAGCTTAATGGTGAACCCAGCCCGGGGAGGAGA	602
Db	543	TGAGACAGGGCTCTTCACTCTGAGTGGAGCTTAATGGTGAACCCAGCCCGGGGAGGAGA	602
Qy	603	TCCCGTCCCACTTCTCTGTAGCTTACGCCAGCCAGCCCTTCCCGACACCGGGCTTTGG	662
Db	603	TCCCGTCCCACTTCTCTGTAGCTTACGCCAGCCAGCCCTTCCCGACACCGGGCTTTGG	662
Qy	663	CACAGCCCCATCCAGCCCGTGTGTGGAGGCTGTGCTCTGGAGGAGGTCCCAATTGG	721
Db	663	CACAGCCCCATCCAGCCCGTGTGTGGAGGCTGTGCTCTGGAGGAGGTCCCAATTGG	722
Qy	722	TGGTGGAGCCAGAAAGGTGAGCAGTAGCTTCTGTGTGAACCTGACCTGTGTGAAG	781
Db	723	TGGTGGAGCCAGAAAGGTGAGCAGTAGCTTCTGTGTGAACCTGACCTGTGTGAAG	782
Qy	782	TCCTCGCCAGCCCTCTCTCAATCCACTGGATGAAGGATGGTGTGCCCTTGGCCCTTC	841

APPLICANT: Schmidt, Ann Marie	
APPLICANT: Wu, Jun	
TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES	
FILE REFERENCE: 0575/50159	
CURRENT APPLICATION NUMBER: US/10/850,861	
CURRENT FILING DATE: 2004-05-20	
PRIOR APPLICATION NUMBER: US/08/755,235	
PRIOR FILING DATE: 1996-11-22	
NUMBER OF SEQ ID NOS: 4	
SOFTWARE: PatentIn version 3.1	
SEQ ID NO 3	
LENGTH: 1405	
TYPE: DNA	
ORGANISM: Human	
US-10-850-861-3	

Query Match	93.8%;	Score 957;	DB 18;	Length 1463;
Best Local Similarity	95.5%;	Pred. No. 7e-268;		
Matches 1015;	Conservative 0;	Mismatches 0;	Indels 48;	Gaps 1;

Qy	1	ATGGCAGCGGAACAGCAGTGTGGAGCCCTGGGTGCTGCTCTCAGTCTGTGTGGGGGCGAGTA	60
Db	25	ATGGCAGCGGAACAGCAGTGTGGAGCCCTGGGTGCTGCTCTCAGTCTGTGTGGGGGCGAGTA	84
Qy	61	GTAGTGTCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTCTGAAGTGTAAAGGG	120
Db	85	GTAGTGTCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTCTGAAGTGTAAAGGG	144
Qy	121	GGCCCAAGAAACACCCAGCGGTGGAATGGAAATCTGAACACAGCCCGGACAGAAAGCT	180
Db	145	GGCCCAAGAAACACCCAGCGGTGGAATGGAAATCTGAACACAGCCCGGACAGAAAGCT	204
Qy	181	TGGAAGTCTCTGTCTCCCCAGGAGGAGCCCTTGGGACAGTGTGGTCTGTCTTCCC	240
Db	205	TGGAAGTCTCTGTCTCCCCAGGAGGAGCCCTTGGGACAGTGTGGTCTGTCTTCCC	264
Qy	241	ACGGGTCTCTTCTTCTTCCGGCTGTCCGGATCCAGGATGAGGGATTTTCCGGTGCAG	300

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Db 265 AACGGCTCCCTCTTCCGCTGTGCGGATCCAGGATGAGGGGATTTTCCGGTGCCAG 324
Qy 301 GCAATGACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGCTTACCAATT 360
Db 325 GCAATGACAGGAATGGAAGGAGACCAAGTCCAACTACCGAGTCCGCTGCTTACCAATT 384
Qy 361 CCTGGAAAGCCAGAAATTTGATGATTTCTGCTCTGAACTCAGCGCTGCTGTTCCCAATA-- 418
Db 385 CCTGGAAAGCCAGAAATTTGATGATTTCTGCTCTGAACTCAGCGCTGCTGTTCCCAATAAG 444
Qy 419 -----AGGTGGGACATGT 432
Db 445 GTAGTGGAAAGAACGAGGAGAAGTAGAAAACCGGCCCTGTGAACAGAGAGTGGGACATGT 504
Qy 433 GTGTACAGAGGAAGTACCTTCAGGAGCTTCTAGCTGGCACTTGGATGGGAAGCCCTTG 492
Db 505 GTGTACAGAGGAAGTACCTTCAGGAGCTTCTAGCTGGCACTTGGATGGGAAGCCCTTG 564
Qy 493 GTGCTTAATGAAAGGAGATCTGTGAAGGAAACAGACCAGGAGACACCTTGAGACAGGG 552
Db 565 GTGCTTAATGAAAGGAGATCTGTGAAGGAAACAGACCAGGAGACACCTTGAGACAGGG 624
Qy 553 CTCTTCACACTGCAGTGGAGCTAATGTTGACCCAGCCAGCCCGGGAGGAGATCCCGTCCC 612
Db 625 CTCTTCACACTGCAGTGGAGCTAATGTTGACCCAGCCAGCCCGGGAGGAGATCCCGTCCC 684
Qy 613 ACCTTCTCTGTAGCTTCAGCCAGGCTTCCCGACACCCGGGCTTGGCCAGACAGCCCC 672
Db 685 ACCTTCTCTGTAGCTTCAGCCAGGCTTCCCGACACCCGGGCTTGGCCAGACAGCCCC 744
Qy 673 ATCAGCCCGCTGTCTGGAGCTGTGCTCTGAGAGAGTCCAAATGTTGTTGGAGCCA 732
Db 745 ATCAGCCCGCTGTCTGGAGCTGTGCTCTGAGAGAGTCCAAATGTTGTTGGAGCCA 804
Qy 733 GAAGTGGAGCAGTAGCTCTGTGGAAACCGTACCTGACCTGACCTGACCTGACCTGACCT 792
Db 805 GAAGTGGAGCAGTAGCTCTGTGGAAACCGTACCTGACCTGACCTGACCTGACCTGACCT 864
Qy 793 CCTCTCTCAATCCACTGGATGAAGGATGTTGCTGCTTCCCTTCCCTTCCCTTCCCTTCCCT 852
Db 865 CCTCTCTCAATCCACTGGATGAAGGATGTTGCTGCTTCCCTTCCCTTCCCTTCCCTTCCCT 924
Qy 853 GTGCTGATCTCCTGATAGAGGCTCAGGACACAGGACCTTACAGCTGTGTGGCCACC 912
Db 925 GTGCTGATCTCCTGATAGAGGCTCAGGACACAGGACCTTACAGCTGTGTGGCCACC 984
Qy 913 CATTCAGCCACGGGCCCCAGGAAAGCCGTGTGTGATCAGCATCAGCATCAGCATCAGCAT 972
Db 985 CATTCAGCCACGGGCCCCAGGAAAGCCGTGTGTGATCAGCATCAGCATCAGCATCAGCAT 1044
Qy 973 GAGGAGGGGCAACTGAGGCTCTGTGGAGGATCAGGCTGG 1015
Db 1045 GAGGAGGGGCAACTGAGGCTCTGTGGAGGATCAGGCTGG 1087
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RESULT 10

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US-10-309-290-99
; Sequence 99, Application US/10309290
; Publication No. US2004002341A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chilikuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
```

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; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glennda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
```

```
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10309,290
```

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; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 99
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1170)
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US-10-309-290-99
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Query Match 90.3%; Score 921; DB 17; Length 1173;
Best Local Similarity 95.9%; Pred. No. 2e-257;
Matches 973; Conservative 0; Mismatches 0; Indels 42; Gaps 1;
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Qy 1 ATGGCAGCCGGAACAGCAGTTGGAGCCTGGTGTCTCTCAGTCTGTGGGGGCGAGTA 60
Db 1 ATGGCAGCCGGAACAGCAGTTGGAGCCTGGTGTCTCTCAGTCTGTGGGGGCGAGTA 60
Qy 61 GTAGTGTCTCAAAACATCACAGCCCGGATTTGGGAGCCACTGGTGTGTAAGTGTAGGGG 120
Db 61 GTAGTGTCTCAAAACATCACAGCCCGGATTTGGGAGCCACTGGTGTGTAAGTGTAGGGG 120
Qy 121 GCCCCCAAGAAACACACCCAGCGGCTGGAAATGGAACCTGAACACAGCCCGGACAGAGCT 180
Db 121 GCCCCCAAGAAACACACCCAGCGGCTGGAAATGGAACCTGAACACAGCCCGGACAGAGCT 180
Qy 181 TGGAGGTCTGTCTCTCCCGGAGGAGGCGCCCTGGGACAGTGTGGCTGTGCTCTTCCC 240
Db 159 -----GGAGAGGAGGCGCCCTGGGACAGTGTGGCTGTGCTCTTCCC 198
Qy 241 AACGGCTCCCTCTTCTTCCCGGCTGTCCGGATCCAGGATCAGGGGATTTTCCCGTGCAG 300
Db 199 AACGGCTCCCTCTTCTTCCCGGCTGTCCGGATCCAGGATCAGGGGATTTTCCCGTGCAG 258
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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1015	99.5	1215	9	AY421473	Homo sapi
2	953.8	93.5	1163	9	AY421474	Pan trogl
3	716.8	70.3	1194	5	BQ067161	AGENCOURT
4	695.8	68.2	841	4	BI7171266	BI7171266
5	678	66.5	777	4	BG545464	603572696
6	672.8	66.0	1209	9	AY421475	Mus muscu
7	649.4	63.7	724	4	BG536369	602564760
8	648.2	63.5	750	4	BG548202	603575359
9	647	63.4	715	4	BG506672	601861271
10	642.8	63.0	715	4	BG5298918	602558918
11	642.4	63.0	729	4	BG545652	602572917
12	641	62.8	1347	3	AK004802	Mus muscu
13	635.4	62.3	1296	7	CF110468	Shultzomi
14	612.6	60.1	755	4	BG529866	602558957
15	611.4	59.9	822	4	BG540930	602569259
16	610.4	59.8	736	4	BG540452	602568768
17	604.6	59.3	832	4	BG548148	602575303
18	581.6	57.0	853	4	BG535354	602563012
19	576.4	56.5	810	4	BG569848	602590474
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21	567.4	55.6	692	4	BG483796	602503447
22	557.8	54.7	698	4	BG537129	602565523
23	554.8	54.4	613	4	BG570489	602591356
24	554	54.3	723	4	BG534930	602554119

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 16, 2005, 02:38:05 ; Search time 80 Seconds
(without alignments)
1638.897 Million cell updates/sec

Title: US-10-091-019-3

Perfect score: 339

Sequence: 1 MAAGTAGVAGWLVLSWGA.....IIEPGEGBTAGSGVGLV 339

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	339	100.0	339	5	ABB82164 Human sol
2	338	99.7	340	2	AAM44199 Human sol
3	338	99.7	340	2	AAM33753 Human RAG
4	338	99.7	391	8	ADP19666 Human LP2
5	338	99.7	402	7	ADP95564 Human NOV
6	338	99.7	404	4	AAB81925 Extracorp
7	338	99.7	404	5	ADP65011 Human rec
8	338	99.7	404	8	ADP31292 Human rec
9	338	99.7	404	8	ADP42983 Human rec
10	338	99.7	404	8	ADK00129 Human RAG
11	337	99.4	339	5	AAM48746 Human SRA
12	337	99.4	404	5	AAM48745 Human RAG
13	331	97.6	347	5	ABB82298 Human sol
14	331	97.6	347	7	ADG37044 Receptor
15	331	97.6	352	8	ADP19656 Human LP2
16	316	93.2	318	2	AAM44200 Human mat
17	316	93.2	318	2	AAM33754 Human RAG
18	275	81.1	360	8	ADP19664 Human LP2
19	274	80.8	298	8	ADP19658 Human LP2
20	274	80.8	325	8	ADM80782 Human CAD
21	271	79.9	390	7	ADP95566 Human NOV
22	271	79.9	390	7	ADP95568 Human NOV
23	271	79.9	390	8	ADP19670 Human LP2
24	271	79.9	421	6	ABR43188 Human REM
25	251	74.0	381	8	ADS10986 Human the

26	241	71.1	332	3	AAV52130	Human Rec
27	238	70.2	404	5	AAU77543	Human rec
28	238	70.2	404	5	AAE23219	Human rec
29	238	70.2	404	7	AAE39510	Human RAG
30	238	70.2	404	7	ADG32004	Human hom
31	230	67.8	250	6	ABR43202	Human REM
32	207	61.1	342	7	ADJ68835	Human hea
33	198	58.4	420	5	ABP65012	Human pro
34	198	58.4	425	8	ADP19660	Human LP2
35	191	56.3	368	8	ADP19662	Human LP2
36	172	50.7	585	8	ADK00127	Human RAG
37	119	35.1	128	6	ABR43201	Human REM
38	114	33.6	127	8	ADP19668	Human LP2
39	112	33.0	112	5	AAM48747	Human RAG
40	40	11.8	40	8	ADK00131	Human RAG
41	30	8.8	30	2	AAV09349	Human RAG
42	30	8.8	30	3	AAV52134	Human Rec
43	30	8.8	30	5	AAM48748	Human RAG
44	26	7.7	343	8	ADK00124	Murine so
45	26	7.7	403	5	AAU77544	Murine re

ALIGNMENTS

RESULT 1
ABB82164
ID ABB82164 standard; protein; 339 AA.
XX
AC ABB82164;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human soluble RAGE (sRAGE).
XX
KW Receptor for Advanced Glycated end product; RAGE; recombinant; nontropic;
KW antihypertensive; antidiabetic; cytotatic; nephrotropic; vasotropic;
KW neuroprotective; antiinflammatory; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO200270667-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US006881.
XX
PR 05-MAR-2001; 2001US-0273418P.
XX
PA (TRAN-) TRANSTECH PHARMA INC.
XX
PI Harris R, Shen J, Shabbaz M;
XX
DR WPI; 2002-713443/77.
DR N-PSDB; ABQ79956.
XX
PT High level expression of recombinant Receptors for Advanced Glycated end products (RAGE) proteins for treating increased levels of advanced glycosylation end products, comprises infecting cells with a high titer recombinant virus.
XX
PS Example; Fig 2B; 51pp; English.
XX
CC The invention relates to a method for high level expression of recombinant forms of the Receptor for Advanced Glycated end products (RAGE) or its fragments. The method involves (i) subcloning a nucleotide sequence encoding RAGE or its fragment into a virus; (ii) preparing a high titer stock of recombinant virus; and (iii) infecting host cells with the high titer recombinant virus under conditions such that predetermined levels of RAGE or its fragment is produced, where the predetermined levels of RAGE comprises at least 25 mg recombinant protein per liter of culture. The method is useful for high level expression of recombinant RAGE polypeptide or its fragment which may be useful in

CC preventing, treating or ameliorating diseases associated with increased
 CC levels of advanced glycosylation end products, such as atherosclerosis,
 CC diabetes and its symptoms, amyloidosis, kidney failure, Alzheimer's
 CC disease, inflammation, systemic lupus nephritis, inflammatory lupus
 CC nephritis, cancer or erectile dysfunction. The present sequence
 CC represents the amino acid sequence of human sRAGE (soluble, extracellular
 CC portion of RAGE)
 XX
 XX Sequence 339 AA;
 Query Match 100.0%; Score 339; DB 5; Length 339;
 Best Local Similarity 100.0%; Pred. No. 4e-309;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAGTAGAWLVLSLWGA VVGAQNITARI GEPVLVKCKGAPKPPQRLWKLTGRTEA 60
 DB 1 MAAGTAGAWLVLSLWGA VVGAQNITARI GEPVLVKCKGAPKPPQRLWKLTGRTEA 60
 QY 61 WKVLSPOGGP WDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQI 120
 DB 61 WKVLSPOGGP WDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQI 120
 QY 121 PKGPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQTRRH 180
 DB 121 PKGPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDRPTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
 DB 181 PETGLFTLQSELMTVPARGGDRPTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
 QY 241 VVEPEGGA VAPGGTVTLTCEVPAQSPQIHMMKDGVPPLPPSPVLILPEIGPDQGTYS 300
 DB 241 VVEPEGGA VAPGGTVTLTCEVPAQSPQIHMMKDGVPPLPPSPVLILPEIGPDQGTYS 300
 QY 301 CVATHSSHGPQESRAVSIISIIPEGEGPTAGSVGGSLV 339
 DB 301 CVATHSSHGPQESRAVSIISIIPEGEGPTAGSVGGSLV 339
 RESULT 2
 AAW44199
 ID AAW44199 standard; protein; 340 AA.
 AC AAW44199;
 XX
 XX 14-MAY-1998 (first entry)
 DT Human soluble receptor to an advanced glycosylation end product.
 DE Human; soluble receptor; advanced glycosylation end product; RAGE; AGE;
 XX antibody; vascular permeability; diabetes mellitus.
 KW
 KW Homo sapiens.
 XX
 XX WO9739125-A1.
 PN 23-OCT-1997.
 PD 11-APR-1997; 97WO-EP001834.
 XX 16-APR-1996; 96US-00633148.
 PR (SCHD) SCHERING PATENTE AG.
 XX
 XX Morser MJ, Nagashima M, Hollander DA;
 PI WPI; 1997-558580/51.
 DR N-PSDB; AAV12394.
 XX
 XX Anti-advanced glycosylation end product polypeptide antibody - prevents
 PT receptor binding and therefore reduces vascular permeability, useful to
 PT treat diabetes mellitus.
 XX

PS Claim 2; Page 40-41; 90pp; English.
 XX The present sequence represents a soluble human receptor to an advanced
 CC glycosylation end product (RAGE) polypeptide. The present invention
 CC describes an isolated antibody (Ab), specifically immunoreactive with
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are non-
 CC enzymatically glycosylated proteins, which accumulate in vascular tissue
 CC in ageing, and at an accelerated rate in individuals with diabetes. The
 CC Ab, which prevents the interaction between an AGE and it's receptor
 CC (RAGE), reduces vascular permeability. The Ab can be used to treat
 CC diabetes mellitus symptoms, e.g. microvasculopathy, occlusive vascular
 CC disorders, neuropathy, nephropathy, retinopathy, haemodialysis associated
 CC amyloidosis or atherosclerosis. The Ab can also be used for the isolation
 CC and purification of human RAGE polypeptide
 XX
 XX Sequence 340 AA;
 Query Match 99.7%; Score 338; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 3.5e-308;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAGTAGAWLVLSLWGA VVGAQNITARI GEPVLVKCKGAPKPPQRLWKLTGRTEA 60
 DB 1 MAAGTAGAWLVLSLWGA VVGAQNITARI GEPVLVKCKGAPKPPQRLWKLTGRTEA 60
 QY 61 WKVLSPOGGP WDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQI 120
 DB 61 WKVLSPOGGP WDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQI 120
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 DB 121 PKGPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDRPTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
 DB 181 PETGLFTLQSELMTVPARGGDRPTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
 QY 241 VVEPEGGA VAPGGTVTLTCEVPAQSPQIHMMKDGVPPLPPSPVLILPEIGPDQGTYS 300
 DB 241 VVEPEGGA VAPGGTVTLTCEVPAQSPQIHMMKDGVPPLPPSPVLILPEIGPDQGTYS 300
 QY 301 CVATHSSHGPQESRAVSIISIIPEGEGPTAGSVGGSL 338
 DB 301 CVATHSSHGPQESRAVSIISIIPEGEGPTAGSVGGSL 338
 RESULT 3
 AAW33753
 ID AAW33753 standard; protein; 340 AA.
 AC AAW33753;
 XX
 XX 08-MAY-1998 (first entry)
 DT Human RAGE polypeptide (340 amino acid residues).
 DE Advanced glycosylation end-product receptor; RAGE; screening; AGE;
 XX KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;
 KW Alzheimer's disease.
 XX
 XX Homo sapiens.
 XX
 XX WO9739121-A1.
 PN 23-OCT-1997.
 PD 11-APR-1997; 97WO-EP001832.
 XX 16-APR-1996; 96US-00633147.
 PR (SCHD) SCHERING AG.
 XX
 XX Morser MJ, Nagashima M;
 PI

XX WPI; 1997-526458/48.
 DR N-PSDB; AAV06517.
 XX
 PT New soluble advanced glycosylation end-product receptor polypeptide -
 PT used for reducing vascular permeability, complications of diabetes etc.,
 PT also for purification and to screen for modulators.
 XX
 PS Claim 3; Fig 1A; 91pp; English.
 PS
 XX This is a human advanced glycosylation end-product receptor (RAGE)
 CC polypeptide (340 amino acid residues). The RAGE polypeptides and its
 CC active fragments or their mimetics, inhibit interaction between advanced
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They
 CC are used to treat diseases associated with AGE/RAGE interaction, such as
 CC increased vascular permeability, diabetes mellitus (particularly
 CC complications such as micro- or macro- vasculopathy or occlusive vascular
 CC disorders such as neuropathy, nephropathy, retinopathy or
 CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or
 CC age-related disorders such as oxidative stress. These RAGE polypeptides
 CC are also used, when immobilised, to purify AGE from a protein mixture and
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE
 CC interaction. They can also be used diagnostically to detect abnormal
 CC levels of AGE. Antibodies against RAGE polypeptides are useful as
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of
 CC interaction between AGE and RAGE or other receptors and for purification
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are
 CC used to express recombinant RAGE and as probes for isolating related
 CC genes
 XX
 SQ Sequence 340 AA;
 Query Match 99.7%; Score 338; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 3.5e-308;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAGTAVGAWVLVLSLWAGVGAQNTARIGEPVLKCKGAPKPPORLEWKLNTGRTA 60
 DB 1 MAAGTAVGAWVLVLSLWAGVGAQNTARIGEPVLKCKGAPKPPORLEWKLNTGRTA 60
 QY 61 WKVLSQQGGPNDVSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETSRYRVYQI 120
 DB 61 WKVLSQQGGPNDVSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETSRYRVYQI 120
 QY 121 PGKPEIVDSASELTAGVPNKVGTVCSEGSYPAGTILSWHLDGKPLVNEKGVSKVQTRRH 180
 DB 121 PGKPEIVDSASELTAGVPNKVGTVCSEGSYPAGTILSWHLDGKPLVNEKGVSKVQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDPRTFTSCFSPLGPRHRLRTAPIQRYVMEPVLPLEEVQL 240
 DB 181 PETGLFTLQSELMTVPARGGDPRTFTSCFSPLGPRHRLRTAPIQRYVMEPVLPLEEVQL 240
 QY 241 VVEPEGAVAPGTVTLTCEVPAQPSQIHKMKDGVPLPSPVLILPEIGPDQGTYS 300
 DB 241 VVEPEGAVAPGTVTLTCEVPAQPSQIHKMKDGVPLPSPVLILPEIGPDQGTYS 300
 QY 301 CVATHSHGPQESRAVYSIIEPGERGPTAGSVGGSL 338
 DB 301 CVATHSHGPQESRAVYSIIEPGERGPTAGSVGGSL 338
 RESULT 4
 ID ADP19666
 XX ADP19666 standard; protein; 391 AA.
 AC ADP19666;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human LP2005 protein SEQ ID.NO:12.
 XX
 KW human; LP2005; antidiabetic; neuroprotective; neurotropic;

XX antinflammatory; antirheumatic; antiarthritic; vulnerary; cytostatic;
 KW immunosuppressive; nephrotropic; dermatologic; gene therapy; diabetes;
 KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;
 KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;
 KW systemic lupus erythematosus.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= signal
 FT Protein 24..391
 FT /label= LP2005
 XX
 PN WO2004044126-A2.
 PD
 XX 27-MAY-2004.
 XX
 PF 05-NOV-2003; 2003WO-US032734.
 XX
 PR 14-NOV-2002; 2002US-0426253P.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Na S, Perkins DR;
 XX
 DR WPI; 2004-411705/38.
 DR N-PSDB; ADP19665.
 XX
 PT New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or
 PT LP2003) for diagnosing or treating disorders associated with aberrant
 PT levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome
 PT identification.
 XX
 PS Claim 9; SEQ ID NO 12; 111pp; English.
 XX
 CC The present sequence represents human LP2005, which is used in the
 CC exemplification of the present invention. The present invention
 CC describes: (1) an isolated nucleic acid (I) comprising DNA having at
 CC least 95% sequence identity to a polynucleotide selected from the group
 CC consisting of: (a) a polynucleotide having a nucleotide sequence as shown
 CC in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a
 CC polypeptide or mature form of a polypeptide having the amino acid
 CC sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide
 CC fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide
 CC having a nucleotide sequence which is complementary to the nucleotide
 CC sequence of a polynucleotide as in (a), (b) or (c); (2) a vector
 CC comprising (1); (3) a host cell comprising the vector; (4) producing an
 CC LP polypeptide; (5) an isolated polypeptide produced by the above method
 CC and comprising an amino acid sequence comprising about 95% sequence
 CC identity to a sequence of amino acid residues comprising LP2001, LP2003,
 CC LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric
 CC molecule comprising an LP polypeptide fused to a heterologous amino acid
 CC sequence; (7) an antibody which specifically binds to an LP polypeptide
 CC described above; (8) a composition (C) comprising a therapeutic amount of
 CC an active agent selected from an LP polypeptide, an agonist to an LP
 CC polypeptide, an antagonist to an LP polypeptide, an LP polypeptide
 CC antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a
 CC polynucleotide in combination with a pharmaceutical carrier; and (9)
 CC diagnosing or treating a mammal suffering from a disease, condition or
 CC disorder associated with aberrant levels of an LP-polypeptide. (C) has
 CC antidiabetic, neuroprotective, nootropic, antiinflammatory,
 CC antirheumatic, antiarthritic, vulnerary, cytostatic, immunosuppressive,
 CC nephrotropic and dermatological activities, and can be used in gene
 CC therapy. The compositions (C) and methods are useful for diagnosing or
 CC treating disorders associated with aberrant levels of an LP polypeptide,
 CC such as diabetes and its complications, Alzheimer's disease,
 CC inflammation, rheumatoid arthritis, wounds, autoimmune disease,
 CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They
 CC may also be used for chromosome identification. The LP polypeptide can
 CC also be used in manufacturing a medicament for the treatment of the above
 CC -mentioned diseases, conditions or disorders associated with aberrant
 CC levels of the LP polypeptide.

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XX SQ Sequence 391 AA;
Query Match          99.7%; Score 338; DB 8; Length 391;
Best Local Similarity 100.0%; Pred. No. 3.9e-308;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACTAVGAWLVLSLWGAVVGAQNITARIGEPVLVLCCKGAPKPPORLEWKLNTGRTEA 60
Db 1 MAACTAVGAWLVLSLWGAVVGAQNITARIGEPVLVLCCKGAPKPPORLEWKLNTGRTEA 60

QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQI 120
Db 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQI 120

QY 121 PGKPEIVDSASELTAGVPNKVGTCSGSGYPAGTLSWHLDDKPLVNEKGVSKVKEQTRRH 180
Db 121 PGKPEIVDSASELTAGVPNKVGTCSGSGYPAGTLSWHLDDKPLVNEKGVSKVKEQTRRH 180

QY 181 PETGLFTLOSELMTVPARGDPRPTFSCFSFGLPRHRALRTAPIQPRVWEPVPLEEVOL 240
Db 181 PETGLFTLOSELMTVPARGDPRPTFSCFSFGLPRHRALRTAPIQPRVWEPVPLEEVOL 240

QY 241 VVEPEGNAVAPGGTTLTCEVPAQPSQIHWMDKGVPLPLPPSPVLLPIGPDQGTYS 300
Db 241 VVEPEGNAVAPGGTTLTCEVPAQPSQIHWMDKGVPLPLPPSPVLLPIGPDQGTYS 300

QY 301 CVATHSHGQESRAVSISIIIEGEGTPTAGSVGGSL 338
Db 301 CVATHSHGQESRAVSISIIIEGEGTPTAGSVGGSL 338

RESULT 5
ADE95564
ID ADE95564 standard; protein; 402 AA.
XX AC ADE95564;
XX AC ADE95564;
DT 12-FEB-2004 (first entry)
XX DE Human NOVX16c protein.
XX KW NOVX protein; biochemical stimulation; physiological stimulation;
KW cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
KW antirheumatic; antiarthritic; antidiabetic; nephroprotective; dermatological;
KW immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;
KW antipruritic; antipsoriatic; antiparkinsonian; antiasthmatic; neuroleptic;
KW antidepressant; antiallergic; gynaecological; gene therapy; vaccine;
KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;
KW cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;
KW psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;
KW Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;
KW depression; allergy; fertility disorder; NOVX16c.
XX OS Homo sapiens.
XX OS
XX PN W02003050245-A2.
XX PD
XX PF 19-JUN-2003.
XX PF 03-DEC-2002; 2002WO-US038594.
XX PR 05-DEC-2001; 2001US-0336600P.
XX PR 07-DEC-2001; 2001US-0338285P.
XX PR 12-DEC-2001; 2001US-0341346P.
XX PR 17-DEC-2001; 2001US-0341477P.
XX PR 20-DEC-2001; 2001US-0341540P.
XX PR 27-DEC-2001; 2001US-0342592P.
XX PR 31-DEC-2001; 2001US-0344297P.
XX PR 17-APR-2002; 2001US-0344903P.
XX PR 15-MAY-2002; 2002US-0373288P.
XX PR 17-MAY-2002; 2002US-0380981P.
XX PR 17-MAY-2002; 2002US-0381495P.

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PR 28-MAY-2002; 2002US-0383534P.
PR 28-MAY-2002; 2002US-0383744P.
PR 29-MAY-2002; 2002US-0383829P.
PR 29-MAY-2002; 2002US-0384024P.
PR 07-AUG-2002; 2002US-0401788P.
PR 26-AUG-2002; 2002US-0406353P.
PR 31-OCT-2002; 2002US-0401788.
PR 02-DEC-2002; 2002US-0406353.
XX (CURA-) CURAGEN CORP.
XX PA
XX PI Alsbrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru RA;
PI Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X;
PI Jeffers ME, Ji W, Li L, Malyankar UM, Miller CE, Murphy R;
PI Ratturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG;
PI Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;
XX WPI; 2003-513974/48.
XX DR N-PSDB; ADE95563.
XX DR
XX PT New NOVX polypeptides and nucleic acids, useful for preventing or
XX PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
XX PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
XX PT pharmacogenomics.
XX PS Claim 2; SEQ ID NO 96; 211pp; English.
XX CC This invention relates to novel NOVX proteins, and the DNA sequence which
XX CC encode them, having properties related to stimulation of biochemical or
XX CC physiological responses in a cell, a tissue, an organ or an organism.
XX CC Compounds which modulate the proteins of the invention may have cardiant,
XX CC antiarteriosclerotic, hypotensive, cytostatic, anorectic, antirheumatic,
XX CC antiarthritic, antidiabetic, nephroprotective, dermatological,
XX CC immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,
XX CC neurotic, antipsoriatic, antiparkinsonian, antiasthmatic, neuroleptic,
XX CC antidepressant, antiallergic or gynaecological activities. The DNA
XX CC sequences of the invention may be useful for gene therapy whilst the
XX CC protein sequences may allow the development of a vaccine. The protein is
XX CC useful in the manufacture of a medicament for treating a syndrome
XX CC associated with a human disease. The invention may be useful in
XX CC diagnosing, treating or preventing NOVX-associated disorders, for example
XX CC cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
XX CC rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin
XX CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
XX CC Parkinson's disease, asthma, schizophrenia, depression, allergies or
XX CC fertility disorders. The nucleic acids may further be used as
XX CC hybridisation probes, in chromosome mapping, tissue typing, preventive
XX CC medicine, and pharmacogenomics. The present sequence is the amino acid
XX CC sequence of the human NOVX16c protein of the invention.
XX SQ Sequence 402 AA;
Query Match          99.7%; Score 338; DB 7; Length 402;
Best Local Similarity 100.0%; Pred. No. 4e-308;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACTAVGAWLVLSLWGAVVGAQNITARIGEPVLVLCCKGAPKPPORLEWKLNTGRTEA 60
Db 1 MAACTAVGAWLVLSLWGAVVGAQNITARIGEPVLVLCCKGAPKPPORLEWKLNTGRTEA 60

QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQI 120
Db 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQI 120

QY 121 PGKPEIVDSASELTAGVPNKVGTCSGSGYPAGTLSWHLDDKPLVNEKGVSKVKEQTRRH 180
Db 121 PGKPEIVDSASELTAGVPNKVGTCSGSGYPAGTLSWHLDDKPLVNEKGVSKVKEQTRRH 180

QY 181 PETGLFTLOSELMTVPARGDPRPTFSCFSFGLPRHRALRTAPIQPRVWEPVPLEEVOL 240
Db 181 PETGLFTLOSELMTVPARGDPRPTFSCFSFGLPRHRALRTAPIQPRVWEPVPLEEVOL 240

QY 241 VVEPEGNAVAPGGTTLTCEVPAQPSQIHWMDKGVPLPLPPSPVLLPIGPDQGTYS 300

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Db 241 VVEPEGAVAGGTGTTTCEVPAQSPQIHHMKDGVPLPLPPSPVLILPEIGPDQGTYS 300
QY 301 CVATHSHGPGQESRAVSISIIERCEGPTAGSVGGSL 338
Db 301 CVATHSHGPGQESRAVSISIIERCEGPTAGSVGGSL 338
RESULT 6
AAB81925
ID AAB81925 standard; protein; 404 AA.
XX
AC AAB81925;
XX
DT 15-JUN-2001 (first entry)
XX
DE Extracorporeal circulation material receptor protein.
XX
KW Extracorporeal circulation; carbonyl stress product; receptor; diabetes;
KW vascular lesion; excretory dysfunction.
XX
OS Unidentified.
XX
PN WC200118060-A1.
XX
PD 15-MAR-2001.
XX
PF 08-SEP-2000; 2000MO-JP006172.
XX
PR 08-SEP-1999; 99JP-00254463.
XX
PA (TORA ) TORAY IND INC.
XX
PI Shimizu S, Kubota M, Akiyama H, Usui M;
XX
WPI; 2001-290314/30.
XX
Material for extracorporeal circulation, applicable in selective
PT elimination of diabetic complication factors such as carbonyl stress
PT products caused by abnormally promoted carbonyl stress from excretory
PT dysfunction in vascular lesions.
XX
PS Claim 1; Page 31-32; 36pp; Japanese.
XX
The present invention describes a material for extracorporeal circulation
CC which is made from a water-insoluble carrier immobilized with a protein
CC having the sequence shown here. The materials of the invention, including
CC adsorbents, are for extracorporeal circulation, which are applicable in
CC the selective elimination of diabetic complication factors from a body
CC fluid, and are therefore useful in treating vascular lesions like
CC arteriosclerosis due to carbonyl stress products caused by abnormally
CC promoted carbonyl stress from excretory dysfunction
XX
SQ Sequence 404 AA;
Query Match 99.7%; Score 338; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 46-308;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAGTAGAWVLVLSLWGA VVGAVGQNTARIGELVLKCKGAPKPPORLEWKLNTGRTEA 60
Db 1 MAAGTAGAWVLVLSLWGA VVGAVGQNTARIGELVLKCKGAPKPPORLEWKLNTGRTEA 60
QY 61 WKVLSFGGGPWBDSVARVLPNGSLFLPAVGIDEGIFRCQAMRNKGTNSYRVRYQI 120
Db 61 WKVLSFGGGPWBDSVARVLPNGSLFLPAVGIDEGIFRCQAMRNKGTNSYRVRYQI 120
QY 121 PKRPEIVDSASELTAGVPNKVGTGCVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQETRRH 180
Db 121 PKRPEIVDSASELTAGVPNKVGTGCVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQETRRH 180
QY 181 PETGLFTLQSELMTVPARGDPRPTSCFSFGLPHRLALRTAPIQPRVWEPVPLEVQL 240
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Db 181 PETGLFTLQSELMTVPARGDPRPTSCFSFGLPHRLALRTAPIQPRVWEPVPLEVQL 240
QY 241 VVEPEGAVAGGTGTTTCEVPAQSPQIHHMKDGVPLPLPPSPVLILPEIGPDQGTYS 300
Db 241 VVEPEGAVAGGTGTTTCEVPAQSPQIHHMKDGVPLPLPPSPVLILPEIGPDQGTYS 300
QY 301 CVATHSHGPGQESRAVSISIIERCEGPTAGSVGGSL 338
Db 301 CVATHSHGPGQESRAVSISIIERCEGPTAGSVGGSL 338
RESULT 7
ABP65011
ID ABP65011 standard; protein; 404 AA.
XX
AC ABP65011;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human protein SEQ ID 671.
XX
KW Human; expressed sequence tag; EST; haematopoietic disorder;
KW central nervous system disease; viral infection;
KW peripheral nervous system disease; non-healing wound; infectious disease;
KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;
KW fungal infection; autoimmune disorder; coagulation disorder; neutropenic;
KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;
KW cytostatic; haemostatic; virucide; antibacterial; fungicide;
KW immunostimulant; cerebroprotective.
XX
OS Homo sapiens.
XX
PN WC200259260-A2.
XX
PD 01-AUG-2002.
XX
PF 16-NOV-2001; 2001WO-US042950.
XX
PR 17-NOV-2000; 2000US-00714936.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QH;
PI Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
WPI; 2002-590824/63.
XX
N-PSDB; ABQ99597.
XX
New isolated polynucleotide, useful in research, diagnostic or
PT therapeutic methods, e.g. preventing or treating disorders involving
PT aberrant protein expression or biological activity.
XX
PS Claim 20; SEQ ID NO 671; 394pp; English.
XX
The present invention relates to novel human coding sequences (ABQ99268-
CC ABQ99608) and proteins (ABP64682-ABP65022). The sequences are useful in
CC therapeutic, diagnostic and research methods. The polynucleotides may be
CC used in the field of molecular biology as hybridisation probes, primers
CC for PCR, for chromosome and gene mapping, for the recombinant production
CC of protein, or in generation of anti-sense DNA or RNA. The
CC polynucleotides are useful in diagnostics as expressed sequence tags
CC (ESTs) for identifying expressed genes or for physical mapping of the
CC human genome. The proteins may be used as molecular weight markers, or as
CC nutritional sources or supplements. The proteins may be used to maintain
CC and expand cell population in a totipotent or pluripotent state,
CC useful for re-engineering damaged or diseased tissues, transplantation,
CC manufacture of bio-pharmaceuticals or the development of bio-sensors. The
CC polynucleotides and proteins are useful for preventing, treating or
CC ameliorating disorders involving aberrant protein expression or
CC biological activity, e.g. haematopoietic disorders, central/peripheral
CC nervous system diseases, mechanical and traumatic disorders, non-healing
CC wounds, immune deficiencies and disorders, infectious diseases caused by
CC viral, bacterial or fungal infection, autoimmune disorders, allergic
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CC reactions and conditions, coagulation disorders, or cancer. The
 CC polynucleotide sequences of the invention were assembled from ESTs
 CC isolated mainly by sequencing by hybridisation, and in some cases,
 CC sequences obtained from one or more public databases. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 404 AA;

Query Match 99.7%; Score 338; DB 5; Length 404;
 Best Local Similarity 100.0%; Pred. No. 4e-308;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGAVGVAQNTARIGEPVLKCKGAPKPPQRLWKLTGRTEA 60
 DB 1 MAAGTAVGAWLVLSLWGAVGVAQNTARIGEPVLKCKGAPKPPQRLWKLTGRTEA 60
 QY 61 WKVLSPOGGGPDWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120
 DB 61 WKVLSPOGGGPDWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120
 QY 121 PGKPEIVDSASBLTAGVKNKVGTCVSEGSYPAGTLSWHLDGKPLVPNEKGVSKVEQTRRH 180
 DB 121 PGKPEIVDSASBLTAGVKNKVGTCVSEGSYPAGTLSWHLDGKPLVPNEKGVSKVEQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDPRTFSCSFGLPRHRLRTAPIQPRVWEPVLEEVOL 240
 DB 181 PETGLFTLQSELMTVPARGGDPRTFSCSFGLPRHRLRTAPIQPRVWEPVLEEVOL 240
 QY 241 VVEPEGGA VAGTGTTLTCEVPAQPSQIHWMDGVPLPLPPSPVLILPEIGPDQGTYS 300
 DB 241 VVEPEGGA VAGTGTTLTCEVPAQPSQIHWMDGVPLPLPPSPVLILPEIGPDQGTYS 300
 QY 301 CVATHSHGPOESRAVSISIIIEEGEGTAGSVGGSGL 338
 DB 301 CVATHSHGPOESRAVSISIIIEEGEGTAGSVGGSGL 338

RESULT 8
 ADF31292
 ID ADF31292 standard; protein; 404 AA.
 XX
 AC ADF31292;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human receptor of advanced glycation end products (RAGE).
 XX
 KW human; receptor; advanced glycation end product; RAGE;
 KW receptor of advanced glycation end product; high yield; high purity.
 XX
 OS Homo sapiens.
 XX
 PN JP2003306500-A.
 XX
 PD 28-OCT-2003.
 XX
 PF 05-FEB-2003; 2003JP-00027992.
 XX
 PR 15-FEB-2002; 2002JP-00038380.
 XX
 PA (TORA) TORAY IND INC.
 XX
 DR WPI; 2004-015267/02.
 XX
 PT Purifying receptor of advanced glycation end products derivative
 PT containing Igv domain of receptor of advanced glycation end product using
 PT one or more affinity columns.
 XX
 PS Disclosure; SEQ ID NO 1; 13pp; Japanese.
 XX
 CC The invention relates to a method of purifying a receptor of advanced

CC Glycation end products (RAGE) derivative. The method is useful for
 CC purifying receptor of advanced glycation end product derivative. The
 CC method enables simple, rapid with high yield and high purity manufacture
 CC of RAGE derivative. The present sequence represents the amino acid
 CC sequence of human receptor of advanced glycation end products (RAGE).
 XX
 SQ Sequence 404 AA;

Query Match 99.7%; Score 338; DB 8; Length 404;
 Best Local Similarity 100.0%; Pred. No. 4e-308;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGAVGVAQNTARIGEPVLKCKGAPKPPQRLWKLTGRTEA 60
 DB 1 MAAGTAVGAWLVLSLWGAVGVAQNTARIGEPVLKCKGAPKPPQRLWKLTGRTEA 60
 QY 61 WKVLSPOGGGPDWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120
 DB 61 WKVLSPOGGGPDWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120
 QY 121 PGKPEIVDSASBLTAGVKNKVGTCVSEGSYPAGTLSWHLDGKPLVPNEKGVSKVEQTRRH 180
 DB 121 PGKPEIVDSASBLTAGVKNKVGTCVSEGSYPAGTLSWHLDGKPLVPNEKGVSKVEQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDPRTFSCSFGLPRHRLRTAPIQPRVWEPVLEEVOL 240
 DB 181 PETGLFTLQSELMTVPARGGDPRTFSCSFGLPRHRLRTAPIQPRVWEPVLEEVOL 240
 QY 241 VVEPEGGA VAGTGTTLTCEVPAQPSQIHWMDGVPLPLPPSPVLILPEIGPDQGTYS 300
 DB 241 VVEPEGGA VAGTGTTLTCEVPAQPSQIHWMDGVPLPLPPSPVLILPEIGPDQGTYS 300
 QY 301 CVATHSHGPOESRAVSISIIIEEGEGTAGSVGGSGL 338
 DB 301 CVATHSHGPOESRAVSISIIIEEGEGTAGSVGGSGL 338

RESULT 9
 ADF42983
 ID ADF42983 standard; protein; 404 AA.
 XX
 AC ADF42983;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human receptor of advanced glycation (RAGE) protein.
 XX
 KW diabetic complication factor; receptor of advanced glycation end product;
 KW RAGE binding substance adsorption ligand; water-insoluble carrier;
 KW biological evaluation; diabetic complication; renal disease; human.
 XX
 OS Homo sapiens.
 XX
 PN JP2003306499-A.
 XX
 PD 28-OCT-2003.
 XX
 PF 05-FEB-2003; 2003JP-00027991.
 XX
 PR 15-FEB-2002; 2002JP-00038378.
 XX
 PA (TORA) TORAY IND INC.
 XX
 DR WPI; 2004-015266/02.
 XX
 PT Obtaining diabetic complication factor comprises contacting biological
 PT fluid with adsorbent, and immobilizing receptor of advanced glycation end
 PT products binding substance ligand on carrier.
 XX
 PS Disclosure; SEQ ID NO 1; 18pp; Japanese.
 XX
 CC This invention relates to a novel method of obtaining a diabetic
 CC complication factor which comprises contacting liquid from a biological

CC fluid with an adsorbent which immobilises a receptor of advanced
CC glycation end products (RAGE) binding substance adsorption ligand on a
CC water-insoluble carrier, cleaning the adsorbent in an aqueous solution,
CC separating and recovering the diabetically complicated factor by contacting
CC the adsorbent with the aqueous solution. The method is useful for
CC carrying out biological evaluation which involves determining advanced
CC degree of diabetic complication or degree of a renal-disease.
XX
SQ Sequence 404 AA;

Query Match 99.7%; Score 338; DB 8; Length 404;
Best Local Similarity 100.0%; Pred. No. 4e-308;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGA VVGAQNITARI GEPLV LKCKGAPKPPQRLWKLTGRTEA 60
DB 1 MAAGTAVGAWLVLSLWGA VVGAQNITARI GEPLV LKCKGAPKPPQRLWKLTGRTEA 60

QY 61 WKVLS PQGGPWDSVARVLPNGSLFLPAVG IQDEGIFRCQAMNRNGKETKSNYRVVYQI 120
DB 61 WKVLS PQGGPWDSVARVLPNGSLFLPAVG IQDEGIFRCQAMNRNGKETKSNYRVVYQI 120

QY 121 PGKPEIVDSASELTAGVPNKVGTCSVSEGSYPAGTILSWHLDGKPLVNEKGVSKQTRRH 180
DB 121 PGKPEIVDSASELTAGVPNKVGTCSVSEGSYPAGTILSWHLDGKPLVNEKGVSKQTRRH 180

QY 181 PETGLFTLQSELMVTPARGDPRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVOL 240
DB 181 PETGLFTLQSELMVTPARGDPRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVOL 240

QY 241 VVEPEGGA VAPGTVTLTCEVPAQSPQIHMMKDGVP LPLPPSPVLLPEIGPDQGTYS 300
DB 241 VVEPEGGA VAPGTVTLTCEVPAQSPQIHMMKDGVP LPLPPSPVLLPEIGPDQGTYS 300

QY 301 CVATHSSHGPQBSRAVSISIIIEPGEETAGSVGGSGL 338
DB 301 CVATHSSHGPQBSRAVSISIIIEPGEETAGSVGGSGL 338

RESULT 10
ADK00129
ID ADK00129 standard; protein; 404 AA.
XX
AC ADK00129;
DT 20-MAY-2004 (first entry)
XX
DE Human RAGE protein.
XX
KW Advanced Glycation End Product Ligand Binding Element; RAGE-LBE;
KW Cystostatic; Antidiabetic; Nootropic; Antiarthritic; Osteopathic;
KW Neuroprotective; Antiinflammatory; Dermatological; Immunosuppressive;
KW Vasotropic; Antipruritic; Antibacterial; Antiartherosclerotic;
KW amyloidosis; cancer; Crohn's disease; diabetes; Alzheimer's disease;
KW chronic inflammatory disease; osteoarthritis; irritable bowel disease;
KW multiple sclerosis; psoriasis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004016229-A2.
XX
PD 26-FEB-2004.
XX
PP 18-AUG-2003; 2003WO-US025996.
XX
PR 16-AUG-2002; 2002US-0404205P.
XX
PA (AMHP) WYETH.
XX
PI Pittman DD, Clancy B, Larsen G, Trepicchio WL, Brennan FM;
PI Feldmann M, Foxwell BJM, Feldman JL;

DR WPI; 2004-192067/18.
XX N-PSDB; ADK00130.
XX New fusion protein comprising a Receptor for Advanced Glycation End
PT Product Ligand Binding Element (RAGE-LBE) and an Immunoglobulin element,
PT useful for preparing a composition for treating e.g., Alzheimer's
PT disease.
XX
PS Disclosure; SEQ ID NO 43; 100pp; English.
XX
CC The present invention relates to a new fusion protein comprising a
CC Receptor for Advanced Glycation End Product Ligand Binding Element (RAGE-
CC LBE) and an immunoglobulin element. The fusion protein is useful for
CC preparing a composition for treating RAGE-associated disorders such as
CC amyloidosis, cancer, Crohn's disease, diabetes, complications of
CC diabetes, prion-related disorders, vasculitis, nephropathies,
CC retinopathies and/or neuropathies; Alzheimer's disease, chronic
CC inflammatory disease e.g., rheumatoid arthritis, osteoarthritis,
CC irritable bowel disease, multiple sclerosis, psoriasis or lupus, acute
CC inflammatory disease e.g., sepsis, or cardiovascular disease, e.g.,
CC atherosclerosis or restenosis. The present sequence represents human RAGE
CC protein.
XX
SQ Sequence 404 AA;

Query Match 99.7%; Score 338; DB 8; Length 404;
Best Local Similarity 100.0%; Pred. No. 4e-308;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGA VVGAQNITARI GEPLV LKCKGAPKPPQRLWKLTGRTEA 60
DB 1 MAAGTAVGAWLVLSLWGA VVGAQNITARI GEPLV LKCKGAPKPPQRLWKLTGRTEA 60

QY 61 WKVLS PQGGPWDSVARVLPNGSLFLPAVG IQDEGIFRCQAMNRNGKETKSNYRVVYQI 120
DB 61 WKVLS PQGGPWDSVARVLPNGSLFLPAVG IQDEGIFRCQAMNRNGKETKSNYRVVYQI 120

QY 121 PGKPEIVDSASELTAGVPNKVGTCSVSEGSYPAGTILSWHLDGKPLVNEKGVSKQTRRH 180
DB 121 PGKPEIVDSASELTAGVPNKVGTCSVSEGSYPAGTILSWHLDGKPLVNEKGVSKQTRRH 180

QY 181 PETGLFTLQSELMVTPARGDPRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVOL 240
DB 181 PETGLFTLQSELMVTPARGDPRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVOL 240

QY 241 VVEPEGGA VAPGTVTLTCEVPAQSPQIHMMKDGVP LPLPPSPVLLPEIGPDQGTYS 300
DB 241 VVEPEGGA VAPGTVTLTCEVPAQSPQIHMMKDGVP LPLPPSPVLLPEIGPDQGTYS 300

QY 301 CVATHSSHGPQBSRAVSISIIIEPGEETAGSVGGSGL 338
DB 301 CVATHSSHGPQBSRAVSISIIIEPGEETAGSVGGSGL 338

RESULT 11
AAM48746
ID AAM48746 standard; protein; 339 AA.
XX
AC AAM48746;
XX
DT 02-APR-2002 (first entry)
XX
DE Human BRAGE protein SEQ ID NO 2.
XX
KW Human; RAGE; receptor for advanced glycosylated endproduct; receptor;
KW antidiabetic; neuroprotective; cystostatic; antiinflammatory; vasotropic;
KW nephrotropic; dermatological; antiarteriosclerotic; nootropic; diabetes;
KW Alzheimer's disease; cancer; inflammation; kidney failure;
KW systemic lupus; nephritis; erectile dysfunction; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200192892-A2.

XX PD 06-DEC-2001.
 XX PF 30-MAY-2001; 2001WO-US017447.
 XX PR 30-MAY-2000; 2000US-0207342P.
 XX PR 05-MAR-2001; 2001US-00799152.
 XX PA (TRAN-) TRANS TECH PHARMA.
 XX PI Shahbaz M;
 XX PI WPI; 2002-114372/15.
 XX DR
 XX PT Detecting a receptor for advanced glycosylated endproducts (RAGE) modulators,
 XX PT for treating e.g., cancer, diabetes or inflammation, comprises measuring
 XX PT the amount of bound anti-RAGE antibody.
 XX PS Claim 2; Fig 2; 49pp; English.
 XX CC The invention relates to detecting receptor for advanced glycosylated
 XX CC endproducts (RAGE) modulators comprising determining the amount of RAGE
 XX CC protein or its fragment bound to the pre-adsorbed ligand by measuring the
 XX CC amount of anti-RAGE antibody bound to the solid surface. The method is
 XX CC useful for rapid, high-throughput identification of compounds that
 XX CC modulate RAGE. The compounds are useful for treating symptoms of diabetes
 XX CC and symptoms of diabetic late complications, amyloidosis, Alzheimer's
 XX CC disease, cancer, inflammation, kidney failure, systemic lupus nephritis
 XX CC or inflammatory lupus nephritis, erectile dysfunction and atherosclerosis
 XX SQ Sequence 339 AA;
 Query Match 99.4%; Score 337; DB 5; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3e-307;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AAGTAVGAWLVLSLWGA VVGAQNITARI GEPLVLCCKGAPKPPORLEWKLNTGRTEAM 61
 DB 2 AAGTAVGAWLVLSLWGA VVGAQNITARI GEPLVLCCKGAPKPPORLEWKLNTGRTEAM 61
 QY 62 KVLSPQGGPWDSVARVLPNGSLFLPAVG IQDEGIFRCQAMNRNGKETKSNYRVVYQIP 121
 DB 62 KVLSPQGGPWDSVARVLPNGSLFLPAVG IQDEGIFRCQAMNRNGKETKSNYRVVYQIP 121
 QY 122 GKPEIVDSASLTAGVPNKVGTVCVSEGSYPAGTLSWHL DKGKPLVPNEKGVSKQETRRHP 181
 DB 122 GKPEIVDSASLTAGVPNKVGTVCVSEGSYPAGTLSWHL DKGKPLVPNEKGVSKQETRRHP 181
 QY 182 ETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVQIV 241
 DB 182 ETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVQIV 241
 QY 242 VEPEGGA VAPGGT VTLTCEVPAQPSQIHWMDGVLPPLPPSPVLILPEIGPDQGTYS 301
 DB 242 VEPEGGA VAPGGT VTLTCEVPAQPSQIHWMDGVLPPLPPSPVLILPEIGPDQGTYS 301
 QY 302 VATHSHGHPQESRAVSIIEPEGEGPTAGSVGSGSL 338
 DB 302 VATHSHGHPQESRAVSIIEPEGEGPTAGSVGSGSL 338
 RESULT 12
 AAM48745
 ID AAM48745 standard; protein; 404 AA.
 XX AAM48745;
 AC XX
 DT 02-APR-2002 (first entry)
 XX Human RAGE protein SEQ ID NO 1.
 XX Human; RAGE; receptor for advanced glycosylated endproduct; receptor;
 XX antidiabetic; neuroprotective; cytosolic; antiinflammatory; vasotropic;

KW nephrotropic; dermatological; antiarteriosclerotic; nootropic; diabetes;
 KW Alzheimer's disease; cancer; inflammation; kidney failure;
 KW systemic lupus; nephritis; erectile dysfunction; atherosclerosis.
 OS Homo sapiens.
 XX WO200192892-A2.
 PN 06-DEC-2001.
 PD 30-MAY-2001; 2001WO-US017447.
 XX 30-MAY-2000; 2000US-0207342P.
 XX 05-MAR-2001; 2001US-00799152.
 XX (TRAN-) TRANS TECH PHARMA.
 XX PA Shahbaz M;
 XX PI WPI; 2002-114372/15.
 XX DR
 XX PT Detecting a receptor for advanced glycosylated endproducts (RAGE) modulators,
 XX PT for treating e.g., cancer, diabetes or inflammation, comprises measuring
 XX PT the amount of bound anti-RAGE antibody.
 XX PS Claim 1; Fig 2; 49pp; English.
 XX CC The invention relates to detecting receptor for advanced glycosylated
 XX CC endproducts (RAGE) modulators comprising determining the amount of RAGE
 XX CC protein or its fragment bound to the pre-adsorbed ligand by measuring the
 XX CC amount of anti-RAGE antibody bound to the solid surface. The method is
 XX CC useful for rapid, high-throughput identification of compounds that
 XX CC modulate RAGE. The compounds are useful for treating symptoms of diabetes
 XX CC and symptoms of diabetic late complications, amyloidosis, Alzheimer's
 XX CC disease, cancer, inflammation, kidney failure, systemic lupus nephritis
 XX CC or inflammatory lupus nephritis, erectile dysfunction and atherosclerosis
 XX SQ Sequence 404 AA;
 Query Match 99.4%; Score 337; DB 5; Length 404;
 Best Local Similarity 100.0%; Pred. No. 3.5e-307;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AAGTAVGAWLVLSLWGA VVGAQNITARI GEPLVLCCKGAPKPPORLEWKLNTGRTEAM 61
 DB 2 AAGTAVGAWLVLSLWGA VVGAQNITARI GEPLVLCCKGAPKPPORLEWKLNTGRTEAM 61
 QY 62 KVLSPQGGPWDSVARVLPNGSLFLPAVG IQDEGIFRCQAMNRNGKETKSNYRVVYQIP 121
 DB 62 KVLSPQGGPWDSVARVLPNGSLFLPAVG IQDEGIFRCQAMNRNGKETKSNYRVVYQIP 121
 QY 122 GKPEIVDSASLTAGVPNKVGTVCVSEGSYPAGTLSWHL DKGKPLVPNEKGVSKQETRRHP 181
 DB 122 GKPEIVDSASLTAGVPNKVGTVCVSEGSYPAGTLSWHL DKGKPLVPNEKGVSKQETRRHP 181
 QY 182 ETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVQIV 241
 DB 182 ETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVQIV 241
 QY 242 VEPEGGA VAPGGT VTLTCEVPAQPSQIHWMDGVLPPLPPSPVLILPEIGPDQGTYS 301
 DB 242 VEPEGGA VAPGGT VTLTCEVPAQPSQIHWMDGVLPPLPPSPVLILPEIGPDQGTYS 301
 QY 302 VATHSHGHPQESRAVSIIEPEGEGPTAGSVGSGSL 338
 DB 302 VATHSHGHPQESRAVSIIEPEGEGPTAGSVGSGSL 338
 RESULT 13
 ABB82298
 ID ABB82298 standard; protein; 347 AA.
 XX ABB82298;
 AC ABB82298;

```
XX 08-JAN-2003 (first entry)
XX Human soluble RAGE protein.
XX RAGE; receptor; advanced glycation endproduct; antidiabetic; nootropic;
XX neuroprotective; antiarteriosclerotic; antiulcer; human.
XX Homo sapiens.
XX WO200274805-A1.
XX 26-SEP-2002.
XX 19-MAR-2002; 2002WO-JP002623.
XX 19-MAR-2001; 2001JP-00078409.
XX 10-AUG-2001; 2001JP-00243114.
XX 25-FEB-2002; 2002JP-00048182.
XX (UYKA-) UNIV JAPAN KANAZAWA.
XX Yamamoto H, Yonekura H, Yamamoto Y, Sakurai S, Watanabe T;
XX WPI; 2002-740851/80.
XX N-PSDB; ABV73151.
XX Soluble advanced glycation endproduct receptor polypeptides and
XX substances modifying their activity for treatment and prevention of
XX disorders associated with diabetes and aging.
XX Claim 1; Page 118-120; 127pp; Japanese.
XX The invention relates to soluble receptor polypeptides for advanced
XX glycation endproducts (soluble RAGE) and encoding polynucleotides. The
XX soluble RAGE protein can be prepared by standard recombinant methodology.
XX The protein, polynucleotide and modulators can be used for the
XX prevention, treatment and diagnosis of diabetic complications, diseases
XX of aging, disorders of glycation of metabolic proteins, Alzheimer's
XX disease, arteriosclerosis and ulceration, and study of the mechanism and
XX pathology of these diseases. The present sequence represents the human
XX soluble RAGE protein
XX Sequence 347 AA;
Query Match 97.6%; Score 331; DB 5; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.3e-301;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAGTAVGAWLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60
DB 1 MAAGTAVGAWLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60
QY 61 WKVLSPPQGGPWSVARVLPNGSLFPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120
DB 61 WKVLSPPQGGPWSVARVLPNGSLFPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120
QY 121 PKPEIVDSASELTAGVPNKVGTCSSEGSYPAGTILSHWLDGKPLVPNEKGVSKQTRRH 180
DB 121 PKPEIVDSASELTAGVPNKVGTCSSEGSYPAGTILSHWLDGKPLVPNEKGVSKQTRRH 180
QY 181 PETGLFTLQSELMVTTPARGDPRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVQL 240
DB 181 PETGLFTLQSELMVTTPARGDPRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVQL 240
QY 241 VVEPEGGA VAPGGTTLTCEVPAQPSQIHWKMDGVLPPLPSPVLILPEIGPDQGTYS 300
DB 241 VVEPEGGA VAPGGTTLTCEVPAQPSQIHWKMDGVLPPLPSPVLILPEIGPDQGTYS 300
QY 301 CVATHSHGPGQESRAVSIISIEPGBEGPTAG 331
DB 301 CVATHSHGPGQESRAVSIISIEPGBEGPTAG 331
RESULT 14
ADG37044
ID ADG37044 standard; protein; 347 AA.
XX
XX ADG37044;
AC
XX
XX 26-FEB-2004 (first entry)
DT
XX
XX Receptor for advanced glycation endproducts (RAGE).
DE
XX receptor for advanced glycation endproducts; RAGE; diabetic complication;
KW glycosuria nephropathy; glycosuria retinopathy; Alzheimer's disease;
KW atherosclerosis; Down's syndrome; multiple sclerosis; amyloidosis;
KW autoimmune disease; inflammation; cancer; wound healing; human; receptor.
XX
XX Homo sapiens.
OS
XX
XX JP2003230382-A.
PN
XX
XX 19-AUG-2003.
PD
XX
XX 08-FEB-2002; 2002JP-00032155.
PF
XX
XX 08-FEB-2002; 2002JP-00032155.
PR
XX
XX (KANA-) KANAZAWA DAIGAKUCHO.
PA
XX
XX WPI; 2003-820207/77.
DR
XX
XX N-PSDB; ADG37043.
DR
XX
XX New advanced glycation endproducts-receptor for advanced glycation
XX endproducts antagonist useful for treating or preventing diabetic
XX complication, glycosuria nephropathy, and glycosuria retinopathy.
XX Example 1; SEQ ID NO 2; 23pp; Japanese.
XX The invention relates to a receptor for advanced glycation endproducts
XX (RAGE). An AGE-RAGE antagonist composition is useful for treating or
XX preventing diabetic complication (e.g., glycosuria nephropathy,
XX glycosuria retinopathy), Alzheimer's disease, atherosclerosis, Down's
XX syndrome, multiple sclerosis, amyloidosis, autoimmune disease,
XX inflammation, cancer, wound healing, etc. The present sequence represents
XX the amino acid sequence of the receptor for advanced glycation
XX endproducts (RAGE).
XX Sequence 347 AA;
Query Match 97.6%; Score 331; DB 7; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.3e-301;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAGTAVGAWLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60
DB 1 MAAGTAVGAWLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60
QY 61 WKVLSPPQGGPWSVARVLPNGSLFPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120
DB 61 WKVLSPPQGGPWSVARVLPNGSLFPAVGIDEGIFRCQAMNRNGKETKSNYRVYQI 120
QY 121 PKPEIVDSASELTAGVPNKVGTCSSEGSYPAGTILSHWLDGKPLVPNEKGVSKQTRRH 180
DB 121 PKPEIVDSASELTAGVPNKVGTCSSEGSYPAGTILSHWLDGKPLVPNEKGVSKQTRRH 180
QY 181 PETGLFTLQSELMVTTPARGDPRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVQL 240
DB 181 PETGLFTLQSELMVTTPARGDPRPTFSCFSFGLPRHRLARTAPIQPRVWEPVPLEEVQL 240
QY 241 VVEPEGGA VAPGGTTLTCEVPAQPSQIHWKMDGVLPPLPSPVLILPEIGPDQGTYS 300
DB 241 VVEPEGGA VAPGGTTLTCEVPAQPSQIHWKMDGVLPPLPSPVLILPEIGPDQGTYS 300
QY 301 CVATHSHGPGQESRAVSIISIEPGBEGPTAG 331
```

Db 301 CVATHSHGPOESRAVSIIIEPGEETAG 331
RESULT 15
ADP19656
ID ADP19656 standard; protein; 352 AA.
AC ADP19656;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human LP2000 protein SEQ ID NO:2.
XX
KW human; LP2000; antidiabetic; neuroprotective; nontropic;
KW antiinflammatory; antihemorrhagic; antiarthritic; vulnary; cytoskeletal;
KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;
KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;
KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;
KW systemic lupus erythematosus.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= signal
FT Protein 24..352
FT /label= LP2000
XX
FN WO200404126-A2.
XX
PD 27-MAY-2004.
XX
PF 05-NOV-2003; 2003WO-US032734.
XX
PR 14-NOV-2002; 2002US-0426253P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Na S, Perkins DR;
XX
PI WPI; 2004-411705/38.
XX
DR N-PSDB; ADP19655.
XX
XX
XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or
XX LP2003) for diagnosing or treating disorders associated with aberrant
XX levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome
XX identification.
XX
XX Disclosure; SEQ ID NO 2; 11pp; English.
XX
XX The present sequence represents human LP2000, which is used in the
XX exemplification of the present invention. The present invention
XX describes: (1) an isolated nucleic acid (I) comprising DNA having at
XX least 95% sequence identity to a polynucleotide selected from the group
XX consisting of: (a) a polynucleotide having a nucleotide sequence as shown
XX in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a
XX polypeptide or mature form of a polypeptide having the amino acid
XX sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide
XX fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide
XX having a nucleotide sequence which is complementary to the nucleotide
XX sequence of a polynucleotide as in (a), (b) or (c); (2) a vector
XX comprising (1); (3) a host cell comprising the vector; (4) producing an
XX LP polypeptide; (5) an isolated polypeptide produced by the above method
XX and comprising an amino acid sequence comprising about 95% sequence
XX identity to a sequence of amino acid residues comprising LP2001, LP2003,
XX LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric
XX molecule comprising an LP polypeptide fused to a heterologous amino acid
XX sequence; (7) an antibody which specifically binds to an LP polypeptide
XX described above; (8) a composition (C) comprising a therapeutic amount of
XX an active agent selected from an LP polypeptide, an agonist to an LP
XX polypeptide, an antagonist to an LP polypeptide, an LP polypeptide
XX antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a

CC polynucleotide in combination with a pharmaceutical carrier; and (9)
CC diagnosing or treating a mammal suffering from a disease, condition or
CC disorder associated with aberrant levels of an LP-polypeptide. (C) has
CC antidiabetic, neuroprotective, nontropic, antiinflammatory,
CC antirheumatic, antiarthritic, vulnary, cytoskeletal, immunosuppressive,
CC nephrotropic and dermatological activities, and can be used in gene
CC therapy. The compositions (C) and methods are useful for diagnosing or
CC treating disorders associated with aberrant levels of an LP polypeptide,
CC such as diabetes and its complications, Alzheimer's disease,
CC inflammation, rheumatoid arthritis, wounds, autoimmune disease,
CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. Multiple
CC may also be used for chromosome identification. The LP polypeptide can
CC also be used in manufacturing a medicament for the treatment of the above
CC mentioned diseases, conditions or disorders associated with aberrant
XX levels of the LP polypeptide.
XX
SQ Sequence 352 AA;
Query Match 97.6%; Score 331; DB 8; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.3e-301; Indels 0; Gaps 0;
Matches 331; Conservative 0; Mismatches 0;
QY 1 MAAGTAVGAWLVLSLWGA VVGAQNITARIGSEPLVLCCKGAPKPPQRLKWLNTGRTEA 60
DB 1 MAAGTAVGAWLVLSLWGA VVGAQNITARIGSEPLVLCCKGAPKPPQRLKWLNTGRTEA 60
QY 61 WKVLSPOGGGPDWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTKSNRYRVYQI 120
DB 61 WKVLSPOGGGPDWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTKSNRYRVYQI 120
QY 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTSLSHLDGKPLVPNEKGVSKQTRRH 180
DB 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTSLSHLDGKPLVPNEKGVSKQTRRH 180
QY 181 PETGLFTLOSLMVTTPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
DB 181 PETGLFTLOSLMVTTPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
QY 241 VVEPEGGA VAPGGTVTLTCEVPAQPSQIHWKDGVPPLPSPVLILPEIGPODQGTYS 300
DB 241 VVEPEGGA VAPGGTVTLTCEVPAQPSQIHWKDGVPPLPSPVLILPEIGPODQGTYS 300
QY 301 CVATHSHGPOESRAVSIIIEPGEETAG 331
DB 301 CVATHSHGPOESRAVSIIIEPGEETAG 331
Search completed: March 16, 2005, 06:03:30
Job time : 83 secs

Result No.	Score	Query Match	Length	DB	ID	Description	
1	338	99.7	340	2	US-08-633-148-2	Sequence 2, Appli	
2	338	99.7	404	4	US-09-949-016-11025	Sequence 11025, A	
3	316	93.2	318	2	US-08-633-148-4	Sequence 4, Appli	
4	316	93.2	332	4	US-09-062-363-1	Sequence 1, Appli	
5	238	70.2	404	4	US-09-638-649-3	Sequence 3, Appli	
6	238	70.2	404	4	US-09-638-648-3	Sequence 3, Appli	
7	216	63.7	405	4	US-08-755-235-4	Sequence 4, Appli	
8	207	61.1	278	2	US-08-432-016-5	Sequence 5, Appli	
9	207	61.1	278	2	US-08-684-594-5	Sequence 5, Appli	
10	30	8.8	30	4	US-09-062-365-5	Sequence 5, Appli	
11	30	8.8	30	4	US-08-948-131-1	Sequence 1, Appli	
12	26	7.7	403	4	US-09-638-649-5	Sequence 5, Appli	
13	26	7.7	403	4	US-09-638-648-5	Sequence 5, Appli	
14	24	7.1	416	4	US-09-638-649-1	Sequence 1, Appli	
15	24	7.1	416	4	US-08-755-235-2	Sequence 2, Appli	
16	24	7.1	416	4	US-09-638-648-1	Sequence 1, Appli	
17	22	6.5	22	2	US-09-062-363-2	Sequence 2, Appli	
18	16	4.7	16	2	US-08-633-148-18	Sequence 18, Appli	
19	15	4.4	15	2	US-08-633-148-12	Sequence 12, Appli	
20	13	3.8	30	4	US-08-948-131-2	Sequence 2, Appli	
21	11	3.2	11	2	US-08-633-148-9	Sequence 9, Appli	
22	11	3.2	11	2	US-08-633-148-15	Sequence 15, Appli	
23	11	3.2	30	4	US-08-948-131-3	Sequence 3, Appli	
24	10	2.9	10	2	US-08-633-148-5	Sequence 5, Appli	
25	10	2.9	10	2	US-08-633-148-7	Sequence 7, Appli	
26	10	2.9	10	2	US-08-633-148-8	Sequence 8, Appli	
27	10	2.9	10	2	US-08-633-148-11	Sequence 11, Appli	

QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTKSNRYRVYQI 120
DB 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTKSNRYRVYQI 120
QY 121 PKPEIVDSASELTAGVPNKVGTCSGSGSPAGTSLSHWLDGKPLVPNEKGVSKQTRRH 180
DB 121 PKPEIVDSASELTAGVPNKVGTCSGSGSPAGTSLSHWLDGKPLVPNEKGVSKQTRRH 180
QY 181 PETGLFTLQSELMVTARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEPVLEEVOL 240
DB 181 PETGLFTLQSELMVTARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEPVLEEVOL 240
QY 241 VVEPEGGAAPGGTTLTCEVPAQSPQIHWKMDGVPPLPPSPVLILPEIGPDQGTYS 300
DB 241 VVEPEGGAAPGGTTLTCEVPAQSPQIHWKMDGVPPLPPSPVLILPEIGPDQGTYS 300
QY 301 CVATHSSHGPOESRAVSISIIIEPGEPTAGSVGGSL 338
DB 301 CVATHSSHGPOESRAVSISIIIEPGEPTAGSVGGSL 338
RESULT 2
US-09-949-016-11025
; Sequence 11025, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11025
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11025
Query Match 99.7%; Score 338; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.2e-310; Mismatches 0; Indels 0; Gaps 0;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAGTAGAWLVLSLWGAIVGGAQNTARIGBPLVLKCKGAPKPPQRLWKLTGRTEA 60
DB 1 MAAGTAGAWLVLSLWGAIVGGAQNTARIGBPLVLKCKGAPKPPQRLWKLTGRTEA 60
QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTKSNRYRVYQI 120
DB 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKTKSNRYRVYQI 120
QY 121 PKPEIVDSASELTAGVPNKVGTCSGSGSPAGTSLSHWLDGKPLVPNEKGVSKQTRRH 180
DB 121 PKPEIVDSASELTAGVPNKVGTCSGSGSPAGTSLSHWLDGKPLVPNEKGVSKQTRRH 180
QY 181 PETGLFTLQSELMVTARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEPVLEEVOL 240
DB 181 PETGLFTLQSELMVTARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEPVLEEVOL 240
QY 241 VVEPEGGAAPGGTTLTCEVPAQSPQIHWKMDGVPPLPPSPVLILPEIGPDQGTYS 300
DB 241 VVEPEGGAAPGGTTLTCEVPAQSPQIHWKMDGVPPLPPSPVLILPEIGPDQGTYS 300
QY 301 CVATHSSHGPOESRAVSISIIIEPGEPTAGSVGGSL 338
DB 301 CVATHSSHGPOESRAVSISIIIEPGEPTAGSVGGSL 338

DB 301 CVATHSSHGPOESRAVSISIIIEPGEPTAGSVGGSL 338
RESULT 3
US-08-633-148-4
; Sequence 4, Application US/08633148
; Patent No. 5864018
; GENERAL INFORMATION:
; APPLICANT: MORSE, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; APPLICANT: HOLLANDER, DORIS A.
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND
; CITY: TWO EMBARCADERO CENTER, 8TH FLOOR
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,148
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 014618-005600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-633-148-4
Query Match 93.2%; Score 316; DB 2; Length 318;
Best Local Similarity 100.0%; Pred. No. 5.4e-290; Mismatches 0; Indels 0; Gaps 0;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 AQNTARIGEPLVLKCKGAPKPPQRLWKLTGRTEAWKLVSPQGGPWSVARVLPNG 82
DB 1 AQNTARIGEPLVLKCKGAPKPPQRLWKLTGRTEAWKLVSPQGGPWSVARVLPNG 60
QY 83 SLFLPAVGIDEGIFRCQAMNRNGKTKSNRYRVYQIPKPEIVDSASELTAGVPNKVG 142
DB 61 SLFLPAVGIDEGIFRCQAMNRNGKTKSNRYRVYQIPKPEIVDSASELTAGVPNKVG 120
QY 143 TCVSEGSYPAGTSLSHWLDGKPLVPNEKGVSKQTRRHPTGLTLOSELMVTARGDGP 202
DB 121 TCVSEGSYPAGTSLSHWLDGKPLVPNEKGVSKQTRRHPTGLTLOSELMVTARGDGP 180
QY 203 RPTFSCSPGLPRHRLRTAPIQPRVWEPVLEEVOLVVEPEGGAAPGGTTLTCEVP 262
DB 181 RPTFSCSPGLPRHRLRTAPIQPRVWEPVLEEVOLVVEPEGGAAPGGTTLTCEVP 240
QY 263 AQSPQIHWKMDGVPPLPPSPVLILPEIGPDQGTYSVCVATHSSHGPOESRAVSISII 322
DB 241 AQSPQIHWKMDGVPPLPPSPVLILPEIGPDQGTYSVCVATHSSHGPOESRAVSISII 300
QY 323 PGEPTAGSVGGSL 338
DB 301 PGEPTAGSVGGSL 316

RESULT 4
US-09-062-365-1
; Sequence 1, Application US/09062365
; Patent No. 645422
; GENERAL INFORMATION:
; APPLICANT: Stern, David
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A
; FILE OF INVENTION: SUBJECT
; FILE REFERENCE: 55424
; CURRENT APPLICATION NUMBER: US/09/062,365
; CURRENT FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Human
; US-09-062-365-1

Query Match 93.2%; Score 316; DB 4; Length 332;
Best Local Similarity 100.0%; Pred. No. 5.6e-290;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 AQNITARIGEPLVKCKGAPKPPQRLWKLTGRTEAMKVLSPQGGPMDVARVLPNG 82
DB 1 AQNITARIGEPLVKCKGAPKPPQRLWKLTGRTEAMKVLSPQGGPMDVARVLPNG 60
QY 83 SLPLPAVGTDGIFRCQAMNRNGKTKSNRYRVVYQIPGKPEIVDSASELTAGVNPVKVG 142
DB 61 SLPLPAVGTDGIFRCQAMNRNGKTKSNRYRVVYQIPGKPEIVDSASELTAGVNPVKVG 120
QY 143 TCVSEGSYPAGTSLWHLCKPLVNEKGVSVKEOTRRHPETGLTLOSELMTVPARGGDP 202
DB 121 TCVSEGSYPAGTSLWHLCKPLVNEKGVSVKEOTRRHPETGLTLOSELMTVPARGGDP 180
QY 203 RTFSCSFSGLPRLRALTAIQRVWPEVPLEEVLVVEGGAVAPGGTTLTCEVP 262
DB 181 RTFSCSFSGLPRLRALTAIQRVWPEVPLEEVLVVEGGAVAPGGTTLTCEVP 240
QY 263 AQPSPQIHMWDGVPPLPSPVLLILPEIGPQDQGTYSVATHSHGPOESRAVSISIE 322
DB 241 AQPSPQIHMWDGVPPLPSPVLLILPEIGPQDQGTYSVATHSHGPOESRAVSISIE 300
QY 323 PGESEGTAGSVGSGSL 338
DB 301 PGESEGTAGSVGSGSL 316

RESULT 5
US-09-638-649-3
; Sequence 3, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
; US-09-638-649-3

Query Match 70.2%; Score 238; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 2.8e-216;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 101 AMNRNGKTKSNRYRVVYQIPGKPEIVDSASELTAGVNPKNKGTCTVSEGSYPAGTSLWHL 160
DB 101 AMNRNGKTKSNRYRVVYQIPGKPEIVDSASELTAGVNPKNKGTCTVSEGSYPAGTSLWHL 160
QY 161 GKPLVPNEKGVSVKEOTRRHPETGLTLOSELMTVPARGGDPRTFSCSFSGLPRLRAL 220
DB 161 GKPLVPNEKGVSVKEOTRRHPETGLTLOSELMTVPARGGDPRTFSCSFSGLPRLRAL 220
QY 221 RTAPIQPRVWPEVPLEEVLVVEGGAVAPGGTTLTCEVPAQSPQIHMWDGVPPL 280
DB 221 RTAPIQPRVWPEVPLEEVLVVEGGAVAPGGTTLTCEVPAQSPQIHMWDGVPPL 280
QY 281 PPSVLLILPEIGPQDQGTYSVATHSHGPOESRAVSISIIIEPGEGETAGSVGSGSL 338
DB 281 PPSVLLILPEIGPQDQGTYSVATHSHGPOESRAVSISIIIEPGEGETAGSVGSGSL 338

RESULT 6
US-09-638-648-3
; Sequence 3, Application US/09638648
; Patent No. 6825164
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; APPLICANT: Zlokovic, Berislav
; TITLE OF INVENTION: A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID
; FILE OF INVENTION: ANGIOPATHY
; FILE REFERENCE: 0575/62097
; CURRENT APPLICATION NUMBER: US/09/638,648
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
; US-09-638-648-3

Query Match 70.2%; Score 238; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 2.8e-216;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 101 AMNRNGKTKSNRYRVVYQIPGKPEIVDSASELTAGVNPKNKGTCTVSEGSYPAGTSLWHL 160
DB 101 AMNRNGKTKSNRYRVVYQIPGKPEIVDSASELTAGVNPKNKGTCTVSEGSYPAGTSLWHL 160
QY 161 GKPLVPNEKGVSVKEOTRRHPETGLTLOSELMTVPARGGDPRTFSCSFSGLPRLRAL 220
DB 161 GKPLVPNEKGVSVKEOTRRHPETGLTLOSELMTVPARGGDPRTFSCSFSGLPRLRAL 220
QY 221 RTAPIQPRVWPEVPLEEVLVVEGGAVAPGGTTLTCEVPAQSPQIHMWDGVPPL 280
DB 221 RTAPIQPRVWPEVPLEEVLVVEGGAVAPGGTTLTCEVPAQSPQIHMWDGVPPL 280
QY 281 PPSVLLILPEIGPQDQGTYSVATHSHGPOESRAVSISIIIEPGEGETAGSVGSGSL 338
DB 281 PPSVLLILPEIGPQDQGTYSVATHSHGPOESRAVSISIIIEPGEGETAGSVGSGSL 338

RESULT 7
US-08-755-235-4
; Sequence 4, Application US/08755235
; Patent No. 6790443
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES

FILE REFERENCE: 0575/50159
CURRENT APPLICATION NUMBER: US/08/755,235
CURRENT FILING DATE: 1996-11-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent in version 3.1
SEQ ID NO 4
LENGTH: 405
TYPE: PRT
ORGANISM: Human
US-08-755-235-4

Query Match 63.7%; Score 216; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 1.6e-195;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	101	AMNRNGKTKSNRYRVVQIPGKPEIVDSASELTAGVKNKVTGTCVSEGSYPAGTILSWHLD	160
Db	101	AMNRNGKTKSNRYRVVQIPGKPEIVDSASELTAGVKNKVTGTCVSEGSYPAGTILSWHLD	160
QY	161	GKPLVPNEKGVSVKEQTRRHPTGLFTLQSELMTVPARGDPRPTFCSPGLPRHRL	220
Db	161	GKPLVPNEKGVSVKEQTRRHPTGLFTLQSELMTVPARGDPRPTFCSPGLPRHRL	220
QY	221	RTAPIQPRVWPVPLEEVQVVEEGGAVAPGGTTLTCEVPAQPSQIHWKDGVPPL	280
Db	221	RTAPIQPRVWPVPLEEVQVVEEGGAVAPGGTTLTCEVPAQPSQIHWKDGVPPL	280
QY	281	PPSPVLLILPEIGPODQGTYSVATHSSHGPOESRAV	316
Db	281	PPSPVLLILPEIGPODQGTYSVATHSSHGPOESRAV	316

RESULT 8
US-08-432-016-5
Sequence 5, Application US/08432016
Patent No. 5968768
GENERAL INFORMATION:
APPLICANT: HAYNES, BARTON F.
APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: PATEL, DHAVALKUMAR
APPLICANT: BOWEN, MICHAEL A.
APPLICANT: MARQUARDT, HANS
TITLE OF INVENTION: CD6 LIGAND
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,016
FILING DATE: 01-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,350
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,903
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-432-016-5

Query Match 61.1%; Score 207; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 3.5e-187;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	101	AMNRNGKTKSNRYRVVQIPGKPEIVDSASELTAGVKNKVTGTCVSEGSYPAGTILSWHLD	160
Db	72	AMNRNGKTKSNRYRVVQIPGKPEIVDSASELTAGVKNKVTGTCVSEGSYPAGTILSWHLD	131
QY	161	GKPLVPNEKGVSVKEQTRRHPTGLFTLQSELMTVPARGDPRPTFCSPGLPRHRL	220
Db	132	GKPLVPNEKGVSVKEQTRRHPTGLFTLQSELMTVPARGDPRPTFCSPGLPRHRL	191
QY	221	RTAPIQPRVWPVPLEEVQVVEEGGAVAPGGTTLTCEVPAQPSQIHWKDGVPPL	280
Db	192	RTAPIQPRVWPVPLEEVQVVEEGGAVAPGGTTLTCEVPAQPSQIHWKDGVPPL	251
QY	281	PPSPVLLILPEIGPODQGTYSVATHSS	307
Db	252	PPSPVLLILPEIGPODQGTYSVATHSS	278

RESULT 9
US-08-684-594-5
Sequence 5, Application US/08684594
Patent No. 5998172
GENERAL INFORMATION:
APPLICANT: HAYNES, BARTON F.
APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: PATEL, DHAVALKUMAR
APPLICANT: BOWEN, MICHAEL A.
APPLICANT: MARQUARDT, HANS
TITLE OF INVENTION: CD6 LIGAND
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,594
FILING DATE: 18-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,016
FILING DATE: 01-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,350
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,903
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000

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; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-684-594-5

Query Match 61.1%; Score 207; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 3.5e-187; Indels 0; Gaps 0;
Matches 207; Conservative 0; Mismatches 0;

QY 101 ANNNGKTKSNYRVYQIPGKPEIVDSASELTAGVKNKVGTCVSEGSYPAGTILSHWLD 160
DB 72 ANNNGKTKSNYRVYQIPGKPEIVDSASELTAGVKNKVGTCVSEGSYPAGTILSHWLD 131
QY 161 GKPLVPNEKGVSKQTRRHPTGLTLOSELMTVPARGDPRPTFSCFSFGLPRHRAL 220
DB 132 GKPLVPNEKGVSKQTRRHPTGLTLOSELMTVPARGDPRPTFSCFSFGLPRHRAL 191
QY 221 RTAPIQPRVWEVPLEEVLVVEPEGGA VAPGTVTLTCEVPAQSPQLHWMKDGVPPLP 280
DB 192 RTAPIQPRVWEVPLEEVLVVEPEGGA VAPGTVTLTCEVPAQSPQLHWMKDGVPPLP 251
QY 281 PPSVLLPEIGPDQDGTYSVCVATHSS 307
DB 252 PPSVLLPEIGPDQDGTYSVCVATHSS 278

RESULT 10
US-09-062-365-5
; Sequence 5, Application US/09062365
; Patent No. 6465422
; GENERAL INFORMATION:
; APPLICANT: Stern, David
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A
; FILE REFERENCE: 55424
; CURRENT APPLICATION NUMBER: US/09/062,365
; CURRENT FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human
US-09-062-365-5

Query Match 8.8%; Score 30; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.9e-21; Indels 0; Gaps 0;
Matches 30; Conservative 0; Mismatches 0;

QY 23 AQNITARIGEPLVKCKGAPKPPQRLWK 52
DB 1 AQNITARIGEPLVKCKGAPKPPQRLWK 30

RESULT 12
US-09-638-649-5
; Sequence 5, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Murine
US-09-638-649-5

Query Match 7.7%; Score 26; DB 4; Length 403;
Best Local Similarity 100.0%; Pred. No. 3.3e-16; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0;

QY 137 VPKVGTGTCVSEGSYPAGTILSHWLDGK 162
DB 136 VPKVGTGTCVSEGSYPAGTILSHWLDGK 161

RESULT 13
US-09-638-648-5
; Sequence 5, Application US/09638648
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; Patent No. 6825164
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; APPLICANT: Zlokovic, Berislav
; TITLE OF INVENTION: A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID
; TITLE OF INVENTION: ANGIOPATHY
; FILE REFERENCE: 0575/62097
; CURRENT APPLICATION NUMBER: US/09/638,648
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mouse
US-09-638-648-5

Query Match          7.7%; Score 26; DB 4; Length 403;
Best Local Similarity 100.0%; Pred. No. 3.3e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 VPKNVGTCSVSEGSYPAGTSLSHLDGK 162
Db 136 VPKNVGTCSVSEGSYPAGTSLSHLDGK 161

RESULT 14
US-09-638-649-1
; Sequence 1, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Bos Taurus
US-09-638-649-1

Query Match          7.1%; Score 24; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 EVQLVVEPEGGAVAPGGITVLTCE 260
Db 247 EVQLVVEPEGGAVAPGGITVLTCE 270

RESULT 15
US-08-755-235-2
; Sequence 2, Application US/08755235
; Patent No. 6790443
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Bovine
US-08-755-235-2

Query Match          7.1%; Score 24; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 EVQLVVEPEGGAVAPGGITVLTCE 260
Db 247 EVQLVVEPEGGAVAPGGITVLTCE 270

Search completed: March 16, 2005, 06:04:32
Job time : 28 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 16, 2005, 06:04:08 ; Search time 326 Seconds
(without alignments)
343.722 Million cell updates/sec

Title: US-10-091-019-3
Perfect score: 339
Sequence: 1 MAAGTAVGAWVLVLSLWGAV.....IIEPGEPTAGSVGGSLV 339

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1401741 seqs, 330541175 residues

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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

- Database : Published Applications_AA.*
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 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	339	100.0	339	14	US-10-091-019-3 Sequence 3, Appli
2	338	99.7	404	15	US-10-309-290-96 Sequence 96, Appli
3	331	97.6	347	17	US-10-472-507A-2 Sequence 2, Appli
4	316	93.2	332	9	US-09-872-185B-2 Sequence 1, Appli
5	316	93.2	332	9	US-09-851-071-1 Sequence 2, Appli
6	271	79.9	390	15	US-10-309-290-98 Sequence 98, Appli
7	271	79.9	390	15	US-10-309-290-100 Sequence 100, App
8	216	63.7	405	8	US-08-755-235-4 Sequence 4, Appli
9	207	61.1	342	16	US-10-408-765A-641 Sequence 641, App
10	112	33.0	112	9	US-09-872-185B-1 Sequence 1, Appli
11	30	8.8	30	8	US-08-948-131-1 Sequence 1, Appli
12	30	8.8	30	9	US-09-872-185B-3 Sequence 3, Appli
13	30	8.8	30	9	US-09-872-185B-7 Sequence 7, Appli

14	30	8.8	30	9	US-09-851-071-5	Sequence 5, Appli
15	24	7.1	416	8	US-08-755-235-2	Sequence 2, Appli
16	22	6.5	22	9	US-09-851-071-2	Sequence 2, Appli
17	13	3.8	30	8	US-08-948-131-2	Sequence 4, Appli
18	13	3.8	30	9	US-09-872-185B-4	Sequence 4, Appli
19	11	3.2	30	8	US-08-948-131-3	Sequence 3, Appli
20	11	3.2	30	9	US-09-872-185B-5	Sequence 5, Appli
21	10	2.9	10	8	US-08-948-131-5	Sequence 5, Appli
22	10	2.9	10	9	US-09-872-185B-8	Sequence 8, Appli
23	10	2.9	10	9	US-09-851-071-6	Sequence 6, Appli
24	10	2.9	30	8	US-08-948-131-4	Sequence 4, Appli
25	10	2.9	30	9	US-09-872-185B-6	Sequence 6, Appli
26	9	2.7	25	16	US-10-327-598-238	Sequence 238, App
27	9	2.7	25	16	US-10-327-598-241	Sequence 241, App
28	9	2.7	25	16	US-10-327-598-243	Sequence 243, App
29	9	2.7	25	16	US-10-327-598-244	Sequence 244, App
30	9	2.7	89	17	US-10-872-932A-28	Sequence 28, Appl
31	9	2.7	89	17	US-10-872-932A-29	Sequence 29, Appl
32	9	2.7	98	15	US-10-308-817-118	Sequence 118, App
33	9	2.7	98	15	US-10-308-817-119	Sequence 119, App
34	9	2.7	98	15	US-10-308-817-120	Sequence 120, App
35	9	2.7	98	15	US-10-453-698-118	Sequence 118, App
36	9	2.7	98	15	US-10-453-698-119	Sequence 119, App
37	9	2.7	98	15	US-10-453-698-120	Sequence 120, App
38	9	2.7	105	14	US-10-029-386-33917	Sequence 33917, A
39	9	2.7	108	10	US-09-848-798-51	Sequence 51, Appl
40	9	2.7	108	10	US-09-848-798-52	Sequence 52, Appl
41	9	2.7	108	10	US-09-848-798-53	Sequence 53, Appl
42	9	2.7	108	10	US-09-848-798-166	Sequence 166, App
43	9	2.7	112	16	US-10-327-598-809	Sequence 809, App
44	9	2.7	118	16	US-10-327-598-1106	Sequence 1106, App
45	9	2.7	119	15	US-10-291-265-720	Sequence 720, App

ALIGNMENTS

RESULT 1
US-10-091-019-3
; Sequence 3, Application US/10091019
; Publication No. US20030166063A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Shen, Jane M.
; APPLICANT: Shahbaz, Manouchehr M.
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins
; FILE REFERENCE: 41305-270555
; CURRENT APPLICATION NUMBER: US/10/091,019
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/273,418
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-091-019-3

Query Match	100.0%;	Score 339;	DB 14;	Length 339;
Best Local Similarity	100.0%;	Pred. No. 3.3e-309;		
Matches 339;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MAAGTAVGAWVLVLSLWGAVGCAQNTARIGPLVKCKGAPKPPORLEWKINTGRTA	60	
Db	1	MAAGTAVGAWVLVLSLWGAVGCAQNTARIGPLVKCKGAPKPPORLEWKINTGRTA	60	
QY	61	WKVLPQGGPQWDSVARVLPNGSLFLPAVIGIQDEGIFRCQAMNRNGKETKSNYRVVYQI	120	
Db	61	WKVLPQGGPQWDSVARVLPNGSLFLPAVIGIQDEGIFRCQAMNRNGKETKSNYRVVYQI	120	
QY	121	PKPKEIVDSASBLTAGVPKNVKGTCVSEGSYPAGTISWHLDGKPLVPNEKGVSKETRHH	180	

Db 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTILSHWLDGKPLVPNEKGVSVKEQTRRH 180
QY 181 PETGLFTLQSELMVTPARGGDPRTFSCFSGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
Db 181 PETGLFTLQSELMVTPARGGDPRTFSCFSGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
QY 241 VVEPEGGAVAGGTGTTLTCEVPAQSPQIHMMKDGVPPLPPLPSVLILPEIGPDQGTYS 300
Db 241 VVEPEGGAVAGGTGTTLTCEVPAQSPQIHMMKDGVPPLPPLPSVLILPEIGPDQGTYS 300
QY 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSLV 339
Db 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSLV 339

RESULT 2

US-10-309-290-96
; Sequence 96, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chilikuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274

; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 96
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-290-96

Query Match 99.7%; Score 338; DB 15; Length 404;
Best Local Similarity 100.0%; Pred. No. 3.3e-308;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGA VVGAQNITARIGEPVLVKCKGAPKKPQRLWKLTGRTGA 60
Db 1 MAAGTAVGAWLVLSLWGA VVGAQNITARIGEPVLVKCKGAPKKPQRLWKLTGRTGA 60

QY 61 WKVLSPOGGPMDSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVVYQI 120
Db 61 WKVLSPOGGPMDSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNYRVVYQI 120

QY 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTILSHWLDGKPLVPNEKGVSVKEQTRRH 180
Db 121 PGKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTILSHWLDGKPLVPNEKGVSVKEQTRRH 180

QY 181 PETGLFTLQSELMVTPARGGDPRTFSCFSGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
Db 181 PETGLFTLQSELMVTPARGGDPRTFSCFSGLPRHRLRTAPIQPRVWEPVPLEEVOL 240

QY 241 VVEPEGGAVAGGTGTTLTCEVPAQSPQIHMMKDGVPPLPPLPSVLILPEIGPDQGTYS 300
Db 241 VVEPEGGAVAGGTGTTLTCEVPAQSPQIHMMKDGVPPLPPLPSVLILPEIGPDQGTYS 300

QY 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSL 338
Db 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSL 338

RESULT 3

US-10-472-507A-2
; Sequence 2, Application US/10472507A
; Publication No. US20050033017A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, Hiroshi
; APPLICANT: Yonekura, Hideto
; APPLICANT: Yamamoto, Yasuhiko
; APPLICANT: Sakurai, Shigeru
; APPLICANT: Watanabe, Takuo
; TITLE OF INVENTION: Soluble Rage Protein
; FILE REFERENCE: 026350-089
; CURRENT APPLICATION NUMBER: US/10/472,507A
; CURRENT FILING DATE: 2003-09-22
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: PCT/JP02,02623
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: JP 2001-78409
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: JP 2001-243114
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: JP 2002-48182
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-472-507A-2

Query Match 97.6%; Score 331; DB 17; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.1e-301;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGA VVGAQNITARIGEPVLVKCKGAPKKPQRLWKLTGRTGA 60
Db 1 MAAGTAVGAWLVLSLWGA VVGAQNITARIGEPVLVKCKGAPKKPQRLWKLTGRTGA 60

QY 61 WKVLSPOGGPNDVSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTKSNYRVVYQI 120
Db 61 WKVLSPOGGPNDVSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTKSNYRVVYQI 120
QY 121 PKKPEIVDSASELTAGVPNNKVTGCVSEGSYPAGTLSWHLDGKPLVNEKGVSKQETRRH 180
Db 121 PKKPEIVDSASELTAGVPNNKVTGCVSEGSYPAGTLSWHLDGKPLVNEKGVSKQETRRH 180
QY 181 PETGLFTLQSELMVTPARGDPRPTSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
Db 181 PETGLFTLQSELMVTPARGDPRPTSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
QY 241 VVEPEGAVAPGCTVTLTCEVPAQPSQIHMMDGVPLPLPSPVLILPEIGPDQGTYS 300
Db 241 VVEPEGAVAPGCTVTLTCEVPAQPSQIHMMDGVPLPLPSPVLILPEIGPDQGTYS 300
QY 301 CVATHSSHGPOESRAVSIIEPEGEGTAG 331
Db 301 CVATHSSHGPOESRAVSIIEPEGEGTAG 331

RESULT 4
US-09-872-185B-2
; Sequence 2, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevin
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Human
US-09-872-185B-2

Query Match 93.2%; Score 316; DB 9; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.2e-287;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLCCKGAPKPPORLEWKLNTGRTEAMKVLSPQGGPNDVSVARVLPNG 82
Db 1 AQNITARIGEPLVLCCKGAPKPPORLEWKLNTGRTEAMKVLSPQGGPNDVSVARVLPNG 60
QY 83 SLFLPAVGIQDEGIFRCQAMNRNGKTKSNYRVVYQI PKKPEIVDSASELTAGVPNNKVG 142
Db 61 SLFLPAVGIQDEGIFRCQAMNRNGKTKSNYRVVYQI PKKPEIVDSASELTAGVPNNKVG 120
QY 143 TCVSEGSYPAGTLSWHLDGKPLVNEKGVSKQETRRHPETGLFTLQSELMVTPARGGDP 202
Db 121 TCVSEGSYPAGTLSWHLDGKPLVNEKGVSKQETRRHPETGLFTLQSELMVTPARGGDP 180
QY 203 RPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVOLVVEPEGAVAPGCTVTLTCEVP 262
Db 181 RPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVOLVVEPEGAVAPGCTVTLTCEVP 240
QY 263 AQPSQIHMMDGVPLPLPSPVLILPEIGPDQGTYS CVATHSSHGPOESRAVSIIE 322
Db 241 AQPSQIHMMDGVPLPLPSPVLILPEIGPDQGTYS CVATHSSHGPOESRAVSIIE 300
QY 323 PCEEGTAGSVGSGSL 338
Db 301 PCEEGTAGSVGSGSL 316

RESULT 5
US-09-851-071-1
; Sequence 1, Application US/09851071
; Patent No. US20020177550A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Anne Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: A METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A SUBJECT
; FILE REFERENCE: 0575/55424-Z/JPW/SHS/MVM
; CURRENT APPLICATION NUMBER: US/09/851,071
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Human
US-09-851-071-1

Query Match 93.2%; Score 316; DB 9; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.2e-287;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLCCKGAPKPPORLEWKLNTGRTEAMKVLSPQGGPNDVSVARVLPNG 82
Db 1 AQNITARIGEPLVLCCKGAPKPPORLEWKLNTGRTEAMKVLSPQGGPNDVSVARVLPNG 60
QY 83 SLFLPAVGIQDEGIFRCQAMNRNGKTKSNYRVVYQI PKKPEIVDSASELTAGVPNNKVG 142
Db 61 SLFLPAVGIQDEGIFRCQAMNRNGKTKSNYRVVYQI PKKPEIVDSASELTAGVPNNKVG 120
QY 143 TCVSEGSYPAGTLSWHLDGKPLVNEKGVSKQETRRHPETGLFTLQSELMVTPARGGDP 202
Db 121 TCVSEGSYPAGTLSWHLDGKPLVNEKGVSKQETRRHPETGLFTLQSELMVTPARGGDP 180
QY 203 RPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVOLVVEPEGAVAPGCTVTLTCEVP 262
Db 181 RPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVOLVVEPEGAVAPGCTVTLTCEVP 240
QY 263 AQPSQIHMMDGVPLPLPSPVLILPEIGPDQGTYS CVATHSSHGPOESRAVSIIE 322
Db 241 AQPSQIHMMDGVPLPLPSPVLILPEIGPDQGTYS CVATHSSHGPOESRAVSIIE 300
QY 323 PCEEGTAGSVGSGSL 338
Db 301 PCEEGTAGSVGSGSL 316

RESULT 6
US-10-309-290-98
; Sequence 98, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.

```

; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; PRIOR FILING DATE: 2002-12-02
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 98
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-290-98

Query Match 79.9%; Score 271; DB 15; Length 390;
Best Local Similarity 100.0%; Pred. No. 2.2e-245;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 GGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQIPGKPEIV 127
Db 54 GGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQIPGKPEIV 113

Qy 128 DSASELTAGVPNKVGTGCVSEGSYPAGTILSWHLDGKPLVNEKGVSKQTRRHPTGLFT 187
Db 114 DSASELTAGVPNKVGTGCVSEGSYPAGTILSWHLDGKPLVNEKGVSKQTRRHPTGLFT 173

Qy 188 LQSELMVTARGDPRPTFSCSFGPLPRHRLARTAPIQPRVWEPVPLEEVVVEPEGG 247
Db 174 LQSELMVTARGDPRPTFSCSFGPLPRHRLARTAPIQPRVWEPVPLEEVVVEPEGG 233

RESULT 7
US-10-309-290-100
; Sequence 100, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Sheroy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; PRIOR FILING DATE: 2002-12-02
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 100
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-290-100

Query Match 79.9%; Score 271; DB 15; Length 390;
Best Local Similarity 100.0%; Pred. No. 2.2e-245;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 GGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQIPGKPEIV 127
Db 54 GGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQIPGKPEIV 113

Qy 128 DSASELTAGVPNKVGTGCVSEGSYPAGTILSWHLDGKPLVNEKGVSKQTRRHPTGLFT 187
Db 114 DSASELTAGVPNKVGTGCVSEGSYPAGTILSWHLDGKPLVNEKGVSKQTRRHPTGLFT 173

Qy 188 LQSELMVTARGDPRPTFSCSFGPLPRHRLARTAPIQPRVWEPVPLEEVVVEPEGG 247
Db 174 LQSELMVTARGDPRPTFSCSFGPLPRHRLARTAPIQPRVWEPVPLEEVVVEPEGG 233
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```
QY 248 AVAPGGTTLTCEVPAQSPQIHHMKDGVPLPLPPSPVLILPEIGPDQDGTSCVATHSS 307
DB 234 AVAPGGTTLTCEVPAQSPQIHHMKDGVPLPLPPSPVLILPEIGPDQDGTSCVATHSS 293
QY 308 HGPQESRAVSISIIIEPGEPTAGSVGGGSL 338
DB 294 HGPQESRAVSISIIIEPGEPTAGSVGGGSL 324

RESULT 8
US-08-755-235-4
; Sequence 4, Application US/08755235
; Publication No. US20030059423A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Human
US-08-755-235-4

Query Match 63.7%; Score 216; DB 8; Length 405;
Best Local Similarity 100.0%; Pred. No. 8.7e-194;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVPNKVGTCSVSEGSYPAGTILSHWLD 160
DB 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVPNKVGTCSVSEGSYPAGTILSHWLD 160
QY 161 GKPLVNEKGVSVKEQTRRHPTGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRL 220
DB 161 GKPLVNEKGVSVKEQTRRHPTGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRL 220
QY 221 RTAPIQPRVWEVPVLEEVQVLEPEGAVAPGGTTLTCEVPAQSPQIHHMKDGVPLPL 280
DB 221 RTAPIQPRVWEVPVLEEVQVLEPEGAVAPGGTTLTCEVPAQSPQIHHMKDGVPLPL 280
QY 281 PPSVLILPEIGPDQDGTSCVATHSSHGQESRAV 316
DB 281 PPSVLILPEIGPDQDGTSCVATHSSHGQESRAV 316

RESULT 9
US-10-408-765A-641
; Sequence 641, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 641
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens

QY 248 AVAPGGTTLTCEVPAQSPQIHHMKDGVPLPLPPSPVLILPEIGPDQDGTSCVATHSS 307
DB 234 AVAPGGTTLTCEVPAQSPQIHHMKDGVPLPLPPSPVLILPEIGPDQDGTSCVATHSS 293
QY 308 HGPQESRAVSISIIIEPGEPTAGSVGGGSL 338
DB 294 HGPQESRAVSISIIIEPGEPTAGSVGGGSL 324

RESULT 8
US-08-755-235-4
; Sequence 4, Application US/08755235
; Publication No. US20030059423A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Human
US-08-755-235-4

Query Match 63.7%; Score 216; DB 8; Length 405;
Best Local Similarity 100.0%; Pred. No. 8.7e-194;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVPNKVGTCSVSEGSYPAGTILSHWLD 160
DB 101 AMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVPNKVGTCSVSEGSYPAGTILSHWLD 160
QY 161 GKPLVNEKGVSVKEQTRRHPTGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRL 220
DB 161 GKPLVNEKGVSVKEQTRRHPTGLFTLQSELMTVPARGDPRPTFSCFSFGLPRHRL 220
QY 221 RTAPIQPRVWEVPVLEEVQVLEPEGAVAPGGTTLTCEVPAQSPQIHHMKDGVPLPL 280
DB 221 RTAPIQPRVWEVPVLEEVQVLEPEGAVAPGGTTLTCEVPAQSPQIHHMKDGVPLPL 280
QY 281 PPSVLILPEIGPDQDGTSCVATHSSHGQESRAV 316
DB 281 PPSVLILPEIGPDQDGTSCVATHSSHGQESRAV 316

RESULT 9
US-10-408-765A-641
; Sequence 641, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 641
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
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```
US-10-408-765A-641
Query Match 61.1%; Score 207; DB 16; Length 342;
Best Local Similarity 100.0%; Pred. No. 2.1e-185;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 GGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNRYRVYQIPGKPEIV 127
DB 54 GGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNRYRVYQIPGKPEIV 113
QY 128 DSASELTAGVPNKVGTCSVSEGSYPAGTILSHWLDGKPLVNEKGVSVKEQTRRHPTGLFT 187
DB 114 DSASELTAGVPNKVGTCSVSEGSYPAGTILSHWLDGKPLVNEKGVSVKEQTRRHPTGLFT 173
QY 188 LQSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEVPVLEEVQVLEPEGG 247
DB 174 LQSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEVPVLEEVQVLEPEGG 233
QY 248 AVAPGGTTLTCEVPAQSPQIHHMKD 274
DB 234 AVAPGGTTLTCEVPAQSPQIHHMKD 260

RESULT 10
US-09-872-185B-1
; Sequence 1, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Human
US-09-872-185B-1

Query Match 33.0%; Score 112; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 9.4e-97;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVKCKGAPKPPQRLWKLTNGRTEAMKVLSPQGGPWDSVARVLPNG 82
DB 1 AQNITARIGEPLVKCKGAPKPPQRLWKLTNGRTEAMKVLSPQGGPWDSVARVLPNG 60
QY 83 SLFLPAVGIQDEGIFRCQAMNRNGKETKSNRYRVYQIPGKPEIVDSASELT 134
DB 61 SLFLPAVGIQDEGIFRCQAMNRNGKETKSNRYRVYQIPGKPEIVDSASELT 112

RESULT 11
US-08-948-131-1
; Sequence 1, Application US/08948131
; Publication No. US20010053357A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: Ligand Binding Site of Rage and Uses
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
```

STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,131
FILING DATE: 09-OCT-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 53447
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-948-131-1

Query Match 8.8%; Score 30; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.3e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 AQNITARIGEPLVLKCKGAPKPPORLEWK 52
DB 1 AQNITARIGEPLVLKCKGAPKPPORLEWK 30

RESULT 12
US-09-872-185B-3
Sequence 3, Application US/09872185B
Patent No. US20020122799A1
GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Herold, Kewan
APPLICANT: Yan, Shi Du
APPLICANT: Schmidt, Ann Marie
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
FILE REFERENCE: 0575/64080
CURRENT APPLICATION NUMBER: US/09/872,185B
CURRENT FILING DATE: 2001-06-01
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 30
TYPE: PRT
ORGANISM: Human
US-09-872-185B-3

Query Match 8.8%; Score 30; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.3e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 AQNITARIGEPLVLKCKGAPKPPORLEWK 52
DB 1 AQNITARIGEPLVLKCKGAPKPPORLEWK 30

RESULT 13
US-09-872-185B-7
Sequence 7, Application US/09872185B
Patent No. US20020122799A1
GENERAL INFORMATION:

APPLICANT: Stern, David M.
APPLICANT: Herold, Kewan
APPLICANT: Yan, Shi Du
APPLICANT: Schmidt, Ann Marie
APPLICANT: Lamster, Ira
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
FILE REFERENCE: 0575/64080
CURRENT APPLICATION NUMBER: US/09/872,185B
CURRENT FILING DATE: 2001-06-01
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 30
TYPE: PRT
ORGANISM: Human
US-09-872-185B-7

Query Match 8.8%; Score 30; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.3e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 AQNITARIGEPLVLKCKGAPKPPORLEWK 52
DB 1 AQNITARIGEPLVLKCKGAPKPPORLEWK 30

RESULT 14
US-09-851-071-5
Sequence 5, Application US/09851071
Patent No. US2002017550A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Anne Marie
APPLICANT: Stern, David
TITLE OF INVENTION: A METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A SUBJECT
FILE REFERENCE: 0575/55424-Z/JPW/SHS/MVM
CURRENT APPLICATION NUMBER: US/09/851,071
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 30
TYPE: PRT
ORGANISM: Human
US-09-851-071-5

Query Match 8.8%; Score 30; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.3e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 AQNITARIGEPLVLKCKGAPKPPORLEWK 52
DB 1 AQNITARIGEPLVLKCKGAPKPPORLEWK 30

RESULT 15
US-08-755-235-2
Sequence 2, Application US/08755235
Publication No. US20030059423A1
GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Schmidt, Ann Marie
APPLICANT: Wu, Jun
TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
FILE REFERENCE: 0575/50159
CURRENT APPLICATION NUMBER: US/08/755,235
CURRENT FILING DATE: 1996-11-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 416
TYPE: PRT
ORGANISM: Bovine
US-08-755-235-2

Query Match 7.1%; Score 24; DB 8; Length 416;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 EVQLVVEPEGGAVAPGGTVTLTCE 260
DB 247 EVQLVVEPEGGAVAPGGTVTLTCE 270

Search completed: March 16, 2005, 08:08:47
Job time : 326 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2005, 02:39:20 ; Search time 24 Seconds
(without alignments)
1359.062 Million cell updates/sec

Title: US-10-091-019-3
Perfect score: 339
Sequence: 1 MAAGTAGAWNLVLSWGA.....IIEPGEETAGSGVGLV 339

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	338	99.7	404	1 I61596	advanced glycosyla
2	26	7.7	402	2 T09062	probable advanced
3	24	7.1	416	1 A42879	advanced glycosyla
4	9	2.7	97	2 S36066	Ig lambda chain -
5	9	2.7	98	2 S36063	Ig lambda chain -
6	9	2.7	98	2 S36062	Ig lambda chain -
7	9	2.7	110	2 S57465	Ig lambda chain V-
8	9	2.7	112	2 S26655	Ig lambda chain V
9	9	2.7	116	2 C27390	Ig lambda chain pr
10	9	2.7	117	1 LVH2	Ig lambda chain pr
11	9	2.7	117	2 S04526	Ig lambda chain pr
12	9	2.7	120	2 S30528	Ig lambda chain V
13	9	2.7	136	2 S42610	ARMWlambda protein
14	9	2.7	235	2 S25749	Ig lambda chain -
15	8	2.4	357	1 K1EBER	thymidine kinase (
16	8	2.4	359	1 K1EBBT	thymidine kinase (
17	8	2.4	394	2 D70674	probable lipid car
18	8	2.4	410	2 T13531	hypothetical prote
19	8	2.4	549	2 JC5926	secreted klotho pr
20	8	2.4	550	2 G70597	probable proteins
21	8	2.4	599	2 G86204	hypothetical prote
22	8	2.4	643	2 I50539	intermediate filam
23	8	2.4	745	2 T51370	hypothetical prote
24	8	2.4	1012	2 JC5925	membrane klotho pr
25	8	2.4	1089	2 T31583	hypothetical prote
26	8	2.4	6831	2 A88852	protein unc-22 (im
27	8	2.4	6839	2 S57242	twichin (similar)
28	8	2.4	7160	2 T27935	hypothetical prote
29	7	2.1	89	2 G96958	ACT domain contain

30	7	2.1	105	2 E75360	conserved hypothet
31	7	2.1	106	2 I48862	tyrosine kinase gr
32	7	2.1	125	2 C72579	hypothetical prote
33	7	2.1	144	2 S23655	superoxide dismuta
34	7	2.1	182	2 C90141	hypothetical prote
35	7	2.1	187	2 H87376	hypothetical prote
36	7	2.1	215	2 T36448	probable methyltra
37	7	2.1	223	2 H64065	mutator muth - Hae
38	7	2.1	236	2 T35095	probable membrane
39	7	2.1	242	2 AG2283	two-component resp
40	7	2.1	253	2 B83332	cis-1,2-dihydroxyc
41	7	2.1	257	2 G87285	hypothetical prote
42	7	2.1	258	2 A96013	probable oxidoredu
43	7	2.1	259	2 A87377	hypothetical prote
44	7	2.1	263	2 S59380	probable membrane
45	7	2.1	267	2 I72882	Fc gamma receptor

ALIGNMENTS

RESULT 1

I61596

advanced glycosylation end-products receptor precursor - human

N;Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprotein

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004

C;Accession: I61596; B42879; S27968

R;Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, H.;

Genomics 23, 408-419, 1994

A;Title: Three genes in the human MHC class III region near the junction with the class I

nterpart of mouse mammary tumor gene int-3.

A;Reference number: A55562; MUID:95137587; PMID:7835890

A;Accession: I61596

A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EHBI

A;Molecule type: DNA

A;Residues: 1-404 <RES>

A;Cross-references: UNIPROT:Q15109; GB:D28769; NID:G561657; PIDN:BAA05958.1; PID:G561659

R;Nepper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; Ste

J. Biol. Chem. 267, 14998-15004, 1992

A;Title: Cloning and expression of a cell surface receptor for advanced glycosylation en

A;Reference number: A42879; MUID:92340547; PMID:1378843

A;Accession: B42879

A;Molecule type: mRNA

A;Residues: 'G', '2-99', 'R', '101-404' <NEE>

A;Cross-references: EMBL:M91211; NID:G190845; PIDN:AAA03574.1; PID:G190846

A;Experimental source: lung

A;Note: sequence extracted from NCBI backbone (NCBIP:109438)

C;Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycosy

cellular function, thus contributing to tissue lesions in diabetes.

C;Comment: This receptor appears also to mediate the effects of amyloid beta peptide on r

ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.

C;Genetics:

A;Gene: GDB:AGER

A;Cross-references: GDB:306354; OMIM:600214

A;Map position: 6p21.3-6p21.3

A;Introns: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2

C;Function:

A;Description: neuronal receptor for amphoterin, a DNA-binding protein involved in neurit

C;Superfamily: advanced glycosylation end products receptor; immunoglobulin homology

C;Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-404/Product: advanced glycosylation end products receptor #status predicted <MAT>

F;23-344/Domain: extracellular #status predicted <EXT>

F;31-101/Domain: immunoglobulin homology <IM1>

F;137-210/Domain: immunoglobulin homology <IM2>

F;252-303/Domain: immunoglobulin homology <IM3>

F;345-362/Domain: transmembrane #status predicted <TMW>

F;363-404/Domain: intracellular #status predicted <INT>

F;25, 81/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;38-99, 144-208, 259-301/Disulfide bonds: #status predicted

Query Match 99.7%; Score 338; DB 1; Length 404;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAGAAGVWVLSLWGAAGVGAQNTARIGEPVLVKCKGAPKKPPORLEWKLNTGRTEA 60
Db 1 MAAGTAGAAGVWVLSLWGAAGVGAQNTARIGEPVLVKCKGAPKKPPORLEWKLNTGRTEA 60
QY 61 WKVLSPOGGFWDVSARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQI 120
Db 61 WKVLSPOGGFWDVSARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQI 120
QY 121 PKRPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTILSHWLDGKPLVPNEKGVSKQOTRRH 180
Db 121 PKRPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTILSHWLDGKPLVPNEKGVSKQOTRRH 180
QY 181 PETGLFTLQSELMTVPARGGDPRTPTSCSPGLPHRRALRTAPIOPRVWPEVPLEEVOL 240
Db 181 PETGLFTLQSELMTVPARGGDPRTPTSCSPGLPHRRALRTAPIOPRVWPEVPLEEVOL 240
QY 241 VVEPEGGAAPGGTGTITCEVPAQPSQIHMMDGVPLPLPSPVLILPEIGPDQGTYS 300
Db 241 VVEPEGGAAPGGTGTITCEVPAQPSQIHMMDGVPLPLPSPVLILPEIGPDQGTYS 300
QY 301 CVATHSHGPOESRAVSIISIEPGERGPTAGSVGGSL 338
Db 301 CVATHSHGPOESRAVSIISIEPGERGPTAGSVGGSL 338

RESULT 2
T09062
Probable advanced glycosylation end-products receptor precursor - mouse
N;Alternate names: RAGE
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09062
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sch
submitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region.
A;Reference number: Z16543
A;Accession: T09062
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-402 <ROW>
A;Cross-references: UNIPROT:Q35444; EMBL:AF030001; NID:g2564945; PID:g2564950
C;Gene: RAGE
A;Map position: 17
A;Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2
C;Superfamily: advanced glycosylation end products receptor; immunoglobulin homology
C;Keywords: receptor; transmembrane protein
F;31-100/Domain: immunoglobulin homology <IMM>

Query Match 7.7%; Score 26; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 9.4e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 VPKNVGTCTVSEGSYPAGTILSHWLDGK 162
Db 136 VPKNVGTCTVSEGSYPAGTILSHWLDGK 161

RESULT 3
A42879
Advanced glycosylation end-products receptor precursor - bovine
N;Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprotein
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Mar-1993 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C;Accession: A42879; A42878; S27949
R;Neepker, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; St
J. Biol. Chem. 267, 14998-15004, 1992
A;Title: Cloning and expression of a cell surface receptor for advanced glycosylation en
A;Reference number: A42879; PMID:92340547; PMID:1378843
A;Accession: A42879
```

```
A;Molecule type: mRNA
A;Residues: 1-416 <NEE>
A;Cross-references: UNIPROT:Q28173; GB:M91212; NID:g163650; PIDN:AAA03575.1; PID:g163651
A;Experimental source: lung
A;Note: sequence extracted from NCBI backbone (NCBIP:109436)
A;Note: parts of this sequence, including the amino end of the mature protein, were deter
J. Schmidt, A.M.; Viana, M.; Gerlach, M.; Brett, J.; Ryan, J.; Kao, J.; Esposito, C.; He
R. Biol. Chem. 267, 14987-14997, 1992
A;Title: Isolation and characterization of two binding proteins for advanced glycosylatic
A;Reference number: A42878; MUID:92340546; PMID:1321822
A;Accession: A42878
A;Molecule type: protein
A;Residues: 23-24,'X',26-37,'X',39-49,'XX',52-54 <SCH>
A;Experimental source: endothelial cells
A;Note: sequence extracted from NCBI backbone (NCBIP:109434)
C;Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycosyl
cellular function, thus contributing to tissue lesions in diabetes.
C;Comment: This receptor appears also to mediate the effects of amyloid beta peptide on r
ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.
C;Function:
A;Description: neuronal receptor for amphoterin, a DNA-binding protein involved in neurit
C;Superfamily: advanced glycosylation end products receptor; immunoglobulin homology
C;Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-416/Product: advanced glycosylation end-products receptor RAGE #status predicted <M
F;23-354/Domain: extracellular #status predicted <EXT>
F;31-100/Domain: immunoglobulin homology <IM1>
F;136-209/Domain: immunoglobulin homology <IM2>
F;262-313/Domain: immunoglobulin homology <IM3>
F;355-372/Domain: transmembrane #status predicted <TM>
F;373-416/Domain: intracellular #status predicted <INT>
F;25.80/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;38-98,143-207,269-311/Disulfide bonds: #status predicted

Query Match 7.1%; Score 24; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 9.8e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 EVQLVVEPEGGAAPGGTIVTLTCE 260
Db 247 EVQLVVEPEGGAAPGGTIVTLTCE 270

RESULT 4
S36066
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-May-1997
C;Accession: S36066
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36066
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <WIL>
A;Cross-references: EMBL:Z22210
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 2.7%; Score 9; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 PGGTIVTLTC 259
Db 14 PGGTIVTLTC 22

RESULT 5
S36063
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
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GenCore version 5.1.6
Copyright: (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2005, 02:46:31 ; Search time 82 Seconds
(without alignments)
2117.010 Million cell updates/sec

Title: US-10-091-019-3
Perfect score: 339
Sequence: 1 MAAGTAVGAWLVLSLWGA.....IIEPGEQTAGSVGGSLV 339

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	338	99.7	404	1	RAGE HUMAN
2	331	97.6	347	2	Q86SN1
3	131	38.6	147	2	Q71BG7
4	30	8.8	50	2	Q71BB6
5	28	8.3	402	1	RAGE RAT
6	28	8.3	402	2	Q6MG86
7	26	7.7	402	2	Q35444
8	26	7.7	403	1	RAGE MOUSE
9	24	7.1	416	1	RAGE BOVIN
10	21	6.2	119	2	Q6TVZ6
11	21	6.2	161	2	Q6UPY5
12	21	6.2	330	2	Q6QP58
13	19	5.6	23	2	Q6SA79
14	17	5.0	17	2	Q71UQ2
15	16	4.7	82	2	Q9UQR5
16	9	2.7	17	2	Q95794
17	9	2.7	32	2	Q9TRQ1
18	9	2.7	117	1	LVQA_HUMAN
19	9	2.7	219	2	Q880R7
20	9	2.7	246	2	Q9ANU6
21	9	2.7	259	2	Q92I71
22	9	2.7	261	2	Q51496
23	9	2.7	270	2	Q93874
24	8	2.4	17	2	Q95795
25	8	2.4	173	2	Q9UFP6
26	8	2.4	220	2	Q9B4G8
27	8	2.4	224	2	Q75613
28	8	2.4	231	2	Q79494
29	8	2.4	231	2	Q7Y9Q9
30	8	2.4	231	2	Q6GNB8
31	8	2.4	233	2	Q6GNH3

32	8	2.4	250	2	Q69XD7	Q69xd7 oryza sativ
33	8	2.4	253	2	Q9X5W5	Q9x5w5 rhodobacter
34	8	2.4	259	2	O52384	O52384 ralestonia s
35	8	2.4	259	2	Q9L5D0	Q9l5d0 comamonas t
36	8	2.4	272	2	Q9LC88	Q9lc88 nocardioides
37	8	2.4	273	2	Q96KM5	Q96kw5 homo sapien
38	8	2.4	285	2	P78977	P78977 yarrowia li
39	8	2.4	299	2	Q6NUK6	Q6nuk6 homo sapien
40	8	2.4	338	2	Q63IS8	Q63is8 burkholderi
41	8	2.4	345	2	Q8WW19	Q8ww19 homo sapien
42	8	2.4	355	2	Q84YW6	Q84yw6 oryza sativ
43	8	2.4	357	1	KITH_BHV16	P24096 bovine herp
44	8	2.4	359	1	KITH_BHV1Q	P24424 bovine herp
45	8	2.4	359	2	Q65560	Q65560 bovine herp

ALIGNMENTS

RESULT 1

RAGE HUMAN

ID RAGE HUMAN STANDARD; PRT; 404 AA.

AC Q15109; Q15279; Q9H2X7; Q9V3R3;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Advanced glycosylation end product-specific receptor precursor

DE (Receptor for advanced glycosylation end products).

GN Name=AGER; Synonyms=RAGE;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Lung;

RX MEDLINE=92340547; PubMed=1378843;

RA Nepper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C., Elliston K., Stern D., Shaw A.;

RT "Cloning and expression of a cell surface receptor for advanced glycosylation end products of proteins.";

RT J. Biol. Chem. 267:14998-15004(1992).

RL [2]

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=95137587; PubMed=7835890;

RA Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A., Inoto H., Ikemura T.;

RT "Three genes in the human MHC class III region near the junction with the class II: gene for receptor of advanced glycosylation end products, PBX2 homeobox gene and a notch homolog, human counterpart of mouse mammary tumor gene int-3.";

RL Genomics 23:408-419(1994).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX Rowen L., Danders C., Baskin D., Faust J., Loretz C., Ahearn M.E., Banta A., Spies T., Hood L.;

RT "Sequence determination of 300 kilobases of the human class III MHC locus.";

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100.

RX Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y., Yamamoto H.;

RT "Molecular heterogeneity of the receptor for advanced glycation endproducts.";

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RX Malherbe P., Richards J., Gaillard H., Thompson A., Diener C., Schuler A., Huber G.;

RT "cDNA cloning of a novel secreted isoform of the human receptor for advanced glycation end products (RAGE) and characterization of cells co-expressing cell-surface scavenger receptors and Swedish mutant


```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22510265; PubMed=12495433; DOI=10.1042/BJ20021371;
RA Yonekura H., Yamamoto Y., Sakurai S., Petrova R.G., Abedin Md.J.,
RA Li H., Yasui K., Takeuchi M., Makita Z., Takasawa S., Okamoto H.,
RA Watanabe T., Yamamoto H.;
RT "Novel splice variants of the receptor for advanced glycation end-
RT products expressed in human vascular endothelial cells and pericytes,
RT and their putative roles in diabetes-induced vascular injury.";
RL Biochem. J. 370:1097-1109(2003).
DR EMBL; AB061668; BAC65465.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor; Signal.
FT SIGNAL 1
SQ SEQUENCE 347 AA; 37050 MW; 519E377C4D6AC62C CRC64;

Query Match 97.6%; Score 331; DB 2; Length 347;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAGAWVLVLSLWGAAGVGAQNTARIGELPLVLCCKGAPKPPQRLWKLNTGRTA 60
DB 1 MAAGTAGAWVLVLSLWGAAGVGAQNTARIGELPLVLCCKGAPKPPQRLWKLNTGRTA 60

QY 61 WKVLSQGGPWPDSVARVLPNGSLFTPAVGIQDEGIFRCQAMNRNGKETKSNYRVYQI 120
DB 61 WKVLSQGGPWPDSVARVLPNGSLFTPAVGIQDEGIFRCQAMNRNGKETKSNYRVYQI 120

QY 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSYPACTLSWHLGKPLVNEKGVSKVQETRRH 180
DB 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSYPACTLSWHLGKPLVNEKGVSKVQETRRH 180

QY 181 PETGLFTLQSELNVTTPARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEVOL 240
DB 181 PETGLFTLQSELNVTTPARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEVOL 240

QY 241 VPEPEGAVAPGTTVLTCEVPAQPSQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYS 300
DB 241 VPEPEGAVAPGTTVLTCEVPAQPSQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYS 300

QY 301 CVATHSHGPOESRAVSISIIIEGEGPTAG 331
DB 301 CVATHSHGPOESRAVSISIIIEGEGPTAG 331

RESULT 3
QY1BG7 PRELIMINARY; PRT; 147 AA.
AC QY1BG7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Advanced glycosylation end product-specific receptor variant sRAGE2
DE (Fragment).
GN Name=AGER;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22510265; PubMed=12495433; DOI=10.1042/BJ20021371;
RA Yonekura H., Yamamoto Y., Sakurai S., Petrova R.G., Abedin Md.J.,
RA Li H., Yasui K., Takeuchi M., Makita Z., Takasawa S., Okamoto H.,
RA Watanabe T., Yamamoto H.;
RT "Novel splice variants of the receptor for advanced glycation end-
RT products expressed in human vascular endothelial cells and pericytes,
RT and their putative roles in diabetes-induced vascular injury.";
RL Biochem. J. 370:1097-1109(2003).
DR EMBL; AB061668; BAC65465.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor; Signal.
FT SIGNAL 1
SQ SEQUENCE 347 AA; 37050 MW; 519E377C4D6AC62C CRC64;

Query Match 97.6%; Score 331; DB 2; Length 347;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAGAWVLVLSLWGAAGVGAQNTARIGELPLVLCCKGAPKPPQRLWKLNTGRTA 60
DB 1 MAAGTAGAWVLVLSLWGAAGVGAQNTARIGELPLVLCCKGAPKPPQRLWKLNTGRTA 60

QY 61 WKVLSQGGPWPDSVARVLPNGSLFTPAVGIQDEGIFRCQAMNRNGKETKSNYRVYQI 120
DB 61 WKVLSQGGPWPDSVARVLPNGSLFTPAVGIQDEGIFRCQAMNRNGKETKSNYRVYQI 120

QY 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSYPACTLSWHLGKPLVNEKGVSKVQETRRH 180
DB 121 PGKPEIVDSASELTAGVPNKVGTCSVSGSYPACTLSWHLGKPLVNEKGVSKVQETRRH 180

QY 181 PETGLFTLQSELNVTTPARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEVOL 240
DB 181 PETGLFTLQSELNVTTPARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEVOL 240

QY 241 VPEPEGAVAPGTTVLTCEVPAQPSQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYS 300
DB 241 VPEPEGAVAPGTTVLTCEVPAQPSQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYS 300

QY 301 CVATHSHGPOESRAVSISIIIEGEGPTAG 331
DB 301 CVATHSHGPOESRAVSISIIIEGEGPTAG 331

RESULT 3
QY1BG7 PRELIMINARY; PRT; 147 AA.
AC QY1BG7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Advanced glycosylation end product-specific receptor variant sRAGE2
DE (Fragment).
GN Name=AGER;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22510265; PubMed=12495433; DOI=10.1042/BJ20021371;
RA Yonekura H., Yamamoto Y., Sakurai S., Petrova R.G., Abedin Md.J.,
RA Li H., Yasui K., Takeuchi M., Makita Z., Takasawa S., Okamoto H.,
RA Watanabe T., Yamamoto H.;
RT "Novel splice variants of the receptor for advanced glycation end-
RT products expressed in human vascular endothelial cells and pericytes,
RT and their putative roles in diabetes-induced vascular injury.";
RL Biochem. J. 370:1097-1109(2003).
DR EMBL; AB061668; BAC65465.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor; Signal.
FT SIGNAL 1
SQ SEQUENCE 347 AA; 37050 MW; 519E377C4D6AC62C CRC64;
```

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RX MEDLINE=22941919; PubMed=14580673; DOI=10.1016/j.bbaexp.2003.08.008;
RA Schlueter C., Hauke S., Flohr A.M., Rogalla P., Bullerdiek J.;
RT "Tissue-specific expression patterns of the RAGE receptor and its
RT soluble forms-a result of regulated alternative splicing?";
RL Biochim. Biophys. Acta 1630:1-6(2003).
DR EMBL; AF536237; AAQ10686.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 147 AA; 15676 MW; F4D9D530B2EAC934 CRC64;

Query Match 38.6%; Score 131; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 5.3e-125;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 DPRPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEVOLVPEEGAVAPGTTVLTCE 260
DB 1 DPRPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEVOLVPEEGAVAPGTTVLTCE 60

QY 261 VPAQSPQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYSVCVATHSHGPOESRAVSIS 320
DB 61 VPAQSPQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYSVCVATHSHGPOESRAVSIS 120

QY 321 IEPGEGPTAG 331
DB 121 IEPGEGPTAG 131

RESULT 4
QY1BB6 PRELIMINARY; PRT; 50 AA.
ID QY1BB6;
AC QY1BB6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Advanced glycosylation end product-specific receptor RAGE3 (Advanced
DE glycosylation end product-specific receptor variant sRAGE1)
DE (Fragment).
GN Name=AGER;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast cancer;
RX MEDLINE=22941919; PubMed=14580673; DOI=10.1016/j.bbaexp.2003.08.008;
RA Schlueter C., Hauke S., Flohr A.M., Rogalla P., Bullerdiek J.;
RT "Tissue-specific expression patterns of the RAGE receptor and its
RT soluble forms-a result of regulated alternative splicing?";
RL Biochim. Biophys. Acta 1630:1-6(2003).
DR EMBL; AF537303; AAQ10782.1; -.
DR EMBL; AF536236; AAQ10685.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 50 AA; 5708 MW; 71A023326D84AD9C CRC64;

Query Match 8.8%; Score 30; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.9e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 DPRPTFSCSPGLPRHRLRTAPIQPRVW 230
DB 1 DPRPTFSCSPGLPRHRLRTAPIQPRVW 230
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Db 1 DRPTFSCSPGLPRHRLTAPIOPRVW 30

RESULT 5

RAGE RAT STANDARD; PRT; 402 AA.

AC Q63495;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Advanced glycosylation end product-specific receptor precursor
 DE (Receptor for advanced glycosylation end products).
 GN Name=Ager; Synonyms=RAGE;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Lung;
 RX MEDLINE=97368045; PubMed=9224812;
 RA Renard C., Chappey O., Wautier M.P., Nagashima M., Lundh E.,
 RA Morser J., Zhao L., Schmidt A.M., Scherzmann J.M., Wautier J.L.;
 RT "Recombinant advanced glycation end product receptor pharmacokinetics
 RT in normal and diabetic rats.";
 RL Mol. Pharmacol. 52:54-62(1997).
 CC -!- FUNCTION: Mediates interactions of advanced glycosylation end
 CC products (AGE). These are nonenzymatically glycosylated proteins
 CC which accumulate in vascular tissue in aging and at an accelerated
 CC rate in diabetes.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Endothelial cells.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----

EMBL; L33413; AAA2027.1; -;
 RD; 69258; Ager.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig C2.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Glycoprotein; Immunoglobulin domain; Repeat; Signal; Transmembrane.

FT SIGNAL 1 22 Potential.
 FT CHAIN 23 402 Advanced glycosylation end product-specific receptor.
 FT DOMAIN 23 341 Extracellular (Potential).
 FT TRANSMEM 342 362 Potential.
 FT DOMAIN 363 402 Cytoplasmic (Potential).
 FT DOMAIN 23 109 Ig-like V-type.
 FT DOMAIN 123 219 Ig-like C2-type 1.
 FT DOMAIN 233 315 Ig-like C2-type 2.
 FT DISULFID 38 98 Potential.
 FT DISULFID 143 206 Potential.
 FT DISULFID 257 299 Potential.
 FT CARBOHYD 25 25 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 80 80 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 402 AA; 42663 MW; 594481BC3A51E94E CRC64;

Query Match 8.3%; Score 28; DB 1; Length 402;
 Best Local Similarity 100.0%; Pred. No. 2e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 VPKNVGTCTVSEGSYPAGTSLWHLGKPL 164
 |||||
 Db 136 VPKNVGTCTVSEGSYPAGTSLWHLGKPL 163

RESULT 6

Q6MG86 PRELIMINARY; PRT; 402 AA.

AC Q6MG86;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Advanced glycosylation end product-specific receptor.
 GN Name=Ager;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brown Norway;
 RX PubMed=15060004; DOI=10.1101/gr.1987704;
 RA Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shina T.,
 RA Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.;
 RT "The genomic sequence and comparative analysis of the rat major
 RT histocompatibility complex.";
 RL Genome Res. 14:631-639(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brown Norway;
 RA Boehm S., Borzym K., Gelling S., Gimmel V., Heitmann K., Kosiura A.,
 RA Lang N., Lehrack S., Thiel J., Sontag M., Hurt P., Himmelbauer H.,
 RA Sudbrak R., Reinhardt R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; EX883044; CAE83960.1; -;
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig C2.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00408; IGC2; 2.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 402 AA; 42644 MW; CEA49453C05E1CA1 CRC64;

Query Match 8.3%; Score 28; DB 2; Length 402;
 Best Local Similarity 100.0%; Pred. No. 2e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 VPKNVGTCTVSEGSYPAGTSLWHLGKPL 164
 |||||
 Db 136 VPKNVGTCTVSEGSYPAGTSLWHLGKPL 163

RESULT 7

O35444 PRELIMINARY; PRT; 402 AA.

AC O35444;
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE RAGE (Advanced glycosylation end product-specific receptor).
 GN Name=RAGE; Synonyms=Ager;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14656967; DOI=10.1101/gr.1736803;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2005, 09:02:00 ; Search time 79 Seconds
(without alignments)
1659.643 Million cell updates/sec

Title: US-10-091-019-3

Perfect score: 1806

Sequence: 1 MAAGTAGVAGWVLVLSWGA.....IIEPGEETAGSVGGSGILV 339

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1806	100.0	339	5	ABB82164 Human sol
2	1802	99.8	340	2	AAW44199 Human sol
3	1802	99.8	340	2	AAW33753 Human RAG
4	1802	99.8	391	8	ADP19666 Human LP2
5	1802	99.8	402	7	ADP95564 Human NOV
6	1802	99.8	404	4	AA881925 Extracorp
7	1802	99.8	404	5	ABP65011 Human pro
8	1802	99.8	404	8	ADF31292 Human rec
9	1802	99.8	404	8	ADF42983 Human rec
10	1802	99.8	404	8	ADK00129 Human RAG
11	1797	99.5	339	5	AAW48746 Human sRA
12	1797	99.5	404	5	AAW48745 Human RAG
13	1796	99.4	381	8	ADSI0986 Human the
14	1793	99.3	404	5	AAU77543 Human rec
15	1793	99.3	404	5	AAE23219 Human rec
16	1793	99.3	404	7	AAE39510 Human RAG
17	1793	99.3	404	7	ADG32004 Human hom
18	1784	98.8	420	5	ABP65012 Human pro
19	1784	98.8	425	8	ADP19660 Human LP2
20	1784	98.8	585	8	ADK00127 Human RAG
21	1768	97.9	347	5	ABB82298 Human sol
22	1768	97.9	347	7	ADG37044 Receptor
23	1768	97.9	352	8	ADP19656 Human LP2
24	1750	96.9	368	8	ADP19662 Human LP2
25	1709	94.6	390	7	ADP95568 Human NOV

26	1709	94.6	390	8	ADP19670	Adp19670 Human LP2
27	1709	94.6	421	6	ABR43188	ABr43188 Human REM
28	1705	94.4	390	7	ADP95566	Adp95566 Human NOV
29	1690	93.6	318	2	AAW44200	AAw44200 Human mat
30	1690	93.6	318	2	AAW33754	AAw33754 Human RAG
31	1687	93.4	332	3	AAV52130	AAv52130 Human Rec
32	1482.5	82.1	360	8	ADP19664	Adp19664 Human LP2
33	1480	81.9	416	5	AAU77542	AAu77542 Bovine re
34	1480	81.9	416	5	AAE23218	AAe23218 Cow recep
35	1480	81.9	416	7	AAE39509	AAe39509 Bovine RA
36	1480	81.9	416	7	ADG32003	Adg32003 Cow lung-
37	1466	81.2	298	8	ADP19658	Adp19658 Human LP2
38	1466	81.2	325	8	ADM80782	Adm80782 Human CAD
39	1404.5	77.8	343	8	ADK00124	Adk00124 Murine so
40	1404.5	77.8	403	5	AAU77544	AAu77544 Murine re
41	1404.5	77.8	403	5	AAE23220	AAe23220 Mouse rec
42	1404.5	77.8	403	7	AAE39511	AAe39511 Murine RA
43	1379.5	76.4	342	7	ADJ68835	Adj68835 Human hea
44	1229	68.1	250	6	ABR43202	ABr43202 Human REM
45	633	35.0	128	6	ABR43201	ABr43201 Human REM

ALIGNMENTS

RESULT 1

ABB82164

ID ABB82164 standard; protein; 339 AA.

XX AC ABB82164;

XX DT 23-DEC-2002 (first entry)

XX DE Human soluble RAGE (sRAGE).

XX KW Receptor for Advanced Glycated end product; RAGE; recombinant; nootropic;

KW antihyperosclerotic; antidiabetic; cytostatic; nephrotropic; vasotropic;

KW neuroprotective; antiinflammatory; gene therapy; human.

XX OS Homo sapiens.

XX PN WO200270667-A2.

XX PD 12-SEP-2002.

XX PF 05-MAR-2002; 2002WO-US006881.

XX PR 05-MAR-2001; 2001US-0273418P.

XX (TRAN-) TRANSTECH PHARMA INC.

XX Harris R, Shen J, Shabbaz M;

XX WPI; 2002-713443/77.

XX N-PSDB; ABQ79956.

High level expression of recombinant Receptors for Advanced Glycated end products (RAGE) proteins for treating increased levels of advanced glycosylation end products, comprises infecting cells with a high titer recombinant virus.

Example; Fig 2B; 51pp; English.

The invention relates to a method for high level expression of recombinant forms of the Receptor for Advanced Glycated end products (RAGE) or its fragments. The method involves (i) subcloning a nucleotide sequence encoding RAGE or its fragment into a virus; (ii) preparing a high titer stock of recombinant virus; and (iii) infecting host cells with the high titer recombinant virus under conditions such that predetermined levels of RAGE or its fragment is produced, where the predetermined levels of RAGE comprises at least 25 mg recombinant protein per liter of culture. The method is useful for high level expression of recombinant RAGE polypeptide or its fragment which may be useful in

CC preventing, treating or ameliorating diseases associated with increased
 CC levels of advanced glycosylation end products, such as atherosclerosis,
 CC diabetes and its symptoms, amyloidosis, kidney failure, Alzheimer's
 CC disease, inflammation, systemic lupus nephritis, inflammatory lupus
 CC nephritis, cancer or erectile dysfunction. The present sequence
 CC represents the amino acid sequence of human sRAGE (soluble, extracellular
 CC portion of RAGE)
 XX
 SQ Sequence 339 AA;

Query Match 100.0%; Score 1806; DB 5; Length 339;
 Best Local Similarity 100.0%; Pred. No. 1.3e-127;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAGTAVGAWVLVLSLWGA VVGAQNITARI GEPLV LKCKGAPKPPQRLWKLTGRTGA 60
 Db 1 MAAGTAVGAWVLVLSLWGA VVGAQNITARI GEPLV LKCKGAPKPPQRLWKLTGRTGA 60
 QY 61 WKVLSPOGGP WDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVYQI 120
 Db 61 WKVLSPOGGP WDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVYQI 120
 QY 121 PGKPEIVDSASLTAGVKNKVTCTVSEGSYPAGTLSWHLGDKPLVPNEKGVSKVKEQTRRH 180
 Db 121 PGKPEIVDSASLTAGVKNKVTCTVSEGSYPAGTLSWHLGDKPLVPNEKGVSKVKEQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDPRTFTSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
 Db 181 PETGLFTLQSELMTVPARGGDPRTFTSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
 QY 241 VVEPEGGA VAPGTVTLTCEVPAQPSQIHHMKDGVPLPLPPSVLILPIGPDQGTYS 300
 Db 241 VVEPEGGA VAPGTVTLTCEVPAQPSQIHHMKDGVPLPLPPSVLILPIGPDQGTYS 300
 QY 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSLV 339
 Db 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSLV 339

RESULT 2
 AAW44199
 ID AAW44199 standard; protein; 340 AA.
 AC AAW44199;
 XX
 XX
 DT 14-MAY-1998 (first entry)
 XX Human soluble receptor to an advanced glycosylation end product.
 DE Human; soluble receptor; advanced glycosylation end product; RAGE; AGE;
 KW antibody; vascular permeability; diabetes mellitus.
 XX Homo sapiens.
 OS
 EN W09739125-A1.
 XX
 XX 23-OCT-1997.
 XX
 XX 11-APR-1997; 97WO-EP001834.
 XX
 XX 16-APR-1996; 96US-00633148.
 XX
 XX (SCHD) SCHERING PATENTE AG.
 PA Morser MJ, Nagashima M, Hollander DA;
 XX WPI; 1997-558580/51.
 XX N-PSDB; AAV12394.
 DR
 DR Anti-advanced glycosylation end product polypeptide antibody - prevents
 PT receptor binding and therefore reduces vascular permeability, useful to
 PT treat diabetes mellitus.
 XX

PS Claim 2; Page 40-41; 90pp; English.
 XX
 CC The present sequence represents a soluble human receptor to an advanced
 CC glycosylation end product (RAGE) polypeptide. The present invention
 CC describes an isolated antibody (Ab), specifically immunoreactive with
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are non-
 CC enzymatically glycosylated proteins, which accumulate in vascular tissue
 CC in ageing, and at an accelerated rate in individuals with diabetes. The
 CC Ab, which prevents the interaction between an AGE and its receptor
 CC (RAGE), reduces vascular permeability. The Ab can be used to treat
 CC diabetes mellitus symptoms, e.g. microvasculopathy, occlusive vascular
 CC disorders, neuropathy, nephropathy, retinopathy, haemodialysis associated
 CC amyloidosis or atherosclerosis. The Ab can also be used for the isolation
 CC and purification of human RAGE polypeptide
 XX
 SQ Sequence 340 AA;

Query Match 99.8%; Score 1802; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 2.7e-127;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAGTAVGAWVLVLSLWGA VVGAQNITARI GEPLV LKCKGAPKPPORLEWKLNTGRTGA 60
 Db 1 MAAGTAVGAWVLVLSLWGA VVGAQNITARI GEPLV LKCKGAPKPPORLEWKLNTGRTGA 60
 QY 61 WKVLSPOGGP WDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVYQI 120
 Db 61 WKVLSPOGGP WDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVYQI 120
 QY 121 PGKPEIVDSASLTAGVKNKVTCTVSEGSYPAGTLSWHLGDKPLVPNEKGVSKVKEQTRRH 180
 Db 121 PGKPEIVDSASLTAGVKNKVTCTVSEGSYPAGTLSWHLGDKPLVPNEKGVSKVKEQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDPRTFTSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
 Db 181 PETGLFTLQSELMTVPARGGDPRTFTSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
 QY 241 VVEPEGGA VAPGTVTLTCEVPAQPSQIHHMKDGVPLPLPPSVLILPIGPDQGTYS 300
 Db 241 VVEPEGGA VAPGTVTLTCEVPAQPSQIHHMKDGVPLPLPPSVLILPIGPDQGTYS 300
 QY 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSL 338
 Db 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSL 338

RESULT 3
 AAW33753
 ID AAW33753 standard; protein; 340 AA.
 XX
 AC AAW33753;
 XX
 XX
 DT 08-MAY-1998 (first entry)
 XX Human RAGE polypeptide (340 amino acid residues).
 DE Advanced glycosylation end-product receptor; RAGE; screening; AGE;
 KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;
 KW Alzheimer's disease.
 XX Homo sapiens.
 OS
 XX W09739121-A1.
 XX
 XX 23-OCT-1997.
 XX
 XX 11-APR-1997; 97WO-EP001832.
 XX
 XX 16-APR-1996; 96US-00633147.
 XX (SCHD) SCHERING AG.
 XX Morser MJ, Nagashima M;
 PI

XX WPI; 1997-526458/48.
 DR N-PSDB; AAV06517.
 XX New soluble advanced glycosylation end-product receptor polypeptide -
 PT used for reducing vascular permeability, complications of diabetes etc.,
 PT also for purification and to screen for modulators.
 XX Claim 3; Fig 1A; 91pp; English.
 XX This is a human advanced glycosylation end-product receptor (RAGE)
 CC polypeptide (340 amino acid residues). The RAGE polypeptides and its
 CC active fragments or their mimetics, inhibit interaction between advanced
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They
 CC are used to treat diseases associated with AGE/RAGE interaction, such as
 CC increased vascular permeability, diabetes mellitus (particularly
 CC complications such as micro- or macro- vasculopathy or occlusive vascular
 CC disorders such as neuropathy, nephropathy, retinopathy or
 CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or
 CC age-related disorders such as oxidative stress. These RAGE polypeptides
 CC are also used, when immobilised, to purify AGE from a protein mixture and
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE
 CC interaction. They can also be used diagnostically to detect abnormal
 CC levels of AGE. Antibodies against RAGE polypeptides are useful as
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of
 CC interaction between AGE and RAGE or other receptors and for purification
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are
 CC used to express recombinant RAGE and as probes for isolating related
 CC genes
 XX Sequence 340 AA;
 SQ

Query Match
 Best Local Similarity 99.8%; Score 1802; DB 2; Length 340;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWAGVGAQNITARIIGBPLVLKCKGAPKPPQRLWKLTGRTEA 60
 DB 1 MAAGTAVGAWLVLSLWAGVGAQNITARIIGBPLVLKCKGAPKPPQRLWKLTGRTEA 60
 QY 61 WKVLSFQGGPNDVARVLNGLSLFLPAVGIQDEGIFRCQNNRNGKETKSNYRVYQI 120
 DB 61 WKVLSFQGGPNDVARVLNGLSLFLPAVGIQDEGIFRCQNNRNGKETKSNYRVYQI 120
 QY 121 PKGPETVDSASELTAGVPKNKVTGCVSEGSYPAGTILSHLDGKPLVNEKGVSKQTRRH 180
 DB 121 PKGPETVDSASELTAGVPKNKVTGCVSEGSYPAGTILSHLDGKPLVNEKGVSKQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDPRTTFCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
 DB 181 PETGLFTLQSELMTVPARGGDPRTTFCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
 QY 241 VVEPEGGAAPGTTLTCEVPAQSPQIHWKMDGVPPLPSPVLLPEIGPQDQGYTS 300
 DB 241 VVEPEGGAAPGTTLTCEVPAQSPQIHWKMDGVPPLPSPVLLPEIGPQDQGYTS 300
 QY 301 CVATHSSHGPQESRAVSIISIEPGEETAGSVGGSL 338
 DB 301 CVATHSSHGPQESRAVSIISIEPGEETAGSVGGSL 338

RESULT 4
 ADP19666
 ID ADP19666 standard; protein; 391 AA.
 XX ADP19666;
 AC ADP19666;
 XX 12-AUG-2004 (first entry)
 DT Human LP2005 protein SEQ ID NO:12.
 DE human; LP2005; antidiabetic; neuroprotective; neurotropic;
 XX

XX antinflammatory; antirheumatic; antiarthritic; vulnery; cytostatic;
 KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;
 KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;
 KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;
 KW systemic lupus erythematosus.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..23
 FT /label= signal
 FT Protein 24..391
 FT /label= LP2005
 XX WO2004044126-A2.
 PD 27-MAY-2004.
 XX 05-NOV-2003; 2003WO-US032734.
 XX 14-NOV-2002; 2002US-0426253P.
 XX (ELIL) LILLY & CO ELI.
 XX Na S, Perkins DR;
 PI WPI; 2004-411705/38.
 DR N-PSDB; ADP19665.
 XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or
 PT LP2003) for diagnosing or treating disorders associated with aberrant
 PT levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome
 PT identification.
 XX Claim 9; SEQ ID NO 12; 111pp; English.
 XX The present sequence represents human LP2005, which is used in the
 CC exemplification of the present invention. The present invention
 CC describes: (1) an isolated nucleic acid (I) comprising DNA having at
 CC least 95% sequence identity to a polynucleotide selected from the group
 CC consisting of: (a) a polynucleotide having a nucleotide sequence as shown
 CC in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a
 CC polypeptide or mature form of a polypeptide having the amino acid
 CC sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide
 CC fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide
 CC having a nucleotide sequence which is complementary to the nucleotide
 CC sequence of a polynucleotide as in (a), (b) or (c); (2) a vector
 CC comprising (1); (3) a host cell comprising the vector; (4) producing an
 CC LP polypeptide; (5) an isolated polypeptide produced by the above method
 CC and comprising an amino acid sequence comprising about 95% sequence
 CC identity to a sequence of amino acid residues comprising LP2001, LP2003,
 CC LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric
 CC molecule comprising an LP polypeptide fused to a heterologous amino acid
 CC sequence; (7) an antibody which specifically binds to an LP polypeptide
 CC described above; (8) a composition (C) comprising a therapeutic amount of
 CC an active agent selected from an LP polypeptide, an agonist to an LP
 CC polypeptide, an antagonist to an LP polypeptide, an LP polypeptide
 CC antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a
 CC polynucleotide in combination with a pharmaceutical carrier; and (9)
 CC diagnosing or treating a mammal suffering from a disease, condition or
 CC disorder associated with aberrant levels of an LP-polypeptide. (C) has
 CC antidiabetic, neuroprotective, neurotropic, antiinflammatory,
 CC antirheumatic, antiarthritic, vulnery, cytostatic, immunosuppressive,
 CC nephrotropic and dermatological activities, and can be used in gene
 CC therapy. The compositions (C) and methods are useful for diagnosing or
 CC treating disorders associated with aberrant levels of an LP polypeptide,
 CC such as diabetes and its complications, Alzheimer's disease,
 CC inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple
 CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They
 CC may also be used for chromosome identification. The LP polypeptide can
 CC also be used in manufacturing a medicament for the treatment of the above
 CC -mentioned diseases, conditions or disorders associated with aberrant
 CC levels of the LP polypeptide.

```

XX SQ      Sequence 391 AA;
Query Match      99.8%; Score 1802; DB 8; Length 391;
Best Local Similarity 100.0%; Pred. No. 3.2e-127;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAGVAGWLVLSLWGA VVGAQNITARI GEPLVKCKGAPKPPQRLWKLTGRTGA 60
DB 1 MAAGTAGVAGWLVLSLWGA VVGAQNITARI GEPLVKCKGAPKPPQRLWKLTGRTGA 60

QY 61 WKVLSPOGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETSRYRVYQI 120
DB 61 WKVLSPOGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETSRYRVYQI 120

QY 121 PKPPIVDSASELTAGVKNKVTGCVSEGSYPAGTILSWHLDGKPLVPNEKGVSKQTRRH 180
DB 121 PKPPIVDSASELTAGVKNKVTGCVSEGSYPAGTILSWHLDGKPLVPNEKGVSKQTRRH 180

QY 181 PETGLFTLOSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVLEEVOL 240
DB 181 PETGLFTLOSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVLEEVOL 240

QY 241 VVEPEGGA VGGTTLTCEVPAQPSQIHWKMDGVPLPPLPPSVLLIPGPDQGTYS 300
DB 241 VVEPEGGA VGGTTLTCEVPAQPSQIHWKMDGVPLPPLPPSVLLIPGPDQGTYS 300

QY 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSL 338
DB 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSL 338

RESULT 5
ADE95564
ID ADE95564 standard; protein; 402 AA.
XX AC ADE95564;
XX DT 12-FEB-2004 (first entry)
XX DE Human NOVX16c protein.
XX KW NOVX protein; biochemical stimulation; physiological stimulation;
KW cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
KW antirheumatic; antiarthritic; antidiabetic; nephrotropic; dermatological;
KW immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;
KW notropic; antipsoriatic; antiparkinsonian; antiasthmatic; neuroleptic;
KW antidepressant; antiallergic; gynaecological; gene therapy; vaccine;
KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;
KW cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;
KW psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;
KW Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;
KW depression; allergy; fertility disorder; NOVX16c.
XX OS Homo sapiens.
XX PN WO2003050245-A2.
XX PD 19-JUN-2003.
XX PF 03-DEC-2002; 2002WO-US038594.
XX PR 05-DEC-2001; 2001US-0336600P.
PR 07-DEC-2001; 2001US-0338285P.
PR 12-DEC-2001; 2001US-0341346P.
PR 17-DEC-2001; 2001US-0341477P.
PR 20-DEC-2001; 2001US-0341540P.
PR 27-DEC-2001; 2001US-0342592P.
PR 31-DEC-2001; 2001US-0344297P.
PR 17-APR-2002; 2001US-0344903P.
PR 15-MAY-2002; 2002US-0373288P.
PR 17-MAY-2002; 2002US-0380981P.
PR 17-MAY-2002; 2002US-0381495P.

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PR 28-MAY-2002; 2002US-0383534P.
PR 28-MAY-2002; 2002US-0383744P.
PR 29-MAY-2002; 2002US-0383829P.
PR 29-MAY-2002; 2002US-0384024P.
PR 07-AUG-2002; 2002US-0401788P.
PR 26-AUG-2002; 2002US-0403533P.
PR 31-OCT-2002; 2002US-04041788.
PR 02-DEC-2002; 2002US-04046353.
XX (CURA-) CURAGEN CORP.
XX PA
XX PI Alsbrook JP, Anderson DW, Boldog FH, Burgess CE, Chillakuru RA;
PI Reinger SR, Gerlach VL, Gorman L, Gould-Rothberg BS, Guo X;
PI Jeffers ME, Ji W, Li L, Malyankar UM, Miller CE, Murphy R;
PI Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG;
PI Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;
XX WPI; 2003-513974/48.
XX DR N-PSDB; ADE95563.
XX PT New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX PS Claim 2; SEQ ID NO 96; 211pp; English.
XX CC This invention relates to novel NOVX proteins, and the DNA sequence which
CC encode them, having properties related to stimulation of biochemical or
CC physiological responses in a cell, a tissue, an organ or an organism.
CC Compounds which modulate the proteins of the invention may have cardiant,
CC antiarteriosclerotic, hypotensive, cytostatic, anorectic, antirheumatic,
CC antiarthritic, antidiabetic, nephrotropic, dermatological,
CC immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,
CC notropic, antipsoriatic, antiparkinsonian, antiasthmatic, neuroleptic,
CC antidepressant, antiallergic or gynaecological activities. The DNA
CC sequences of the invention may be useful for gene therapy whilst the
CC protein sequences may allow the development of a vaccine. The protein is
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease. The invention may be useful in
CC diagnosing, treating or preventing NOVX-associated disorders, for example
CC cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
CC rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin
CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
CC Parkinson's disease, asthma, schizophrenia, depression, allergies or
CC fertility disorders. The nucleic acids may further be used as
CC hybridisation probes, in chromosome mapping, tissue typing, preventive
CC medicine, and pharmacogenomics. The present sequence is the amino acid
CC sequence of the human NOVX16c protein of the invention.
XX SQ      Sequence 402 AA;
Query Match      99.8%; Score 1802; DB 7; Length 402;
Best Local Similarity 100.0%; Pred. No. 3.3e-127;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAGVAGWLVLSLWGA VVGAQNITARI GEPLVKCKGAPKPPQRLWKLTGRTGA 60
DB 1 MAAGTAGVAGWLVLSLWGA VVGAQNITARI GEPLVKCKGAPKPPQRLWKLTGRTGA 60

QY 61 WKVLSPOGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETSRYRVYQI 120
DB 61 WKVLSPOGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETSRYRVYQI 120

QY 121 PKPPIVDSASELTAGVKNKVTGCVSEGSYPAGTILSWHLDGKPLVPNEKGVSKQTRRH 180
DB 121 PKPPIVDSASELTAGVKNKVTGCVSEGSYPAGTILSWHLDGKPLVPNEKGVSKQTRRH 180

QY 181 PETGLFTLOSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVLEEVOL 240
DB 181 PETGLFTLOSELMTVPARGDPRPTFSCFSFGLPRHRLRTAPIQPRVWEPVLEEVOL 240

QY 241 VVEPEGGA VGGTTLTCEVPAQPSQIHWKMDGVPLPPLPPSVLLIPGPDQGTYS 300

```

Db 241 VVEPEGGA... 300
QY 301 CVATHSSHGP... 338
Db 301 CVATHSSHGP... 338
RESULT 6
ID AAB81925 standard; protein; 404 AA.
XX AAB81925;
DT 15-JUN-2001 (first entry)
XX Extracorporeal circulation material receptor protein.
DE Extracorporeal circulation; carbonyl stress product; receptor; diabetes;
KW vascular lesion; excretory dysfunction.
XX Unidentified.
OS WO200118060-A1.
PN 15-MAR-2001.
PD 08-SEP-2000; 2000WO-JP006172.
PF 08-SEP-1999; 99JP-00254463.
PR (TORA) TORAY IND INC.
XX Shimizu S, Kubota M, Akiyama H, Usui M;
PI WPI; 2001-290314/30.
DR Material for extracorporeal circulation, applicable in selective
PT elimination of diabetic complication factors such as carbonyl stress
PT products caused by abnormally promoted carbonyl stress from excretory
PT dysfunction in vascular lesions.
XX Claim 1; Page 31-32; 36pp; Japanese.
PS The present invention describes a material for extracorporeal circulation
XX which is made from a water-insoluble carrier immobilized with a protein
CC having the sequence shown here. The materials of the invention, including
CC adsorbents, are for extracorporeal circulation, which are applicable in
CC the selective elimination of diabetic complication factors from a body
CC fluid, and are therefore useful in treating vascular lesions like
CC arteriosclerosis due to carbonyl stress products caused by abnormally
CC promoted carbonyl stress from excretory dysfunction
XX Sequence 404 AA;
SQ Query Match 99.8%; Score 1802; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 3.3e-127;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAGTAVGAWLVLSLWAGVGAQNTARIGEPVLKCKGAPKPPQRLWKLTGRTEA 60
Db 1 MAAGTAVGAWLVLSLWAGVGAQNTARIGEPVLKCKGAPKPPQRLWKLTGRTEA 60
QY 61 WKVLSPQGGPVDVARVLPNGSLFPAVGIODEGIFRCQAMNRNGKTSNRYRVYQI 120
Db 61 WKVLSPQGGPVDVARVLPNGSLFPAVGIODEGIFRCQAMNRNGKTSNRYRVYQI 120
QY 121 PGKPEIVDSASELTAGVPKNGVTCVSEGSYPAGTSLSHWLDGKPLVNEKGVSKQETRRH 180
Db 121 PGKPEIVDSASELTAGVPKNGVTCVSEGSYPAGTSLSHWLDGKPLVNEKGVSKQETRRH 180
QY 181 PETGLFTLQSELMTVPARGDPRPTSCFSGLPRHRLTAPIQPRVWVEPVLVEVQL 240

Db 181 PETGLFTLQSELMTVPARGDPRPTSCFSGLPRHRLTAPIQPRVWVEPVLVEVQL 240
QY 241 VVEPEGGA... 300
Db 241 VVEPEGGA... 300
QY 301 CVATHSSHGP... 338
Db 301 CVATHSSHGP... 338
RESULT 7
ID ABP65011 standard; protein; 404 AA.
XX ABP65011;
DT 25-FEB-2003. (first entry)
XX Human protein SEQ ID 671.
DE Human; expressed sequence tag; EST; haematopoietic disorder;
KW central nervous system disease; viral infection;
KW peripheral nervous system disease; non-healing wound; infectious disease;
KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;
KW fungal infection; autoimmune disorder; coagulation disorder; neutropenic;
KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;
KW cytostatic; haemostatic; virucide; antibacterial; fungicide;
KW immunostimulant; cerebroprotective.
XX Homo sapiens.
OS WO200259260-A2.
PN 01-AUG-2002.
PD 16-NOV-2001; 2001WO-US042950.
PF 17-NOV-2000; 2000US-00714936.
PR (HYSE-) HYSEQ INC.
XX Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;
PI Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX WPI; 2002-590824/63.
DR N-PSDB; ABQ99597.
XX New isolated polynucleotide, useful in research, diagnostic or
PT therapeutic methods, e.g. preventing or treating disorders involving
PT aberrant protein expression or biological activity.
XX Claim 20; SEQ ID NO 671; 394pp; English.
PS The present invention relates to novel human coding sequences (ABQ99268-
XX ABQ99608) and proteins (ABP64682-ABP65022). The sequences are useful in
CC therapeutic, diagnostic and research methods. The polynucleotides may be
CC used in the field of molecular biology as hybridisation probes, primers
CC for PCR, for chromosome and gene mapping, for the recombinant production
CC of protein, or in generation of anti-sense DNA or RNA. The
CC polynucleotides are useful in diagnostics as expressed sequence tags
CC (ESTs) for identifying expressed genes or for physical mapping of the
CC human genome. The proteins may be used as molecular weight markers, or as
CC nutritional sources or supplements. The proteins may be used to maintain
CC and expand cell population in a totipotent or pluripotent state
CC useful for re-engineering damaged or diseased tissues, transplantation,
CC manufacture of bio-pharmaceuticals or the development of bio-sensors. The
CC polynucleotides and proteins are useful for preventing, treating or
CC ameliorating disorders involving aberrant protein expression or
CC neurological activity, e.g. haematopoietic disorders, central/peripheral
CC nervous system diseases, mechanical and traumatic disorders, non-healing
CC wounds, immune deficiencies and disorders, infectious diseases caused by
CC viral, bacterial or fungal infection, autoimmune disorders, allergic

CC reactions and conditions, coagulation disorders, or cancer. The
 CC polynucleotide sequences of the invention were assembled from ESTs
 CC isolated mainly by sequencing by hybridisation, and in some cases,
 CC sequences obtained from one or more public databases. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 XX
 SQ Sequence 404 AA;

Query Match
 Best Local Similarity 99.8%; Score 1802; DB 5; Length 404;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGA VVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTEA 60
 DB 1 MAAGTAVGAWLVLSLWGA VVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTEA 60
 QY 61 WKVLSPOGGP WDSVARVLPNGSLFLPAVG IQDEGIFRCQAMNRNGKETKSNYRVRYQI 120
 DB 61 WKVLSPOGGP WDSVARVLPNGSLFLPAVG IQDEGIFRCQAMNRNGKETKSNYRVRYQI 120
 QY 121 PGKPEIVDSASELTAGVPNKVGTCSSEGSYPAGTLSWHL DKGKPLVPNEKGSVKEQTRRH 180
 DB 121 PGKPEIVDSASELTAGVPNKVGTCSSEGSYPAGTLSWHL DKGKPLVPNEKGSVKEQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLARTAPIQPRVWEPVPLEEVOL 240
 DB 181 PETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLARTAPIQPRVWEPVPLEEVOL 240
 QY 241 VVEPEGGA VAPGGTVTLTCEVPAQSPQIHWMDGVP LPLPPSPVLILPEIGPDQGTYS 300
 DB 241 VVEPEGGA VAPGGTVTLTCEVPAQSPQIHWMDGVP LPLPPSPVLILPEIGPDQGTYS 300
 QY 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338
 DB 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338

RESULT 8
 ADF31292
 ID ADF31292 standard; protein; 404 AA.
 XX
 AC ADF31292;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human receptor of advanced glycation end products (RAGE).
 XX
 KW human; receptor; advanced glycation end product; RAGE;
 KW receptor of advanced glycation end product; high yield; high purity.
 XX
 OS Homo sapiens.
 XX
 PN JP2003306500-A.
 XX
 PD 28-OCT-2003.
 XX
 PF 05-FEB-2003; 2003JP-00027992.
 XX
 PR 15-FEB-2002; 2002JP-00038380.
 XX
 PA (TORA) TORAY IND INC.
 XX
 DR WPI; 2004-015267/02.
 XX
 PT Purifying receptor of advanced glycation end products derivative
 PT containing IGV domain of receptor of advanced glycation end product using
 PT one or more affinity columns.
 XX
 PS Disclosure; SEQ ID NO 1; 13pp; Japanese.
 XX
 CC The invention relates to a method of purifying a receptor of advanced

CC glycation end products (RAGE) derivative. The method is useful for
 CC purifying receptor of advanced glycation end product derivative. The
 CC method enables simple, rapid with high yield and high purity manufacture
 CC of RAGE derivative. The present sequence represents the amino acid
 CC sequence of human receptor of advanced glycation end products (RAGE).
 XX
 XX
 SQ Sequence 404 AA;

Query Match
 Best Local Similarity 99.8%; Score 1802; DB 8; Length 404;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGA VVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTEA 60
 DB 1 MAAGTAVGAWLVLSLWGA VVGAQNTARIGEPVLVKCKGAPKPPORLEWKLNTGRTEA 60
 QY 61 WKVLSPOGGP WDSVARVLPNGSLFLPAVG IQDEGIFRCQAMNRNGKETKSNYRVRYQI 120
 DB 61 WKVLSPOGGP WDSVARVLPNGSLFLPAVG IQDEGIFRCQAMNRNGKETKSNYRVRYQI 120
 QY 121 PGKPEIVDSASELTAGVPNKVGTCSSEGSYPAGTLSWHL DKGKPLVPNEKGSVKEQTRRH 180
 DB 121 PGKPEIVDSASELTAGVPNKVGTCSSEGSYPAGTLSWHL DKGKPLVPNEKGSVKEQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLARTAPIQPRVWEPVPLEEVOL 240
 DB 181 PETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLARTAPIQPRVWEPVPLEEVOL 240
 QY 241 VVEPEGGA VAPGGTVTLTCEVPAQSPQIHWMDGVP LPLPPSPVLILPEIGPDQGTYS 300
 DB 241 VVEPEGGA VAPGGTVTLTCEVPAQSPQIHWMDGVP LPLPPSPVLILPEIGPDQGTYS 300
 QY 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338
 DB 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338

RESULT 9
 ADF42983
 ID ADF42983 standard; protein; 404 AA.
 XX
 AC ADF42983;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human receptor of advanced glycation (RAGE) protein.
 XX
 KW diabetic complication factor; receptor of advanced glycation end product;
 KW RAGE binding substance adsorption ligand; water-insoluble carrier;
 KW biological evaluation; diabetic complication; renal-disease; human.
 XX
 OS Homo sapiens.
 XX
 PN JP2003306499-A.
 XX
 PD 28-OCT-2003.
 XX
 PF 05-FEB-2003; 2003JP-00027991.
 XX
 PR 15-FEB-2002; 2002JP-00038378.
 XX
 PA (TORA) TORAY IND INC.
 XX
 DR WPI; 2004-015266/02.
 XX
 PT Obtaining diabetic complication factor comprises contacting biological
 PT fluid with adsorbent, and immobilizing receptor of advanced glycation end
 PT products binding substance ligand on carrier.
 XX
 PS Disclosure; SEQ ID NO 1; 18pp; Japanese.
 XX
 CC This invention relates to a novel method of obtaining a diabetic
 CC complication factor which comprises contacting liquid from a biological

CC fluid with an adsorbent which immobilises a receptor of advanced
 CC glycation end products (RAGE) binding substance adsorption ligand on a
 CC water-insoluble carrier, cleaning the adsorbent in an aqueous solution,
 CC separating and recovering the diabetically complicated factor by contacting
 CC the adsorbent with the aqueous solution. The method is useful for
 CC carrying out biological evaluation which involves determining advanced
 CC degree of diabetically complicated or degree of a renal-disease.
 XX
 SQ Sequence 404 AA;

Query Match 99.8%; Score 1802; DB 8; Length 404;
 Best Local Similarity 100.0%; Pred. No. 3.3e-127; Indels 0; Gaps 0;
 Matches 338; Conservative 0; Mismatches 0;

QY 1 MAAGTAVGAWLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60
 DB 1 MAAGTAVGAWLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60
 QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTSNYRVRYQI 120
 DB 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTSNYRVRYQI 120
 QY 121 PGKPEIVDSASELTAGVPKNGVTCVSEGSYPAGTILSHWLDGKPLVNEKGVSKETRHH 180
 DB 121 PGKPEIVDSASELTAGVPKNGVTCVSEGSYPAGTILSHWLDGKPLVNEKGVSKETRHH 180
 QY 181 PETGLFTLQSELMTVPARGGDRPTFSCFSGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
 DB 181 PETGLFTLQSELMTVPARGGDRPTFSCFSGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
 QY 241 VVEPEGAVAPGCTVTLTCEVPAQPSQIHHMKDGVPLPLPSPVLLPEIGPDQGTYS 300
 DB 241 VVEPEGAVAPGCTVTLTCEVPAQPSQIHHMKDGVPLPLPSPVLLPEIGPDQGTYS 300
 QY 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSL 338
 DB 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSL 338

RESULT 10
 ADK00129
 ID ADK00129 standard; protein; 404 AA.
 AC ADK00129;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human RAGE protein.
 XX
 KW Advanced Glycation End Product Ligand Binding Element; RAGE-LBE;
 KW Cytostatic; Antidiabetic; Nootropic; Antiarthritic; Osteopathic;
 KW Neuroprotective; Antiinflammatory; Dermatological; Immunosuppressive;
 KW Vasotropic; Antipruritic; Antibacterial; Antiartherosclerotic;
 KW amyloidosis; cancer; Crohn's disease; diabetes; Alzheimer's disease;
 KW Chronic inflammatory disease; osteoarthritis; irritable bowel disease;
 KW multiple sclerosis; psoriasis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN WO2004016229-A2.
 XX
 PD 26-FEB-2004.
 XX
 PP 18-AUG-2003; 2003WO-US025996.
 XX
 PR 16-AUG-2002; 2002US-040205P.
 XX
 PA (AMHP) WYETH.
 XX
 PI Pittman DD, Clancy B, Larsen G, Trepicchio WL, Brennan FM;
 PI Feldmann M, Foxwell BJM, Feldman JL;
 XX

DR WPI; 2004-192067/18.
 XX N-PSDB; ADK00130.
 XX
 PT New fusion protein comprising a Receptor for Advanced Glycation End
 PT Product Ligand Binding Element (RAGE-LBE) and an immunoglobulin element,
 PT useful for preparing a composition for treating e.g., Alzheimer's
 PT disease.
 XX
 PS Disclosure; SEQ ID NO 43; 100pp; English.
 XX
 CC The present invention relates to a new fusion protein comprising a
 CC Receptor for Advanced Glycation End Product Ligand Binding Element (RAGE-
 CC LBE) and an immunoglobulin element. The fusion protein is useful for
 CC preparing a composition for treating RAGE-associated disorders such as
 CC amyloidosis, cancer, Crohn's disease, diabetes, complications of
 CC retinopathies and/or neuropathies; Alzheimer's disease, chronic
 CC inflammatory disease e.g., rheumatoid arthritis, osteoarthritis,
 CC irritable bowel disease, multiple sclerosis, psoriasis or lupus, acute
 CC inflammatory disease e.g., sepsis, or cardiovascular disease, e.g.,
 CC atherosclerosis or restenosis. The present sequence represents human RAGE
 CC protein.
 XX
 SQ Sequence 404 AA;

Query Match 99.8%; Score 1802; DB 8; Length 404;
 Best Local Similarity 100.0%; Pred. No. 3.3e-127;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60
 DB 1 MAAGTAVGAWLVLSLWGAVVGAQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60
 QY 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTSNYRVRYQI 120
 DB 61 WKVLSPOGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTSNYRVRYQI 120
 QY 121 PGKPEIVDSASELTAGVPKNGVTCVSEGSYPAGTILSHWLDGKPLVNEKGVSKETRHH 180
 DB 121 PGKPEIVDSASELTAGVPKNGVTCVSEGSYPAGTILSHWLDGKPLVNEKGVSKETRHH 180
 QY 181 PETGLFTLQSELMTVPARGGDRPTFSCFSGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
 DB 181 PETGLFTLQSELMTVPARGGDRPTFSCFSGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
 QY 241 VVEPEGAVAPGCTVTLTCEVPAQPSQIHHMKDGVPLPLPSPVLLPEIGPDQGTYS 300
 DB 241 VVEPEGAVAPGCTVTLTCEVPAQPSQIHHMKDGVPLPLPSPVLLPEIGPDQGTYS 300
 QY 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSL 338
 DB 301 CVATHSSHGPOESRAVSISIIIEPGEETAGSVGGSL 338

RESULT 11
 AAM48746
 ID AAM48746 standard; protein; 339 AA.
 XX
 AC AAM48746;
 XX
 DT 02-APR-2002 (first entry)
 XX
 DE Human sRAGE protein SEQ ID NO 2.
 XX
 KW Human; RAGE; receptor for advanced glyated endproduct; receptor;
 KW antidiabetic; neuroprotective; cytostatic; antiinflammatory; vasotropic;
 KW nephrotropic; dermatological; antiatherosclerotic; nootropic; diabetes;
 KW Alzheimer's disease; cancer; inflammation; kidney failure;
 KW systemic lupus; nephritis; erectile dysfunction; atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 FN WO200192892-A2.

XX PD 06-DEC-2001.
 XX PF 30-MAY-2001; 2001WO-US017447.
 XX PR 30-MAY-2000; 2000US-0207342P.
 XX PR 05-MAR-2001; 2001US-00799152.
 XX PA (TRAN-) TRANS TECH PHARMA.
 XX PI Shahbaz M;
 XX DR WPI; 2002-114372/15.
 XX PT Detecting a receptor for advanced glycosylated endproducts (RAGE) modulators,
 XX PT for treating e.g., cancer, diabetes or inflammation, comprises measuring
 XX PT the amount of bound anti-RAGE antibody.
 XX PS Claim 2; Fig 2; 49pp; English.
 XX CC The invention relates to detecting receptor for advanced glycosylated
 XX CC endproducts (RAGE) modulators comprising determining the amount of RAGE
 XX CC protein or its fragment bound to the pre-adsorbed ligand by measuring the
 XX CC amount of anti-RAGE antibody bound to the solid surface. The method is
 XX CC useful for rapid, high-throughput identification of compounds that
 XX CC modulate RAGE. The compounds are useful for treating symptoms of diabetes
 XX CC and symptoms of diabetic late complications, amyloidosis, Alzheimer's
 XX CC disease, cancer, inflammation, kidney failure, systemic lupus nephritis
 XX CC or inflammatory lupus nephritis, erectile dysfunction and atherosclerosis
 XX CC
 XX CC Sequence 339 AA;

Query Match 99.5%; Score 1797; DB 5; Length 339;
 Best Local Similarity 100.0%; Pred. No. 6.3e-127;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AAGTAVGAWLVLSLWGA VVGAQNITARI GEPLVLCCKGAPKPPORLEWKLNTGRTEAW 61
 DB 2 AAGTAVGAWLVLSLWGA VVGAQNITARI GEPLVLCCKGAPKPPORLEWKLNTGRTEAW 61
 QY 62 KVLSPQGGPWDSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQIP 121
 DB 62 KVLSPQGGPWDSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQIP 121
 QY 122 GKPEIVDSASLTAGVPNKVGTCTVSEGSYPAGTLSWHLGDKPLVPNEKGVSKQTRRHP 181
 DB 122 GKPEIVDSASLTAGVPNKVGTCTVSEGSYPAGTLSWHLGDKPLVPNEKGVSKQTRRHP 181
 QY 182 ETGLFTLQSELMTVPARGDPRTFTSCSPGLPRHRLTAPIQPRVWEPVPLEEVQV 241
 DB 182 ETGLFTLQSELMTVPARGDPRTFTSCSPGLPRHRLTAPIQPRVWEPVPLEEVQV 241
 QY 242 VEPEGGA VAPGGTVTLTCEVPAQPSQIHWMDGVPLPLPPSPVLLPEIGPDQGTYS 301
 DB 242 VEPEGGA VAPGGTVTLTCEVPAQPSQIHWMDGVPLPLPPSPVLLPEIGPDQGTYS 301
 QY 302 VATHSHGPOESRAVSISIIIEPEGEGTAGSVGGSL 338
 DB 302 VATHSHGPOESRAVSISIIIEPEGEGTAGSVGGSL 338

RESULT 12
 AAM48745
 ID AAM48745 standard; protein; 404 AA.
 XX AAM48745;
 AC AAM48745;
 XX
 DT 02-APR-2002 (first entry)
 XX Human RAGE protein SEQ ID NO 1.
 DE
 DE Human; RAGE; receptor for advanced glycosylated endproduct; receptor;
 KW antidiabetic; neuroprotective; cytostatic; antiinflammatory; vasotropic;
 KW

KW nephrotropic; dermatological; antiarteriosclerotic; nootropic; diabetes;
 KW Alzheimer's disease; cancer; inflammation; kidney failure;
 KW systemic lupus; nephritis; erectile dysfunction; atherosclerosis.
 XX Homo sapiens.
 OS
 XX
 PN WC200192892-A2.
 PD
 XX 06-DEC-2001.
 XX
 XX 30-MAY-2001; 2001WO-US017447.
 XX
 XX 30-MAY-2000; 2000US-0207342P.
 XX PR 05-MAR-2001; 2001US-00799152.
 XX
 XX (TRAN-) TRANS TECH PHARMA.
 XX PA
 XX Shahbaz M;
 PI
 XX WPI; 2002-114372/15.
 DR
 XX Detecting a receptor for advanced glycosylated endproducts (RAGE) modulators,
 XX PT for treating e.g., cancer, diabetes or inflammation, comprises measuring
 XX PT the amount of bound anti-RAGE antibody.
 XX PS Claim 1; Fig 2; 49pp; English.
 XX CC The invention relates to detecting receptor for advanced glycosylated
 XX CC endproducts (RAGE) modulators comprising determining the amount of RAGE
 XX CC protein or its fragment bound to the pre-adsorbed ligand by measuring the
 XX CC amount of anti-RAGE antibody bound to the solid surface. The method is
 XX CC useful for rapid, high-throughput identification of compounds that
 XX CC modulate RAGE. The compounds are useful for treating symptoms of diabetes
 XX CC and symptoms of diabetic late complications, amyloidosis, Alzheimer's
 XX CC disease, cancer, inflammation, kidney failure, systemic lupus nephritis
 XX CC or inflammatory lupus nephritis, erectile dysfunction and atherosclerosis
 XX CC
 XX CC Sequence 404 AA;

Query Match 99.5%; Score 1797; DB 5; Length 404;
 Best Local Similarity 100.0%; Pred. No. 7.8e-127;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AAGTAVGAWLVLSLWGA VVGAQNITARI GEPLVLCCKGAPKPPORLEWKLNTGRTEAW 61
 DB 2 AAGTAVGAWLVLSLWGA VVGAQNITARI GEPLVLCCKGAPKPPORLEWKLNTGRTEAW 61
 QY 62 KVLSPQGGPWDSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQIP 121
 DB 62 KVLSPQGGPWDSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQIP 121
 QY 122 GKPEIVDSASLTAGVPNKVGTCTVSEGSYPAGTLSWHLGDKPLVPNEKGVSKQTRRHP 181
 DB 122 GKPEIVDSASLTAGVPNKVGTCTVSEGSYPAGTLSWHLGDKPLVPNEKGVSKQTRRHP 181
 QY 182 ETGLFTLQSELMTVPARGDPRTFTSCSPGLPRHRLTAPIQPRVWEPVPLEEVQV 241
 DB 182 ETGLFTLQSELMTVPARGDPRTFTSCSPGLPRHRLTAPIQPRVWEPVPLEEVQV 241
 QY 242 VEPEGGA VAPGGTVTLTCEVPAQPSQIHWMDGVPLPLPPSPVLLPEIGPDQGTYS 301
 DB 242 VEPEGGA VAPGGTVTLTCEVPAQPSQIHWMDGVPLPLPPSPVLLPEIGPDQGTYS 301
 QY 302 VATHSHGPOESRAVSISIIIEPEGEGTAGSVGGSL 338
 DB 302 VATHSHGPOESRAVSISIIIEPEGEGTAGSVGGSL 338

RESULT 13
 ADS10986
 ID ADS10986 standard; protein; 381 AA.
 XX
 AC ADS10986;

XX 16-DEC-2004 (first entry)
XX Human therapeutic protein - SEQ ID 1223.
XX
XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy.
XX
XX Homo sapiens.
XX
XX WO2004080148-A2.
XX
XX 23-SEP-2004.
XX
XX 30-SEP-2003; 2003WO-US030720.
XX
XX 02-OCT-2002; 2002US-0416186P.
XX
XX (NUVE-) NUVELO INC.
XX
XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX
XX WPI; 2004-668857/65.
XX N-PSDB; ADS10302.
XX
XX New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.
XX
XX Claim 20; SEQ ID NO 1223; 718pp; English.
XX
XX The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic protein
CC of the invention. The current sequence is not shown explicitly within the
CC specification but can be accessed from the WIPO web-site.
XX
XX Sequence 381 AA;
XX
XX Query Match 99.4%; Score 1796; DB 8; Length 381;
XX Best Local Similarity 99.7%; Pred. No. 8.7e-127; Indels 0; Gaps 0;
XX Matches 337; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAAAGTAVGAWVLVLSLWGVGAVGAGQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTEA 60
DB 1 MAAAGTAVGAWVLVLSLWGVGAVGAGQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTEA 60
QY 61 WKVLSPPQGGPNDVSARVLPNGSLFLPVGIODEGIFRCQAMNRNGKETKSNYRVRYQI 120
DB 61 WKVLSPPQGGPNDVSARVLPNGSLFLPVGIODEGIFRCQAMNRNGKETKSNYRVRYQI 120
QY 121 PKGPEIVDSASELTAGVPKNKGVTCSEGSYPAGTILSWHLDDGKPLVNEKGVSKQTRRH 180
DB 121 PKGPEIVDSASELTAGVPKNKGVTCSEGSYPAGTILSWHLDDGKPLVNEKGVSKQTRRH 180
QY 181 PETGLFTLQSELMVTPARGCDPRPTSCFSFGLPRHRLARTAPQPRVWEPVPLEEVOL 240
DB 181 PETGLFTLQSELMVTPARGCDPRPTSCFSFGLPRHRLARTAPQPRVWEPVPLEEVOL 240
QY 241 VVEPEGAVAPGTVTLTCEVPAQSPQIHMKDGVPLPLPPSPVLILPEIGPQGGTYS 300
DB 241 VVEPEGAVAPGTVTLTCEVPAQSPQIHMKDGVPLPLPPSPVLILPEIGPQGGTYS 300
QY 301 CVATHSSHGPQBSRAVSIISIBPEGEGPTAGSVGGSL 338
DB 301 CVATHSSHGPQBSRAVSIISIBPEGEGPTAGSVGGSL 338

RESULT 14
AAU77543
ID AAU77543 standard; protein; 404 AA.
XX
XX AC AAU77543;
XX
XX 05-JUN-2002 (first entry)
XX Human receptor for advanced glycosylation end product (RAGE).
XX
XX Receptor for advanced glycation end product; RAGE; receptor;
KW amyloid beta peptide; blood-brain barrier; neurovascular stress;
KW cerebral vasoconstriction suppressor; cerebral blood flow enhancer;
KW cerebral amyloid angiopathy; transgenic animal; amyloid beta precursor;
KW Alzheimer's disease; Down's syndrome; head trauma; stroke; human.
XX
XX OS Homo sapiens.
XX
XX WO200214519-A1.
XX
XX 21-FEB-2002.
XX
XX 14-AUG-2001; 2001WO-US025416.
XX
XX 14-AUG-2000; 2000US-00638648.
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Stern DM, Schmidt AM; Yan SD, Zlokovic B;
PI WPI; 2002-257610/30.
XX N-PSDB; ABK10856.
XX
XX Ameliorating neurovascular stress and decreasing cerebral
PT vasoconstriction in subject suffering from chronic/acute cerebral amyloid
PT angiopathy, by administering inhibitor of receptor for advanced glycation
PT endproduct.
XX
XX Disclosure; Page 16; 68pp; English.
XX
XX The invention describes a method of ameliorating neurovascular stress,
CC and decreasing cerebral vasoconstriction in subject suffering from
CC chronic or acute cerebral amyloid angiopathy, comprising administering an
CC inhibitor (I) of receptor for advanced glycation end product (RAGE). (I)
CC inhibits transcytosis of amyloid beta peptides across blood-brain
CC barrier, thus decreasing cerebral vasoconstriction and increasing
CC cerebral blood flow. (I) is useful for treating amyloid angiopathy in a
CC subject, decreasing cerebral vasoconstriction in a transgenic non-human
CC animal (preferably, transgenic mouse overexpressing mutant human amyloid
CC beta precursor protein) or a human, suffering from chronic or acute
CC cerebral amyloid angiopathy, preferably, Alzheimer's disease, and for
CC ameliorating neurovascular stress comprising cerebral amyloid angiopathy
CC in a subject, where the neurovascular stress is caused by Alzheimer's
CC disease, aging, Down's syndrome, head trauma or stroke. This is the amino
CC acid sequence of human receptor for advanced glycation end product (RAGE)
CC described in the invention
XX
XX Sequence 404 AA;
XX
XX Query Match 99.3%; Score 1793; DB 5; Length 404;
XX Best Local Similarity 99.7%; Pred. No. 1.6e-126;
XX Matches 336; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 AAGTAVGAWVLVLSLWGVGAVGAGQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTEAM 61
DB 2 AAGTAVGAWVLVLSLWGVGAVGAGQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTEAM 61
QY 62 KVLSPQGGPNDVSARVLPNGSLFLPVGIODEGIFRCQAMNRNGKETKSNYRVRYQIP 121
DB 62 KVLSPQGGPNDVSARVLPNGSLFLPVGIODEGIFRCQAMNRNGKETKSNYRVRYQIP 121

QY 122 GKPEIVDSASELTAGVFNKVTCTVSEGSYPAGTILSHWLDGKPLVPNEKGVSVKEQTRRHP 181
 Db 122 GKPEIVDSASELTAGVFNKVTCTVSEGSYPAGTILSHWLDGKPLVPNEKGVSVKEQTRRHP 181
 QY 182 ETGLFTLOSELMTVPARGDPRPTFSCFSFGLPRHRALRTAPIQPRVWEPVPLEEVQLV 241
 Db 182 ETGLFTLOSELMTVPARGDPRPTFSCFSFGLPRHRALRTAPIQPRVWEPVPLEEVQLV 241
 QY 242 VEPGGAVAPGTVTLTCEVPAQSPQIHMMKDGVPPLPRSPVLIILPEIGPODQGTYS 301
 Db 242 VEPGGAVAPGTVTLTCEVPAQSPQIHMMKDGVPPLPRSPVLIILPEIGPODQGTYS 301
 QY 302 VATHSHGQPQSRVAVSIIIEPGEETAGSVGGSG 338
 Db 302 VATHSHGQPQSRVAVSIIIEPGEETAGSVGGSG 338

RESULT 15

AAE23219
 ID AAE23219 standard; protein; 404 AA.

XX AC AAE23219;

XX DT 27-AUG-2002 (first entry)

XX DE Human receptor for advanced glycosylation end product (RAGE) protein.

XX KW Human; Receptor for advanced glycosylation end product; RAGE; cardiant;
 KW tissue growth; neointimal formation; blood vessel; restenosis; diabetes;
 KW myocardial infarction; angioplasty; peripheral vascular surgery; angina;
 KW transgenic animal; acute thrombotic stroke; venous thrombosis.

XX OS Homo sapiens.

XX PN WO200230889-A2.

XX PD 18-APR-2002.

XX PF 12-OCT-2001; 2001WO-US032036.

XX PR 13-OCT-2000; 2000US-00687528.

XX PA (UYCO) UNIV COLUMBIA NEW YORK.

XX PI Stern DM, Schmidt A, Marso S, Topol E, Lincoff AM;

XX DR WPI; 2002-426260/45.

XX DR N-PSDB; AAD36952.

XX PT Inhibiting new tissue growth or neointimal formation in blood vessels of
 PT subject suffering from diabetes, stroke and preventing restenosis,
 PT comprises administering inhibitor of receptor for advance glycation end
 PT product.

XX PS Disclosure; Page 16; 43pp; English.

XX CC The invention relates to a method for inhibiting new tissue growth or
 CC neointimal formation in blood vessels in a subject that has experienced
 CC blood vessel injury and preventing exaggerated restenosis in a diabetic
 CC subject. The method comprises administering an inhibitor of receptor for
 CC advanced glycation/glycosylation end product (RAGE), so as to inhibit new
 CC tissue growth or neointimal formation in subject's blood vessels and
 CC preventing restenosis in the subject. The method is useful for inhibiting
 CC new tissue growth or neointimal formation in blood vessels in a subject
 CC like non-human animal, a transgenic non-human animal or a human suffering
 CC from diabetes, acute thrombotic stroke, venous thrombosis, unstable
 CC angina, myocardial infarction, abrupt closure following angioplasty or
 CC stent placement, or thrombosis as a result of peripheral vascular surgery
 CC The method is also useful for preventing restenosis and for determining
 CC whether a compound inhibits new tissue growth in a blood vessel in a
 CC subject. The present sequence is human receptor for advanced
 CC glycosylation end product (RAGE) protein

XX

SQ Sequence 404 AA;

Query Match 99.3%; Score 1793; DB 5; Length 404;
 Best Local Similarity 99.7%; Pred. No. 1.6e-126;
 Matches 336; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGTAVGAWVLVLSLWGVAVGAQNTARIGEPVLVKCKGAPKKPPORLEWKINTGRTAW 61
 Db 2 AAGTAVGAWVLVLSLWGVAVGAQNTARIGEPVLVKCKGAPKKPPORLEWKINTGRTAW 61
 QY 62 KVLSPQGGGPMDSVARVLPNGSLFLPAVGIODEGIFRCOAMNRNGKETKSNYRVRVYQIP 121
 Db 62 KVLSPQGGGPMDSVARVLPNGSLFLPAVGIODEGIFRCOAMNRNGKETKSNYRVRVYQIP 121
 QY 122 GKPEIVDSASELTAGVFNKVTCTVSEGSYPAGTILSHWLDGKPLVPNEKGVSVKEQTRRHP 181
 Db 122 GKPEIVDSASELTAGVFNKVTCTVSEGSYPAGTILSHWLDGKPLVPNEKGVSVKEQTRRHP 181
 QY 182 ETGLFTLOSELMTVPARGDPRPTFSCFSFGLPRHRALRTAPIQPRVWEPVPLEEVQLV 241
 Db 182 ETGLFTLOSELMTVPARGDPRPTFSCFSFGLPRHRALRTAPIQPRVWEPVPLEEVQLV 241
 QY 242 VEPGGAVAPGTVTLTCEVPAQSPQIHMMKDGVPPLPRSPVLIILPEIGPODQGTYS 301
 Db 242 VEPGGAVAPGTVTLTCEVPAQSPQIHMMKDGVPPLPRSPVLIILPEIGPODQGTYS 301
 QY 302 VATHSHGQPQSRVAVSIIIEPGEETAGSVGGSG 338
 Db 302 VATHSHGQPQSRVAVSIIIEPGEETAGSVGGSG 338

Search completed: March 15, 2005, 11:27:10
 Job time : 81 secs

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OM protein - protein search, using sw model

Run on: March 15, 2005, 10:43:33 ; Search time 27 Seconds
(without alignments)
937.260 Million cell updates/sec

Title: US-10-091-019-3

Perfect score: 1806

Sequence: 1 MAAGTAVGAWVLVSLGWAV.....IIIPGEEGPTAGSVGGSLV 339

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1802	99.8	340	2	US-08-633-148-2
2	1802	99.8	404	4	US-09-949-016-11025
3	1793	99.3	404	4	US-09-638-649-3
4	1793	99.3	404	4	US-09-638-648-3
5	1782.5	98.7	405	4	US-08-755-235-4
6	1690	93.6	318	2	US-08-633-148-4
7	1690	93.6	332	4	US-09-062-365-1
8	1495	82.8	278	2	US-08-432-016-5
9	1495	82.8	278	2	US-08-684-594-5
10	1480	81.9	416	4	US-09-638-649-1
11	1480	81.9	416	4	US-08-755-235-2
12	1480	81.9	416	4	US-09-638-648-1
13	1404.5	77.8	403	4	US-09-638-649-5
14	1404.5	77.8	403	4	US-09-638-648-5
15	223.5	12.4	582	4	US-09-702-705-334
16	223.5	12.4	582	4	US-09-736-457-334
17	223.5	12.4	582	4	US-09-614-124B-334
18	223.5	12.4	582	4	US-09-671-325-334
19	223.5	12.4	582	4	US-09-589-184-334
20	223.5	12.4	582	4	US-09-658-824-334
21	223.5	12.4	604	4	US-09-949-016-9548
22	221.5	12.3	583	2	US-08-432-016-2
23	221.5	12.3	583	2	US-08-684-594-2
24	218.5	12.1	623	4	US-09-949-016-11206
25	218.5	12.1	646	4	US-09-653-961-2
26	217.5	12.0	646	4	US-09-949-016-6728
27	217.5	12.0	646	4	US-09-653-961-4

28	212.5	11.8	466	2	US-08-432-016-4	Sequence 4, Appli
29	212.5	11.8	466	2	US-08-684-594-4	Sequence 4, Appli
30	209	11.6	1651	3	US-09-540-245A-18	Sequence 18, Appli
31	205	11.4	477	2	US-08-432-016-3	Sequence 3, Appli
32	205	11.4	477	2	US-08-684-594-3	Sequence 3, Appli
33	198	11.0	4391	4	US-10-006-011A-2	Sequence 2, Appli
34	197	10.9	486	2	US-08-432-016-6	Sequence 6, Appli
35	197	10.9	486	2	US-08-684-594-6	Sequence 6, Appli
36	190.5	10.3	1953	4	US-09-917-254-92	Sequence 92, Appli
37	186.5	10.3	924	1	US-08-481-130-28	Sequence 28, Appli
38	186.5	10.3	924	1	US-08-656-984A-28	Sequence 28, Appli
39	186.5	10.3	924	1	US-08-485-604-28	Sequence 28, Appli
40	186.5	10.3	924	2	US-08-487-595-28	Sequence 28, Appli
41	185.5	10.3	313	4	US-09-700-397-4	Sequence 3, Appli
42	185.5	10.3	344	4	US-09-700-397-3	Sequence 3, Appli
43	183.5	10.2	1297	3	US-09-540-245A-17	Sequence 17, Appli
44	182.5	10.1	698	2	US-08-602-725-36	Sequence 36, Appli
45	182.5	10.1	702	4	US-09-949-016-6484	Sequence 6484, Ap

ALIGNMENTS

RESULT 1

US-08-633-148-2
; Sequence 2, Application US/08633148
; Patent No. 5864018
; GENERAL INFORMATION:
; APPLICANT: MORSE, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,148
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 014618-00560005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-633-148-2

Query Match 99.8%; Score 1802; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWVLVSLGWAVGVAQNITARIIGPLVLKCKGAPKPPQRLWKLNTGRTEA 60
DB 1 MAAGTAVGAWVLVSLGWAVGVAQNITARIIGPLVLKCKGAPKPPQRLWKLNTGRTEA 60

QY 61 WKVLSPOGGPMDSDVARVLPNGSLFLPAVIGQDEGIFRCQAMNRNGKTKSNYRVYQI 120
 DB 61 WKVLSPOGGPMDSDVARVLPNGSLFLPAVIGQDEGIFRCQAMNRNGKTKSNYRVYQI 120
 QY 121 PKPEIVDSASELTAGVKNKVGTCVSEGSYPAGTLSWHLGDKPLVPNEKGVSVKEQTRRH 180
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 QY 181 PETGLFTLQSELMVTPARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEVQL 240
 DB 181 PETGLFTLQSELMVTPARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEVQL 240
 QY 241 VVEPEGGAAPGTVTLTCEVPAQSPQIHWKMDGVPLPSPVLLPEIGPDQGTYS 300
 DB 241 VVEPEGGAAPGTVTLTCEVPAQSPQIHWKMDGVPLPSPVLLPEIGPDQGTYS 300
 QY 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338
 DB 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338

RESULT 2

US-09-949-016-11025
 ; Sequence 11025, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11025
 ; LENGTH: 404
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-11025

Query Match 99.8%; Score 1802; DB 4; Length 404;
 Best Local Similarity 100.0%; Pred. No. 1.5e-145;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAGAWLVLSLWGA VVGVAQNITARI GEPLVKCKGAPKPPQRLWKLTGRTEA 60
 DB 1 MAAGTAGAWLVLSLWGA VVGVAQNITARI GEPLVKCKGAPKPPQRLWKLTGRTEA 60
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 DB 61 WKVLSPOGGPMDSDVARVLPNGSLFLPAVIGQDEGIFRCQAMNRNGKTKSNYRVYQI 120
 QY 121 PKPEIVDSASELTAGVKNKVGTCVSEGSYPAGTLSWHLGDKPLVPNEKGVSVKEQTRRH 180
 DB 121 PKPEIVDSASELTAGVKNKVGTCVSEGSYPAGTLSWHLGDKPLVPNEKGVSVKEQTRRH 180
 QY 181 PETGLFTLQSELMVTPARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEVQL 240
 DB 181 PETGLFTLQSELMVTPARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEVQL 240
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 DB 241 VVEPEGGAAPGTVTLTCEVPAQSPQIHWKMDGVPLPSPVLLPEIGPDQGTYS 300
 QY 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338

DB 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338

RESULT 3

US-09-638-649-3
 ; Sequence 3, Application US/09638649
 ; Patent No. 6563015
 ; GENERAL INFORMATION:
 ; APPLICANT: Stern, David M.
 ; APPLICANT: Schmidt, Ann Marie
 ; APPLICANT: Yan, Shi Du
 ; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
 ; GLYCANIC ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
 ; TITLE OF INVENTION: USES THEREOF
 ; FILE REFERENCE: 0575/62175
 ; CURRENT APPLICATION NUMBER: US/09/638,649
 ; CURRENT FILING DATE: 2000-08-14
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 404
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-638-649-3

Query Match 99.3%; Score 1793; DB 4; Length 404;
 Best Local Similarity 99.7%; Pred. No. 9e-145;
 Matches 336; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGTAGAWLVLSLWGA VVGVAQNITARI GEPLVKCKGAPKPPQRLWKLTGRTEA 61
 DB 2 AAGTAGAWLVLSLWGA VVGVAQNITARI GEPLVKCKGAPKPPQRLWKLTGRTEA 61
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 DB 62 KVLSPQGGPMDSDVARVLPNGSLFLPAVIGQDEGIFRCQAMNRNGKTKSNYRVYQI 121
 QY 122 GKPEIVDSASELTAGVKNKVGTCVSEGSYPAGTLSWHLGDKPLVPNEKGVSVKEQTRRH 181
 DB 122 GKPEIVDSASELTAGVKNKVGTCVSEGSYPAGTLSWHLGDKPLVPNEKGVSVKEQTRRH 181
 QY 182 ETGLFTLQSELMVTPARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEVQL 241
 DB 182 ETGLFTLQSELMVTPARGDPRPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEVQL 241
 QY 242 VVEPEGGAAPGTVTLTCEVPAQSPQIHWKMDGVPLPSPVLLPEIGPDQGTYS 301
 DB 242 VVEPEGGAAPGTVTLTCEVPAQSPQIHWKMDGVPLPSPVLLPEIGPDQGTYS 301
 QY 302 VATHSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338
 DB 302 VATHSHGPOESRAVSISIIIEPGEETAGSVGGSGL 338

RESULT 4

US-09-638-648-3
 ; Sequence 3, Application US/09638648
 ; Patent No. 6825164
 ; GENERAL INFORMATION:
 ; APPLICANT: Stern, David M.
 ; APPLICANT: Schmidt, Ann Marie
 ; APPLICANT: Yan, Shi Du
 ; APPLICANT: Zlokovic, Barislay
 ; TITLE OF INVENTION: A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID
 ; TITLE OF INVENTION: ANGIOPATHY
 ; FILE REFERENCE: 0575/62097
 ; CURRENT APPLICATION NUMBER: US/09/638,648
 ; CURRENT FILING DATE: 2000-08-14
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 404
 ; TYPE: PRT

ORGANISM: Human
US-08-638-648-3

Query Match 99.3%; Score 1793; DB 4; Length 404;
Best Local Similarity 99.7%; Pred. No. 9e-145;
Matches 336; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 62 KVLSPGGGPDWSDVARVLPNGSLFLPAVGIQDEGIFRCQAMNNGKETSNTYRVRYQIP 121

QY 122 GKPEIVDSASELTAGVPNKVGTCSVSGSPAGTSLWHLGDKPLVPNEKGVSKVKEQTRRP 181
DB 122 GKPEIVDSASELTAGVPNKVGTCSVSGSPAGTSLWHLGDKPLVPNEKGVSKVKEQTRRP 181

QY 182 ETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVQV 241
DB 182 ETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVQV 241

QY 242 VEPEGGAVPGGTVTLTCEVPAQPSQIHHMKDGVPLPLPPSPVLILPEIGPDQGTYS 301
DB 242 VEPEGGAVPGGTVTLTCEVPAQPSQIHHMKDGVPLPLPPSPVLILPEIGPDQGTYS 301

QY 302 VATHSHGQESRAVSIIEPGEPTAGSVGGSL 338
DB 302 VATHSHGQESRAVSIIEPGEPTAGSVGGSL 338

RESULT 5
US-08-755-235-4
; Sequence 4, Application US/08755235
; Patent No. 6790443
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Human
US-08-755-235-4

Query Match 98.7%; Score 1782.5; DB 4; Length 405;
Best Local Similarity 99.4%; Pred. No. 7.1e-144;
Matches 336; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 AGTAVGAWVLVLSLWGVVGAQNIITARIGEPVLVLCCKGAPKPPORLEWKLNTGRTTEAM 61
DB 2 AAGTAVGAWVLVLSLWGVVGAQNIITARIGEPVLVLCCKGAPKPPORLEWKLNTGRTTEAM 61

QY 62 KVLSPGGGPDWSDVARVLPNGSLFLPAVGIQDEGIFRCQAMNNGKETSNTYRVRYQIP 121
DB 62 KVLSPGGGPDWSDVARVLPNGSLFLPAVGIQDEGIFRCQAMNNGKETSNTYRVRYQIP 121

QY 122 GKPEIVDSASELTAGVPNKVGTCSVSGSPAGTSLWHLGDKPLVPNEKGVSKVKEQTRRP 181
DB 122 GKPEIVDSASELTAGVPNKVGTCSVSGSPAGTSLWHLGDKPLVPNEKGVSKVKEQTRRP 181

QY 182 ETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVQV 241
DB 182 ETGLFTLQSELMTVPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVQV 241

QY 242 VEPEGGAVPGGTVTLTCEVPAQPSQIHHMKDGVPLPLPPSPVLILPEIGPDQGTYS 301

DB 242 VEPEGGAVPGGTVTLTCEVPAQPSQIHHMKDGVPLPLPPSPVLILPEIGPDQGTYS 301

QY 302 VATHSHGQESRAVSIIEPGEPTAGSVGGSL 338
DB 302 VATHSHGQESRAVSIIEPGEPTAGSVGGSL 339

RESULT 6
US-08-633-148-4
; Sequence 4, Application US/08633148
; Patent No. 5864018
; GENERAL INFORMATION:
; APPLICANT: MORSE, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; APPLICANT: HOLLANDER, DORIS A.
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,148
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 014618-00560005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-633-148-4

Query Match 93.6%; Score 1690; DB 2; Length 318;
Best Local Similarity 100.0%; Pred. No. 3.9e-136;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPVLVLCCKGAPKPPORLEWKLNTGRTTEAMKVLSPGGGPDWSDVARVLPNG 82
DB 1 AQNITARIGEPVLVLCCKGAPKPPORLEWKLNTGRTTEAMKVLSPGGGPDWSDVARVLPNG 60

QY 83 SLFLPAVGIQDEGIFRCQAMNNGKETSNTYRVRYQIPGKPEIVDSASELTAGVPNKV 142
DB 61 SLFLPAVGIQDEGIFRCQAMNNGKETSNTYRVRYQIPGKPEIVDSASELTAGVPNKV 120

QY 143 TCVSQSGSPAGTSLWHLGDKPLVPNEKGVSKVKEQTRRPETGLFTLQSELMTVPARGGDP 202
DB 121 TCVSQSGSPAGTSLWHLGDKPLVPNEKGVSKVKEQTRRPETGLFTLQSELMTVPARGGDP 180

QY 203 RPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVQVVEPEGGAVPGGTVTLTCEVP 262
DB 181 RPTFSCSPGLPRHRLRTAPIQPRVWEPVPLEEVQVVEPEGGAVPGGTVTLTCEVP 240

QY 263 AQPSPQIHHMKDGVPLPLPPSPVLILPEIGPDQGTYSVATHSHGQESRAVSIIE 322

Db 241 AQPSPQIHWKMDGVLPPLPPSVLILPEIGPDQGTSCVATHSHGQESRAVSIIE 300
QY 323 PGEEGTAGSVGGSL 338
Db 301 PGEEGTAGSVGGSL 316

RESULT 7
US-09-062-365-1
; Sequence 1, Application US/09062365
; Patent No. 6465422
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A
; FILE REFERENCE: 55424
; CURRENT APPLICATION NUMBER: US/09/062.365
; CURRENT FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Human
US-09-062-365-1

Query Match 93.6%; Score 1690; DB 4; Length 332;
Best Local Similarity 100.0%; Pred. No. 4.2e-136; Indels 0; Gaps 0;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AONITARIIGPLVLCCKGAPKPPQRLKNTGRTEAWKVLSPQGGPWSVARVLPNG 82
Db 1 AONITARIIGPLVLCCKGAPKPPQRLKNTGRTEAWKVLSPQGGPWSVARVLPNG 60
QY 83 SLFLPAVGIQDEGIFRCQAMNRNGKTSNYRVVYQIPGKPEIVDSASELTAGVFNKVG 142
Db 61 SLFLPAVGIQDEGIFRCQAMNRNGKTSNYRVVYQIPGKPEIVDSASELTAGVFNKVG 120
QY 143 TCVSSEGYAGTLSWHLGDKPLVPNEKGVSKQTRRHHPETGLFTLQSELMVTPARGGDP 202
Db 121 TCVSSEGYAGTLSWHLGDKPLVPNEKGVSKQTRRHHPETGLFTLQSELMVTPARGGDP 180
QY 203 RPTFSCSFSGLPRLRALRTAPIQPRVWEPVPLEVQVVEPEGGAAPGGTTLTCEVP 262
Db 181 RPTFSCSFSGLPRLRALRTAPIQPRVWEPVPLEVQVVEPEGGAAPGGTTLTCEVP 240
QY 263 AQPSPQIHWKMDGVLPPLPPSVLILPEIGPDQGTSCVATHSHGQESRAVSIIE 322
Db 241 AQPSPQIHWKMDGVLPPLPPSVLILPEIGPDQGTSCVATHSHGQESRAVSIIE 300
QY 323 PGEEGTAGSVGGSL 338
Db 301 PGEEGTAGSVGGSL 316

RESULT 8
US-08-432-016-5
; Sequence 5, Application US/08432016
; Patent No. 5968768
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: PATEL, DHAVALKUMAR
; APPLICANT: BOWEN, MICHAEL A.
; APPLICANT: MARQUARDT, HANS
; TITLE OF INVENTION: CD6 LIGAND
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA

Db 241 AQPSPQIHWKMDGVLPPLPPSVLILPEIGPDQGTSCVATHSHGQESRAVSIIE 300
QY 323 PGEEGTAGSVGGSL 338
Db 301 PGEEGTAGSVGGSL 316

RESULT 9
US-08-684-594-5
; Sequence 5, Application US/08684594
; Patent No. 5998172
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: PATEL, DHAVALKUMAR
; APPLICANT: BOWEN, MICHAEL A.
; APPLICANT: MARQUARDT, HANS
; TITLE OF INVENTION: CD6 LIGAND
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD

; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432.016
; FILING DATE: 01-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,350
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,903
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-432-016-5

Query Match 82.8%; Score 1495; DB 2; Length 278;
Best Local Similarity 99.6%; Pred. No. 1.4e-119;
Matches 277; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 30 IGEPLVLKCKGAPKPPQRLKNTGRTEAWKVLSPQGGPWSVARVLPNGSLFLPAV 89
Db 1 IGEPLVLKCKGAPKPPQRLKNTGRTEAWKVLSPQGGPWSVARVLPNGSLFLPAV 60
QY 90 GIQDEGIFRCQAMNRNGKTSNYRVVYQIPGKPEIVDSASELTAGVFNKVGTCVSEGS 149
Db 61 GIQDEGIFRCQAMNRNGKTSNYRVVYQIPGKPEIVDSASELTAGVFNKVGTCVSEGS 120
QY 150 YPAGTLSWHLGDKPLVPNEKGVSKQTRRHHPETGLFTLQSELMVTPARGGDPPTFSCS 209
Db 121 YPAGTLSWHLGDKPLVPNEKGVSKQTRRHHPETGLFTLQSELMVTPARGGDPPTFSCS 180
QY 210 FSPGLPRHRLRTAPIQPRVWEPVPLEVQVVEPEGGAAPGGTTLTCEVPAQSPQI 269
Db 181 FSPGLPRHRLRTAPIQPRVWEPVPLEVQVVEPEGGAAPGGTTLTCEVPAQSPQI 240
QY 270 HMKDGVLPPLPPSVLILPEIGPDQGTSCVATHSS 307
Db 241 HMKDGVLPPLPPSVLILPEIGPDQGTSCVATHSS 278

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; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,594
; FILING DATE: 18-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/432,016
; FILING DATE: 01-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,350
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,903
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4100
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-684-594-5

Query Match      82.8%; Score 1495; DB 2; Length 278;
Best Local Similarity 99.6%; Pred. No. 1.4e-119;
Matches 277; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 30 IGEPVLVKCKGAPKPPQRLWKLNTGRTAEAWKLSPPQGGPMDVARVLPNGSLFLPAV 89
DB 1 IGEPVLVKCKGAPKPPQRLWKLNTGRTAEAWKLSPPQGGPMDVARVLPNGSLFLPAV 60

QY 90 GIODEGIFRCQAMNRNGKTSNRYRVYQIPGKPEIVDSASELTAGVKNKVGTCVSEGS 149
DB 61 GIODEGIFRCQAMNRNGKTSNRYRVYQIPGKPEIVDSASELTAGVKNKVGTCVSEGS 120

QY 150 YPAGTLSWHLDDGKPLVPNEKGVSKQTRRHPTGLFTLQSELMTVPARGGDPRTFSCS 209
DB 121 YPAGTLSWHLDDGKPLVPNEKGVSKQTRRHPTGLFTLQSELMTVPARGGDPRTFSCS 180

QY 210 FSPGLPRHRLARTAPIQPRWVEVPVLEEVLVPEEGGAVAPGGTTLTCEVPAQSPQI 269
DB 181 FSPGLPRHRLARTAPIQPRWVEVPVLEEVLVPEEGGAVAPGGTTLTCEVPAQSPQI 240

QY 270 HWMKDGVLPLPSPVLILPEIGPQOGTYSCVATHSS 307
DB 241 HWMKDGVLPLPSPVLILPEIGPQOGTYSCVATHSS 278

RESULT 10
US-09-638-649-1
; Sequence 1, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND

; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,594
; FILING DATE: 18-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/432,016
; FILING DATE: 01-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,350
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,903
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4100
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-684-594-5

Query Match      81.9%; Score 1480; DB 4; Length 416;
Best Local Similarity 80.5%; Pred. No. 4.6e-118;
Matches 281; Conservative 22; Mismatches 34; Indels 12; Gaps 2;

QY 1 MAAGTAVGAWLVLSLWGAIVGAQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTAE 60
DB 1 MAAGTAVGAWLVLSLWGAIVGAQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTAE 60

QY 61 WKVLSPPQGGPMDVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKTSNRYRVYQI 120
DB 61 WKVLSPPQGGPMDVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKTSNRYRVYQI 119

QY 121 PGKPEIVDSASELTAGVKNKVGTCVSEGSYPAGTLSWHLDDGKPLVPNEKGVSKQTRRH 180
DB 120 PGKPEIVDSASELTAGVKNKVGTCVSEGSYPAGTLSWHLDDGKPLVPNEKGVSKQTRRH 179

QY 181 PETGLFTLQSELMTVPARGGDPRTFSCSFGSLPRHRLARTAPIQPRVW----- 230
DB 180 PETGLFTLQSELMTVPARGGDPRTFSCSFGSLPRHRLARTAPIQPRVWSEHRGEGPN 239

QY 231 -EPVPLEEVQLVVEPEGGAVAPGGTTLTCEVPAQSPQIHWMKDGVLPLPSPVLILP 289
DB 240 VDAVPLKEVQLVVEPEGGAVAPGGTTLTCEVPAQSPQIHWMKDGVLPLPSPVLILP 299

QY 290 EIGPQOGTYSCVATHSSHPQESRAVSISIEPGEGTAGSVGGSL 338
DB 300 EVGPEQOGTYSCVATHSSHPQESRAVSISIEPGEGTAGSVGGSL 348

RESULT 11
US-08-755-235-2
; Sequence 2, Application US/08755235
; Patent No. 6790443
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Bovine
; US-08-755-235-2

Query Match      81.9%; Score 1480; DB 4; Length 416;
Best Local Similarity 80.5%; Pred. No. 4.6e-118;
Matches 281; Conservative 22; Mismatches 34; Indels 12; Gaps 2;

QY 1 MAAGTAVGAWLVLSLWGAIVGAQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTAE 60
DB 1 MAAGTAVGAWLVLSLWGAIVGAQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTAE 60

QY 61 WKVLSPPQGGPMDVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKTSNRYRVYQI 120
DB 61 WKVLSPPQGGPMDVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKTSNRYRVYQI 119
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[illegible]

RESULT 15

US-09-702-705-334
; Sequence 334, Application US/09702705

; Patent No. 6504010

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; GENERAL INFORMATION:
;
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Fodes, Michael A.
; APPLICANT: Langer, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liguu
;

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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.478C14

; CURRENT APPLICATION NUMBER: US/09/702,705

CURRENT FILING DATE: 2000-10-30

: NUMBER OF SEO ID NOS: 1833

; SOFTWARE: FastSEQ for Windows Version 3.0

: SEO ID NO 334

: LENGTH: 582

: LENGTH: 302
: TYPE: PRT

; LIFE: FKI
: ORGANISM: Homo sapiens

U.S.-09-702-705-334

	Query Match	12.4%; Score 223.5; DB 4;	Length 582;
	Best Local Similarity	25.8%; Pred. No.	1.1e-10;
	Matches 80;	Conservative 46;	Mismatches 133;
		Indels 51;	Gaps 12;
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Db	25 LGHYTVNSAAGDTIIIPCR---LDVPQLNMF-----GK----WKYEKPDSVPIAFRSSTK 74 : : :	: : : :	:
Qy	71 ---PWDSV-----ARVLPNGSLFLPVGIQDEGIIFRCOAMNRNGKETSNY-----RVR 116 : : :	: : : :	:
Db	75 KSVQYDDVP EYKDRLNLSENVTLISINARSIDKRFFVCMLV-----TENVPEAPTIVK 128 : : :	: : : :	:
Qy	117 YVIQPGEPRVIDSASELTAGVPNKGVCHVSSEGSYPAGTLSHWLDCCKPLVFNPKCVSKVKQ 176 : : :	: : : :	:
Db	129 VFQPSKEIIVSKALFLETEQLKKLGPCI SEDSPDGNITYWRNGKVLLPLEGAHWIIFIK 188 : : :	: : : :	:
Qy	177 TRRHPTGLFTLOSELMTVPARGGDPRPTSCS---ESPGLPHRALRTAPIQRVWE-P 232 : : :	: : : :	:
Db	189 KEMDPVQLYTMTISTLEYKITK-AIOMPFTCSVTYYGPS-----GOKTHSEQAEVDIY 242 : : :	: : : :	:
Qy	233 VPLEEVLVVVEPGGAVAGGTVTLTCCEVPAQPSF-QIHMMKGQGVLPPLPPSPVLILPEI 291 : : :	: : : :	:

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2005, 11:27:19 ; Search time 333 Seconds
(without alignments)
335.788 Million cell updates/sec

Title: US-10-091-019-3

Perfect score: 1806

Sequence: 1 MAAGTAGVAGWLVLSLWGA.....IIEPGEGETAGSGVGLV 339

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
- 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
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- 10: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
- 13: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
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- 18: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
- 19: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
- 20: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1806	100.0	339	14	US-10-091-019-3
2	1802	99.8	404	15	US-10-309-290-96
3	1782.5	98.7	405	8	US-08-755-235-4
4	1768	97.9	347	17	US-10-472-507A-2
5	1709	94.6	390	15	US-10-309-290-100
6	1705	94.4	390	15	US-10-309-290-98
7	1690	93.6	332	9	US-09-872-185B-2
8	1690	93.6	332	9	US-09-851-071-1
9	1480	81.9	416	8	US-08-755-235-2
10	1379.5	76.4	342	16	US-10-408-765A-641
11	595	32.9	112	9	US-09-872-185B-1
12	229.5	12.7	3931	15	US-10-120-801-18
13	224.5	12.4	1034	15	US-10-094-749-2631

14	223.5	12.4	570	17	US-10-741-600-1431	Sequence 1431, Ap
15	223.5	12.4	582	9	US-09-736-457-334	Sequence 334, App
16	223.5	12.4	582	9	US-09-902-941-334	Sequence 334, App
17	223.5	12.4	582	9	US-09-849-626-334	Sequence 334, App
18	223.5	12.4	582	10	US-09-476-300-334	Sequence 334, App
19	223.5	12.4	582	14	US-10-017-754-334	Sequence 334, App
20	223.5	12.4	582	14	US-10-113-872-334	Sequence 334, App
21	223.5	12.4	582	15	US-10-283-017-334	Sequence 334, App
22	223.5	12.4	583	17	US-10-741-600-1430	Sequence 1430, Ap
23	222.5	12.3	583	14	US-10-176-847-64	Sequence 64, Appl
24	222.5	12.3	583	14	US-10-205-823-12	Sequence 12, Appl
25	222.5	12.3	583	15	US-10-170-385-277	Sequence 277, App
26	222.5	12.3	583	15	US-10-058-270A-136	Sequence 136, App
27	222.5	12.3	583	17	US-10-741-600-1433	Sequence 1433, Ap
28	217.5	12.0	645	15	US-10-295-027-352	Sequence 352, App
29	217.5	12.0	646	14	US-10-021-660-75	Sequence 75, Appl
30	217.5	12.0	646	14	US-10-021-660-106	Sequence 106, App
31	217.5	12.0	646	15	US-10-211-462-20	Sequence 20, Appl
32	217.5	12.0	646	15	US-10-211-462-125	Sequence 125, App
33	215.5	11.9	3409	16	US-10-367-094-165	Sequence 165, App
34	214	11.8	1479	15	US-10-021-956A-325	Sequence 325, App
35	214	11.8	1496	14	US-10-331-496A-28	Sequence 28, Appl
36	214	11.8	1496	15	US-10-331-496A-28	Sequence 28, Appl
37	214	11.8	1496	15	US-10-211-462-87	Sequence 87, Appl
38	214	11.8	1498	15	US-10-243-552-899	Sequence 899, App
39	214	11.8	1498	15	US-10-276-774-1957	Sequence 1957, Ap
40	212.5	11.8	753	13	US-10-105-934-5	Sequence 5, Appl
41	212.5	11.8	753	17	US-10-895-676-5	Sequence 5, Appl
42	211.5	11.7	532	17	US-10-741-600-1432	Sequence 1432, Ap
43	209	11.6	1477	14	US-10-274-583-20	Sequence 20, Appl
44	209	11.6	1651	14	US-10-289-776-18	Sequence 18, Appl
45	205	11.4	961	15	US-10-162-335-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1

US-10-091-019-3
; Sequence 3, Application US/10091019
; Publication No. US20030166063A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Shen, Jane M.
; APPLICANT: Shabbaz, Manouchehr M.
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins
; FILE REFERENCE: 41305-270555
; CURRENT APPLICATION NUMBER: US/10/091,019
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/273,418
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-091-019-3

Query Match	100.0%	Score	1806	DB	14	Length	339
Best Local Similarity	100.0%	Pred. No.	3.9e-116				
Matches	339	Conservative	0	Mismatches	0	Indels	0
QY	1	MAAGTAGVAGWLVLSLWGA	VGAQNTARIGBPLVKCKGAPKPPQRL	EWKLTNGRT	EA	60	
Db	1	MAAGTAGVAGWLVLSLWGA	VGAQNTARIGBPLVKCKGAPKPPQRL	EWKLTNGRT	EA	60	
QY	61	WKVLSFQGGPQWDSVARVLP	NGSLFPAVGIQDEGIFRCQANNRNGK	ETKSNYRVYQI	120		
Db	61	WKVLSFQGGPQWDSVARVLP	NGSLFPAVGIQDEGIFRCQANNRNGK	ETKSNYRVYQI	120		
QY	121	PKKPISVDSASLTAGVKNVGT	CTVSEGSYPAGTISLWLDGKPLVP	NEKGVSKETRRH	180		
Db	121	PKKPISVDSASLTAGVKNVGT	CTVSEGSYPAGTISLWLDGKPLVP	NEKGVSKETRRH	180		

Db 121 PKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTSLSHLWDGKPLVPNEKGVSKQTRRH 180
QY 181 PETGLFTLQSELMVTPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVLEEVOL 240
Db 181 PETGLFTLQSELMVTPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVLEEVOL 240
QY 241 VVEPEGGAAPGGTTLTCEVPAQSPQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYS 300
Db 241 VVEPEGGAAPGGTTLTCEVPAQSPQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYS 300
QY 301 CVATHSHGPOESRAVSISIEEGEGTSGSVGGSLV 339
Db 301 CVATHSHGPOESRAVSISIEEGEGTSGSVGGSLV 339

RESULT 2

US-10-309-290-96
; Sequence 96, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chilikakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenov, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS, ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274

; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 96
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-290-96

Query Match 99.8%; Score 1802; DB 15; Length 404;
Best Local Similarity 100.0%; Pred. No. 9e-116;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWLVLSLWGAVVGAQNITARIIGBPLVKCKGAPKPPQRLWKLTGRTGA 60
Db 1 MAAGTAVGAWLVLSLWGAVVGAQNITARIIGBPLVKCKGAPKPPQRLWKLTGRTGA 60
QY 61 WKVLSPOGGGPDWSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVQI 120
Db 61 WKVLSPOGGGPDWSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVQI 120
QY 121 PKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTSLSHLWDGKPLVPNEKGVSKQTRRH 180
Db 121 PKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTSLSHLWDGKPLVPNEKGVSKQTRRH 180
QY 181 PETGLFTLQSELMVTPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVLEEVOL 240
Db 181 PETGLFTLQSELMVTPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVLEEVOL 240
QY 241 VVEPEGGAAPGGTTLTCEVPAQSPQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYS 300
Db 241 VVEPEGGAAPGGTTLTCEVPAQSPQIHWKMDGVPLPLPPSPVLILPEIGPDQGTYS 300
QY 301 CVATHSHGPOESRAVSISIEEGEGTSGSVGGSL 338
Db 301 CVATHSHGPOESRAVSISIEEGEGTSGSVGGSL 338

RESULT 3

US-08-755-235-4
; Sequence 4, Application US/08755235
; Publication No. US20030059423A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Human
US-08-755-235-4

Query Match 98.7%; Score 1782.5; DB 8; Length 405;
Best Local Similarity 99.4%; Pred. No. 2e-114;
Matches 336; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 2 AAGTAVGAWLVLSLWGAVVGAQNITARIIGBPLVKCKGAPKPPQRLWKLTGRTGA 61
Db 2 AAGTAVGAWLVLSLWGAVVGAQNITARIIGBPLVKCKGAPKPPQRLWKLTGRTGA 61
QY 62 KVLSPQGGGPDWSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVQI 121
Db 62 KVLSPQGGGPDWSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVQI 121
QY 122 GKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTSLSHLWDGKPLVPNEKGVSKQTRRH 181
Db 122 GKPEIVDSASELTAGVFNKVGTCVSEGSYPAGTSLSHLWDGKPLVPNEKGVSKQTRRH 181
QY 182 ETGLFTLQSELMVTPARGGDPRTFSCSPGLPRHRLRTAPIQPRVWEPVLEEVOL 241

Db 182 ETGLFTLOSELMVTPARGDPRPTFCSPGLPRHRLRTAPIQVRWVEPPLSEVQLV 241
Qy 242 VEPEGGAVAPGGTVTITCEVPAQPSQIHWKDKGVPLPLPPSPVLILPRIGPDQGTYS 301
Db 242 VEPEGGAVAPGGTVTITCEVPAQPSQIHWKDKGVPLPLPPSPVLILPRIGPDQGTYS 301
Qy 302 VATSHSHGQESRA-VSISIIEPGEGBPTAGSVGGSL 338
Db 302 VATSHSHGQESRAVVSISIIEPGEGBPTAGSVGGSL 339

RESULT 4

US-10-472-507A-2
; Sequence 2, Application US/10472507A
; Publication No. US2005033017A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, Hiroshi
; APPLICANT: Yonekura, Hideto
; APPLICANT: Yamamoto, Yasuhiko
; APPLICANT: Sakurai, Shigeru
; APPLICANT: Watanabe, Takuo
; TITLE OF INVENTION: Soluble Rage Protein
; FILE REFERENCE: 026350-089
; CURRENT APPLICATION NUMBER: US/10/472,507A
; PRIOR FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: PCT/JP02,02623
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: JP 2001-78409
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: JP 2001-243114
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: JP 2002-48182
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-472-507A-2

Query Match 97.9%; Score 1768; DB 17; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGTAVGAWLVLSLWGAVGVAQNITARIIGPLVLKCKGAPKPKPQRLWKLTGRTGA 60
Db 1 MAAGTAVGAWLVLSLWGAVGVAQNITARIIGPLVLKCKGAPKPKPQRLWKLTGRTGA 60
Qy 61 WKVLSPPQGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMRNKGTETKSNYRVRYQI 120
Db 61 WKVLSPPQGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMRNKGTETKSNYRVRYQI 120
Qy 121 PKPEIVDSASELTAGVPNKVGTCTSEGSYPAGTILSHWLDGKPLVNEKGVSVKEQTRRH 180
Db 121 PKPEIVDSASELTAGVPNKVGTCTSEGSYPAGTILSHWLDGKPLVNEKGVSVKEQTRRH 180
Qy 181 PETGLFTLOSELMVTPARGDPRPTFCSPGLPRHRLRTAPIQVRWVEPPLSEVQL 240
Db 181 PETGLFTLOSELMVTPARGDPRPTFCSPGLPRHRLRTAPIQVRWVEPPLSEVQL 240
Qy 241 VVEPEGGAVAPGGTVTITCEVPAQPSQIHWKDKGVPLPLPPSPVLILPRIGPDQGTYS 300
Db 241 VVEPEGGAVAPGGTVTITCEVPAQPSQIHWKDKGVPLPLPPSPVLILPRIGPDQGTYS 300
Qy 301 CVATHSHGQESRAVVSISIIEPGEGBPTAG 331
Db 301 CVATHSHGQESRAVVSISIIEPGEGBPTAG 331

RESULT 5

US-10-309-290-100

; Sequence 100, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glennda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 100
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-290-100

Query Match 94.6%; Score 1709; DB 15; Length 390;
Best Local Similarity 95.9%; Pred. No. 2.1e-109;
Matches 324; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
Qy 1 MAAGTAVGAWLVLSLWGAVGVAQNITARIIGPLVLKCKGAPKPKPQRLWKLTGRTGA 60
Db 1 MAAGTAVGAWLVLSLWGAVGVAQNITARIIGPLVLKCKGAPKPKPQRLWKLTGRTGA 60
Qy 61 WKVLSPPQGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMRNKGTETKSNYRVRYQI 120

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Db 54 -----GGGPWDSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQI 106
Qy 121 PGKPEIVDSASLTAGVFNKVTCTVSEGSYPAGTILSHWLDGKPLVPNEKGVSKQTRRH 180
Db 107 PGKPEIVDSASLTAGVFNKVTCTVSEGSYPAGTILSHWLDGKPLVPNEKGVSKQTRRH 166
Qy 181 PETGLFTLQSELMTVPARGGDPRTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
Db 167 PETGLFTLQSELMTVPARGGDPRTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 226
Qy 241 VVEPEGAVAPGGTIVTLTCEVPAQSPQIHWMDGVPLPLPPSVLILPIGPDQGTYS 300
Db 227 VVEPEGAVAPGGTIVTLTCEVPAQSPQIHWMDGVPLPLPPSVLILPIGPDQGTYS 286
Qy 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSL 338
Db 287 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSL 324

RESULT 6
US-10-309-290-98
; Sequence 98, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glennda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
```

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; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 98
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-290-98

Query Match 94.4%; Score 1705; DB 15; Length 390;
Best Local Similarity 95.6%; Pred. No. 4e-109;
Matches 323; Conservative 0; Mismatches 1; Indels 14; Gaps 1;

Qy 1 MAAGTAVGAWLVLSLWGA VVGAQNITARI GEPLV LKCKGAPKPPQRLWK LNTGRTEA 60
Db 1 MAAGTAVGTWLVLSLWGA VVGAQNITARI GEPLV LKCKGAPKPPQRLWK L----- 53

Qy 61 WKVLS PQGGP WDSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQI 120
Db 54 -----GGGPWDSVARVLPNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQI 106

Qy 121 PGKPEIVDSASLTAGVFNKVTCTVSEGSYPAGTILSHWLDGKPLVPNEKGVSKQTRRH 180
Db 107 PGKPEIVDSASLTAGVFNKVTCTVSEGSYPAGTILSHWLDGKPLVPNEKGVSKQTRRH 166

Qy 181 PETGLFTLQSELMTVPARGGDPRTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 240
Db 167 PETGLFTLQSELMTVPARGGDPRTFSCFSFGLPRHRLRTAPIQPRVWEPVPLEEVOL 226

Qy 241 VVEPEGAVAPGGTIVTLTCEVPAQSPQIHWMDGVPLPLPPSVLILPIGPDQGTYS 300
Db 227 VVEPEGAVAPGGTIVTLTCEVPAQSPQIHWMDGVPLPLPPSVLILPIGPDQGTYS 286

Qy 301 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSL 338
Db 287 CVATHSHGPOESRAVSISIIIEPGEETAGSVGGSL 324
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RESULT 7
US-09-872-185B-2
; Sequence 2, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Human
US-09-872-185B-2

Query Match 93.6%; Score 1690; DB 9; Length 332;
Best Local Similarity 100.0%; Pred. No. 3.6e-108;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AQNITARI GEPLV LKCKGAPKPPQRLWK LNTGRTEA WKVLS PQGGP WDSVARVLPNG 82
Db 1 AQNITARI GEPLV LKCKGAPKPPQRLWK LNTGRTEA WKVLS PQGGP WDSVARVLPNG 60

Qy 83 SLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQI PGKPEIVDSASLTAGVFNKVG 142
Db 61 SLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVVYQI PGKPEIVDSASLTAGVFNKVG 120
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QY 143 TCVSEGSYPAGTSLWHLGDKPLVPNEKGVSVKEQTRRHBPETGLFTLQSELMTVPARGGDP 202
DB 121 TCVSEGSYPAGTSLWHLGDKPLVPNEKGVSVKEQTRRHBPETGLFTLQSELMTVPARGGDP 180
QY 203 RPTFSCSFSGPLPRHRLATAPIQPRVWEPVPLEEVQVVEGGAVAPGGTTLTCEVP 262
DB 181 RPTFSCSFSGPLPRHRLATAPIQPRVWEPVPLEEVQVVEGGAVAPGGTTLTCEVP 240
QY 263 AQPSPQIHWKMDGVPLPLPPSPVLLILPEIGPQDQGTYSVATHSSHGPOESRAVSISIIIE 322
DB 241 AQPSPQIHWKMDGVPLPLPPSPVLLILPEIGPQDQGTYSVATHSSHGPOESRAVSISIIIE 300
QY 323 PGEEGTAGSVGSGSL 338
DB 301 PGEEGTAGSVGSGSL 316

RESULT 8
US-09-851-071-1
; Sequence 1, Application US/09851071
; Patent No. US20020177550A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Anne Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: A METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A SUBJECT
; FILE REFERENCE: 0575/55424-Z/JPW/SHS/MVM
; CURRENT APPLICATION NUMBER: US/09/851,071
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Human
US-09-851-071-1

Query Match 93.6%; Score 1690; DB 9; Length 332;
Best Local Similarity 100.0%; Pred. No. 3.6e-108;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AQNITARIGEPLVLCCKGAPKPPQRLWKLTNTRTEANKVLSPOGGGPDWSVARVLPNG 82
DB 1 AQNITARIGEPLVLCCKGAPKPPQRLWKLTNTRTEANKVLSPOGGGPDWSVARVLPNG 60
QY 83 SLFLPAGVIGDDEGIFRCQAMNRNGKETKSNYRVVYQIPCKPEIVDSASELTAGVPNKVG 142
DB 61 SLFLPAGVIGDDEGIFRCQAMNRNGKETKSNYRVVYQIPCKPEIVDSASELTAGVPNKVG 120
QY 143 TCVSEGSYPAGTSLWHLGDKPLVPNEKGVSVKEQTRRHBPETGLFTLQSELMTVPARGGDP 202
DB 121 TCVSEGSYPAGTSLWHLGDKPLVPNEKGVSVKEQTRRHBPETGLFTLQSELMTVPARGGDP 180
QY 203 RPTFSCSFSGPLPRHRLATAPIQPRVWEPVPLEEVQVVEGGAVAPGGTTLTCEVP 262
DB 181 RPTFSCSFSGPLPRHRLATAPIQPRVWEPVPLEEVQVVEGGAVAPGGTTLTCEVP 240
QY 263 AQPSPQIHWKMDGVPLPLPPSPVLLILPEIGPQDQGTYSVATHSSHGPOESRAVSISIIIE 322
DB 241 AQPSPQIHWKMDGVPLPLPPSPVLLILPEIGPQDQGTYSVATHSSHGPOESRAVSISIIIE 300
QY 323 PGEEGTAGSVGSGSL 338
DB 301 PGEEGTAGSVGSGSL 316

RESULT 9
US-08-755-235-2
; Sequence 2, Application US/08755235
; Publication No. US20030059423A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie

; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Bovine
US-08-755-235-2

Query Match 81.9%; Score 1480; DB 8; Length 416;
Best Local Similarity 80.5%; Pred. No. 1.2e-93;
Matches 281; Conservative 22; Mismatches 34; Indels 12; Gaps 2;

QY 1 MAAGTAVGAWVLVLSLWGAIVGAQNTARIGEPVLVLCCKGAPKPPQRLWKLTNTRTEA 60
DB 1 MAAGAVVGAWMLVLSLGGTGTVDQNTARIGKVLNCKGAPKPPQRLWKLTNTRTEA 60
QY 61 WKVLSPOGGGPDWSVARVLPNGSLFLPAGVIGDDEGIFRCQAMNRNGKETKSNYRVVYQI 120
DB 61 WKVLSPO-GDPWDSVARVLPNGSLFLPAGVIGDDEGIFRCQAMNRNGKETKSNYRVVYQI 119
QY 121 PKPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTSLWHLGDKPLVPNEKGVSVKEQTRRH 180
DB 120 PKPEIVDPASBELMAGVNPKNVGTCTVSEGSYPAGTSLWHLGDKPLVPNEKGVSVKEQTRH 179
QY 181 PETGLFTLQSELMTVPARGGDPRTFSCSFSGPLPRHRLATAPIQPRVW----- 230
DB 180 PKTGLFTLHSELMTVPARGGALHPTFSCSFTGLPRRRALHTAPIQLRVMSHRGSGGN 239
QY 231 -BPVPLEEVQVVEGGAVAPGGTTLTCEVPAPSPQIHWKMDGVPLPLPPSPVLLILP 289
DB 240 VDAVPLKEVQVVEGGAVAPGGTTLTCEVPAPSPQIHWKMDGVPLPLPPSPVLLILP 299
QY 290 EIGPQDQGTYSVATHSSHGPOESRAVSISIIIEPGEETAGSVGSGSL 338
DB 300 EVGPEDQGTYSVATHSGPOESRAVSIIETGEGTAGSVGSGSL 348

RESULT 10
US-10-408-765A-641
; Sequence 641, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Roin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 641
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-641

Query Match 76.4%; Score 1379.5; DB 16; Length 342;
Best Local Similarity 78.4%; Pred. No. 7.9e-87;
Matches 279; Conservative 6; Mismatches 28; Indels 43; Gaps 6;
QY 1 MAAGTAVGAWVLVLSLWGAIVGAQNTARIGEPVLVLCCKGAPKPPQRLWKLTNTRTEA 60

Db 1 MAAGTAVGAVWLVLMSLWAGVVAQNITARIAGEPLVLKCKGAPKPPORLEWLK----- 53
 QY 61 WKVLSPOGGGWDVSARVLPNGSLFLPAVGQDEGIFRCQAMNRNGKETKSNRYRVYQI 120
 Db 54 -----GGGPDWSARVLPNGSLFLPAVGQDEGIFRCQAMNRNGKETKSNRYRVYQI 106
 QY 121 PKRPEIVDSASELTAGVFNKVGTCVSEGSYPAGTSLWHLDGKPLVPNEKGVSKVEQTRRH 180
 Db 107 PKRPEIVDSASELTAGVFNKVGTCVSEGSYPAGTSLWHLDGKPLVPNEKGVSKVEQTRRH 166
 QY 181 PETGLFTLOSLLMTVPARGDPRTFSCSPGLPRHRLARTAPIQPRVWEPVLEEVQL 240
 Db 167 PETGLFTLOSLLMTVPARGDPRTFSCSPGLPRHRLARTAPIQPRVWEPVLEEVQL 226
 QY 241 VVEPEGGAAPGGTTLTCEVPAQPSQIHWKMDGVPLPLPPSPVLLPEIGPDQGTYS 300
 Db 227 VVEPEGGAAPGGTTLTCEVPAQPSQIHWKMDVSL-----RGAGRTRGGAN 277
 QY 301 C-----VATHSHG-----PQSR-----AVSIIIEPGEHG- TAGSVGGS 336
 Db 278 CRLCGIRAGNSPGPDGPRGDSRPAHWGHLVAKAATPRGEEGPKPGGRGA 333

RESULT 11

US-09-872-185B-1
 ; Sequence 1, Application US/09872185B
 ; Patent No. US2002012799A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Stern, David M.
 ; APPLICANT: Herold, Kevan
 ; APPLICANT: Yan, Shi Du
 ; APPLICANT: Schmidt, Ann Marie
 ; APPLICANT: Lamster, Ira
 ; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
 ; FILE REFERENCE: 0575/64080
 ; CURRENT APPLICATION NUMBER: US/09/872,185B
 ; CURRENT FILING DATE: 2001-06-01
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 112
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-872-185B-1

Query Match 32.9%; Score 595; DB 9; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.7e-33;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 AQNITARIAGEPLVLKCKGAPKPPORLEWKLNTGRTEAWKVLSPQGGGPDWSARVLPNG 82
 Db 1 AQNITARIAGEPLVLKCKGAPKPPORLEWKLNTGRTEAWKVLSPQGGGPDWSARVLPNG 60
 QY 83 SLFLPAVGQDEGIFRCQAMNRNGKETKSNRYRVYQIPKPEIVDSASELT 134
 Db 61 SLFLPAVGQDEGIFRCQAMNRNGKETKSNRYRVYQIPKPEIVDSASELT 112

RESULT 12

US-10-120-801-18
 ; Sequence 18, Application US/10120801
 ; Publication No. US20030203843A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pena, Carol
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Shimkets, Richard
 ; APPLICANT: Padigar, Muralidhara
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Mehraban, Fuad
 ; APPLICANT: Topper, James N.
 ; APPLICANT: Malvankar, Uriel
 ; APPLICANT: Wasserman, Scott

; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Smithson, Glennda
 ; APPLICANT: Gunther, Erik
 ; APPLICANT: Komuves, Laszlo
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-340
 ; CURRENT APPLICATION NUMBER: US/10/120,801
 ; CURRENT FILING DATE: 2002-04-11
 ; PRIOR APPLICATION NUMBER: 60/285748
 ; PRIOR FILING DATE: 2001-04-23
 ; PRIOR APPLICATION NUMBER: 60/286068
 ; PRIOR FILING DATE: 2001-04-24
 ; PRIOR APPLICATION NUMBER: 60/286292
 ; PRIOR FILING DATE: 2001-04-25
 ; PRIOR APPLICATION NUMBER: 60/288334
 ; PRIOR FILING DATE: 2001-05-03
 ; PRIOR APPLICATION NUMBER: 60/291241
 ; PRIOR FILING DATE: 2001-05-16
 ; PRIOR APPLICATION NUMBER: 60/322284
 ; PRIOR FILING DATE: 2001-09-14
 ; PRIOR APPLICATION NUMBER: 60/285609
 ; PRIOR FILING DATE: 2001-04-20
 ; NUMBER OF SEQ ID NOS: 155
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 18
 ; LENGTH: 3931
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-120-801-18

Query Match 12.7%; Score 229.5; DB 15; Length 3931;
 Best Local Similarity 28.3%; Pred. No. 1.3e-06;
 Matches 86; Conservative 38; Mismatches 127; Indels 53; Gaps 13;
 QY 31 GEPLVLKCKGAPKPPORLEWKLNTGRTEAWKVLSPQGGGPDWSARVLPNGSLFLPAVG 90
 Db 1934 GQEVRLDCE-ADGQPPDVAW-LKDG-----SPLQDGMGPHLRFYLDGSLVLKGLR 1983
 QY 91 IQDEGIFRCQAMNRNGKETKSNRYRVYQIPKPEIVDSASELTAGVFNKVG 148
 Db 1984 ASDAGAYTCVAHNPADEARL-HTVNVLPPTIKQAGDGSGLTVSR-PGELVTWVCPVRG 2041
 QY 149 SYPAGTSLWHLDGKPLVPNEK-----GVSVKQETRRHPETGLTQSELMTVPARGDP 202
 Db 2042 SPPT-HVSWLKDGLPLPLSQRTLLHSGHTLRISKVQLADAGIFTC-----VAASPAQVADR 2097
 QY 203 RPTSCSFPGLPRHRLARTAPIQPRVWEPVLEEVOLVVEPEGGAAPGGTTLTCEVP 262
 Db 2098 NFTLQVQVPP-----VLEPVFQNDVVVVR-----GSLVLPCEAR 2133
 QY 263 AQPSPQIHWKMDGVPL---PLPPSPVLLPEIGPDQGTYSVATHSHGPOESRAVIS 319
 Db 2134 GVPLPLVSWMKDGEPLLSQSLEQPSLOLEAVGAGDSGTSCVAV---SEAGEARRHFOLT 2191
 QY 320 IIEP 323
 Db 2192 VMEP 2195

RESULT 13

US-10-094-749-2631
 ; Sequence 2631, Application US/10094749
 ; Publication No. US20030219741A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: WAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUUKO
 ; APPLICANT: HIO, YURI


```

; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2631
; LENGTH: 1034
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2631

Query Match 12.4%; Score 224.5; DB 15; Length 1034;
Best Local Similarity 24.6%; Pred. No. 6.3e-07;
Matches 84; Conservative 44; Mismatches 132; Indels 81; Gaps 13;

QY 15 SLWGAVGQNTARI-----GEPVLVKCKGAPKPPQRLWKLNTGRT----- 58
DB 51 SLNGSVGPEDPRIIVEQPPDLLVSRGSPATLPCR-AEGRP RPNIEMTKNGARVATVRE 109
QY 59 --EAWKVLSPQGGPWSVARVLNGLSLFLPAV-----GIQDEGIFRCOAMNRNGKETKS 111
DB 110 DPAHRLK-----LPSGALFPFRIHGORARPDEGVTTCTVARVNLGAABR 155
QY 112 NYRVRY-----YQIPGRPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPL 164
DB 156 NASLEVAVLDRDFRQSPGNVW-----AVGEP-AVLECVPPRGHPSPVSMRKGARL 207
QY 165 VNEKGVSVKEQTRRRPETGLTLOSELMTVPARGGDPRTTSCSPGLPRHRLRTAP 224
DB 208 KEEGRITIR-----GKLMMSHTLXSD-AGMYVCVAS-NMAGERESAAA- 250
QY 225 IQPRVWEVPLEEVQLVVEPEGAVAPGTVTLTCEVPAQPSQ-PIHMMKDGVPPLP 279
DB 251 -----EVMVLERPSPLRPPVNVQVLADAPVTLCEVKGDPPLRLWRKEDGELPTGRYE 304
QY 280 LPPSPVLLIPEIGPOQGTCTVATHSSHSGPQESRAVSISI 320
DB 305 IRSDSHLWIGHVSAEDEGTYTCAENSVGRAESGSLSVHV 345

RESULT 14
US-10-741-600-1431
; Sequence 1431, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1431
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1431
```

```

Query Match 12.4%; Score 223.5; DB 17; Length 570;
Best Local Similarity 25.8%; Pred. No. 3.7e-07;
Matches 80; Conservative 46; Mismatches 133; Indels 51; Gaps 12;

QY 21 VQAQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTAEAWKVLSPQGG----- 70
DB 26 LGWYTVNSAYGDTIIIPCR---LDVPQNLMP-----GK---WKYKPDGSPVFIAPRSSTK 75
QY 71 ----PWDSV-----ARVLPNGSLFLPAVGIODEGIFRCOAMNRNGKETKSNY-----RVR 116
DB 76 KSVQYDDVPEYKDRNLNLSNYTSLISNARISDEKRFVCMV-----TEDNVFEAPTIVK 129
QY 117 VYQIPCKPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVNEKGVSVKEQ 176
DB 130 VFQPSKPEIVSKALFLETEQKLKGLDCISESDSPDGNITWYRNGKVLHPLLEGAVVIFK 189
QY 177 TRRHPEETGLTLOSELMTVPARGGDPRTTSCS---FSPGLPRHRLRTAPQPRVWE-P 232
DB 190 KEMDPVTQLYTWTSTLEYKTK-ADIQMPFTCSVTYYGFS-----GQKTIHSEQAVFDIY 243
QY 233 VFLEEVQLVVEPEGAVAPGTVTLTCEVPAQPSQ-PIHMMKDGVPPLPPLPPSPVLILPEI 291
DB 244 YPTEQVTIQVLPKNAIKEGDNITLKCLNGNPPPEEPFLYLPQGOPEGIRSSNTYTLTDV 303
QY 292 GPQDOGTYSK 301
DB 304 RNNATGDYKC 313

RESULT 15
US-09-736-457-334
; Sequence 334, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 334
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-334

Query Match 12.4%; Score 223.5; DB 9; Length 582;
Best Local Similarity 25.8%; Pred. No. 3.8e-07;
Matches 80; Conservative 46; Mismatches 133; Indels 51; Gaps 12;

QY 21 VQAQNTARIGEPVLVKCKGAPKPPQRLWKLNTGRTAEAWKVLSPQGG----- 70
DB 25 LGWYTVNSAYGDTIIIPCR---LDVPQNLMP-----GK---WKYKPDGSPVFIAPRSSTK 74
QY 71 ----PWDSV-----ARVLPNGSLFLPAVGIODEGIFRCOAMNRNGKETKSNY-----RVR 116
DB 75 KSVQYDDVPEYKDRNLNLSNYTSLISNARISDEKRFVCMV-----TEDNVFEAPTIVK 128
QY 117 VYQIPCKPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTLSWHLDGKPLVNEKGVSVKEQ 176
DB 129 VFQPSKPEIVSKALFLETEQKLKGLDCISESDSPDGNITWYRNGKVLHPLLEGAVVIFK 188
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Qy	177	TRRHETGLFTLQSELMVTPARGDPRPTFSCS---	ESFGLPRHRLRTAPIQPRVWE-P	232
Db	189	KEMDPVTQLYWTSTLEVKTKK-ADIQMPFCTSY	YGPS-----GQKTIHSEQAVFDIY	242
Qy	233	VPLEEVLVWEPEGAVAPGGTVTLTCEVPAQSP-Q	IHMMDGVPLPLPPSPVLILPEI	291
Db	243	YPTQEVITQLVPPKNAIKEGDNITLKLGNNGNP	PEEFYLPQGPQEGIRSNNTYLTLDV	302
Qy	292	GPQDQGYSC	301	
Db	303	RNAATGDYKC	312	

Search completed: March 16, 2005, 02:46:23
Job time : 334 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2005, 09:06:31 ; Search time 24 Seconds
(without alignments)
1359.062 Million cell updates/sec

Title: US-10-091-019-3

Perfect score: 1806

Sequence: 1 MAAGTAVGAWVLVLSLWCAV.....IIEPGEGETAGSVGGSLGV 339

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216783 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1802	99.8	404	1	I61596
2	1480	81.9	416	1	A42879
3	1402	77.6	402	2	T09062
4	223.5	12.4	1344	2	T14316
5	222.5	12.3	583	2	I39428
6	217.5	12.0	646	2	I38049
7	212.5	11.8	523	2	I50478
8	212.5	11.8	588	2	A45254
9	210.5	11.7	588	2	JH0506
10	209	11.6	1612	2	T30805
11	204.5	11.3	587	2	JH0464
12	203	11.2	1651	2	T14160
13	198	11.0	4391	2	A38096
14	196	10.9	1033	2	S19247
15	195.5	10.8	584	2	I50419
16	187	10.4	3707	2	S18252
17	185.5	10.3	521	2	S34338
18	183.5	10.2	423	2	T29549
19	183.5	10.2	1273	2	T42405
20	182.5	10.1	702	2	A36319
21	182	10.1	5175	2	T20992
22	182	10.1	5198	2	T43290
23	180.5	10.0	1265	1	A37967
24	180	10.0	6642	2	T29757
25	179.5	9.9	458	2	JC1509
26	175.5	9.7	344	2	I56551
27	174	9.6	739	2	JS0675
28	169.5	9.4	458	1	WNMSR1
29	169.5	9.4	521	2	JC1508

ALIGNMENTS

RESULT 1

I61596

advanced glycosylation end-products receptor precursor - human

N:Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprotein

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004

C:Accession: I61596; B42879; S27968

R:Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, H.;

Genomics 23, 408-419, 1994

A:Title: Three genes in the human MHC class III region near the junction with the class I

interpart of mouse mammary tumor gene int-3.

A:Reference number: A55562; MUID:95137587; PMID:7835890

A:Accession: I61596

A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL

A:Molecule type: DNA

A:Residues: 1-404 <RES>

R:Cross-references: UNIPROT:Q15109; GB:D28769; NID:9561657; PIDN:BA005958.1; PID:9561659

R:Nepper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; Ste

J. Biol. Chem. 267, 14998-15004, 1992

A:Title: Cloning and expression of a cell surface receptor for advanced glycosylation en

A:Reference number: A42879; MUID:92340547; PMID:1378843

A:Accession: B42879

A:Molecule type: mRNA

A:Residues: 'G',2-99,'R',101-404 <NEE>

A:Cross-references: EMBL:M91211; NID:9190845; PIDN:AAA03574.1; PID:g190846

A:Experimental source: lung

A:Note: sequence extracted from NCBI backbone (NCBIP:109438)

C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycosyl

cellular function, thus contributing to tissue lesions in diabetes.

C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide on i

ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.

C:Genetics:

A:Gene: GDB:AGER

A:Cross-references: GDB:306354; OMIM:600214

A:Map position: 6p21.3-6p21.3

A:Introns: 18/1, 53/3, 119/1, 140/3, 170/1, 231/1, 274/3, 322/1, 331/1, 373/2

C:Function:

A:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in neurit

C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology

C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-404/Product: advanced glycosylation end products receptor #status predicted <MAT>

F:23-344/Domain: extracellular #status predicted <EXT>

F:31-101/Domain: immunoglobulin homology <IM1>

F:137-210/Domain: immunoglobulin homology <IM2>

F:252-303/Domain: immunoglobulin homology <IM3>

F:345-362/Domain: transmembrane #status predicted <TM>

F:363-404/Domain: intracellular #status predicted <INT>

F:25.81/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:38-99,144-208,255-301/disulfide bonds: #status predicted

Query Match

99.8%; Score 1802; DB 1; Length 404;

Best Local Similarity 100.0%; Pred. No. 3.4e-113;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGTAVGAWVLVLSLWGAUVGAQNTARIGEPVLVLCCKGAPKPPQRLWKLNTGRTEA 60
Db 1 MAAGTAVGAWVLVLSLWGAUVGAQNTARIGEPVLVLCCKGAPKPPQRLWKLNTGRTEA 60

QY 61 WKVLSPOGGPMDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQI 120
Db 61 WKVLSPOGGPMDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQI 120

QY 121 PKRPEIVDSASELTAGVNPKNVGTCSSEGSYPAGTLSWHLDDGKPLVNEKGVSVKEQTRRH 180
Db 121 PKRPEIVDSASELTAGVNPKNVGTCSSEGSYPAGTLSWHLDDGKPLVNEKGVSVKEQTRRH 180

QY 181 PETGLFTLQSELMTVPARGGDPRTTSCSPGLPRHRLARTAPIQPRVWEVPLEEVOL 240
Db 181 PETGLFTLQSELMTVPARGGDPRTTSCSPGLPRHRLARTAPIQPRVWEVPLEEVOL 240

QY 241 VVPEEGAVAGPCTVTLTCEVPAQSPQIHHMKDGVPLPLPSPVLLIPEIGPDQGTYS 300
Db 241 VVPEEGAVAGPCTVTLTCEVPAQSPQIHHMKDGVPLPLPSPVLLIPEIGPDQGTYS 300

QY 301 CVATHSHGPOESRAVSISIIIEPGEPTAGSVGGSL 338
Db 301 CVATHSHGPOESRAVSISIIIEPGEPTAGSVGGSL 338

RESULT 2
A42879
Advanced glycosylation end-products receptor precursor - bovine
N;Alternate names: advanced glycosylation end product-binding protein, 35k; glycoprotein
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Mar-1993 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
R;Nepper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; St
J. Biol. Chem. 267, 14998-15004, 1992
A;Title: Cloning and expression of a cell surface receptor for advanced glycosylation en
A;Reference number: A42879; MUID:92340547; PMID:1378843
A;Accession: A42879
A;Molecule type: mRNA
A;Residues: 1-416 <NEE>
A;Cross-references: UNIPROT:Q28173; GB:M91212; NID:G163650; PIDN:AAA03575.1; PID:G163651
A;Experimental source: lung
A;Note: sequence extracted from NCBI backbone (NCBIP:109436)
A;Note: parts of this sequence, including the amino end of the mature protein, were dete
R;Schmidt, A.M.; Vianna, M.; Gerlach, M.; Brett, J.; Ryan, J.; Kao, J.; Esposito, C.; He
J. Biol. Chem. 267, 14987-14997, 1992
A;Title: Isolation and characterization of two binding proteins for advanced glycosylati
A;Reference number: A42878; MUID:92340546; PMID:1321822
A;Accession: A42878
A;Molecule type: protein
A;Residues: 23-24,'X',26-37,'X',39-49,'XX',52-54 <SCH>
A;Experimental source: endothelial cells
A;Note: sequence extracted from NCBI backbone (NCBIP:109434)
C;Comment: advanced glycosylation end products are heterogeneous nonenzymatically glycos
cellular function, thus contributing to tissue lesions in diabetes.
C;Comment: this receptor appears also to mediate the effects of amyloid beta peptide on
aces in the neurotoxic pathway that produces dementia in Alzheimer's disease.
C;Function:
A;Description: neuronal receptor for amphoterin, a DNA-binding protein involved in neuro
C;Superfamily: advanced glycosylation end products receptor; immunoglobulin homology
C;Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-416/Product: advanced glycosylation end-products receptor RAGE #status predicted <M
F;23-354/Domain: extracellular #status predicted <EXT>
F;31-100/Domain: immunoglobulin homology <IM1>
F;136-209/Domain: immunoglobulin homology <IM2>
F;262-313/Domain: immunoglobulin homology <IM3>
F;355-372/Domain: transmembrane #status predicted <TM>
F;373-416/Domain: intracellular #status predicted <INT>
F;25.80/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;38-98,143-207,269-311/disulfide bonds: #status predicted

Query Match 81.9%; Score 1480; DB 1; Length 416;
Best Local Similarity 80.5%; Pred. No. 1.1e-91;
Matches 281; Conservative 22; Mismatches 34; Indels 12; Gaps 2;

QY 1 MAAGTAVGAWVLVLSLWGAUVGAQNTARIGEPVLVLCCKGAPKPPQRLWKLNTGRTEA 60
Db 1 MAAGTAVGAWVLVLSLWGAUVGAQNTARIGEPVLVLCCKGAPKPPQRLWKLNTGRTEA 60

QY 61 WKVLSPOGGPMDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQI 120
Db 61 WKVLSPO-GDPMDSVARVLPNGSLFLPAVGIQDEGIFRCATRSRSGKETKSNYRVVYQI 119

QY 121 PKRPEIVDSASELTAGVNPKNVGTCSSEGSYPAGTLSWHLDDGKPLVNEKGVSVKEQTRRH 180
Db 120 PKRPEIVDPASELTASVPKNVGTCSSEGSYPAGTLSWHLDDGKLLIPDGKETLVKEETRRH 179

QY 181 PETGLFTLQSELMTVPARGGDPRTTSCSPGLPRHRLARTAPIQPRVW----- 230
Db 180 PKTGLFTLHSELMTVPARGGALHPTFSCFTPLPRRALHTAPIQLRVWSEHRGEGPN 239

QY 231 -EPVPLESVOLVWPEEGGAVAPGGTIVLTCEVPAQSPQIHHMKDGVPLPLPSPVLLIP 289
Db 240 VDAVPLKEVQLVWPEEGGAVAPGGTIVLTCEAPAQPPQIHWIKDGRPLPLPPGFMILLP 299

QY 290 RIGPDQGTYSQVATHSHGPOESRAVSISIIIEPGEPTAGSVGGSL 338
Db 300 EVGPEDQGTYSQVATHSHGPOESRAVSIIIEGEGTLAGSVGGPL 348

RESULT 3
T09062

Probable advanced glycosylation end-products receptor precursor - mouse

N;Alternate names: RAGE

C;Species: Mus musculus (house mouse)

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: T09062

submitted to the EMBL Data Library, October 1997

A;Description: Sequence of the mouse major histocompatibility locus class III region.

A;Reference number: Z16543

A;Accession: T09062

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA

A;Residues: 1-402 <ROW>

A;Cross-references: UNIPROT:O35444; EMBL:AF030001; NID:G2564945; PID:G2564950

C;Genetics:

A;Gene: RAGE

A;Map position: 17

A;Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2

C;Superfamily: advanced glycosylation end products receptor; immunoglobulin homology

C;Keywords: receptor; transmembrane protein

F;31-100/Domain: immunoglobulin homology <IMW>

Query Match 77.6%; Score 1402; DB 2; Length 402;
Best Local Similarity 78.7%; Pred. No. 1.8e-86;
Matches 266; Conservative 20; Mismatches 50; Indels 2; Gaps 2;

QY 1 MAAGTAVGAWVLVLSLWGAUVGAQNTARIGEPVLVLCCKGAPKPPQRLWKLNTGRTEA 60
Db 1 MPAGTAAAWVLVLAALMGAVAGQNTARIGEPVLVLCCKGAPKPPQRLWKLNTGRTEA 60

QY 61 WKVLSPOGGPMDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVVYQI 120
Db 61 WKVLSPO-GGPMDSVARILPNGSILLPATGIVDEGIFRCATNRRCVKVSNYRVVYQI 119

QY 121 PKRPEIVDSASELTAGVNPKNVGTCSSEGSYPAGTLSWHLDDGKPLVNEKGVSVKEQTRRH 180
Db 120 PKRPEIVDPASELTASVPKNVGTCSSEGSYPAGTLSWHLDDGKLLIPDGKETLVKEETRRH 179

QY 181 PETGLFTLQSELMTVPARGGDPRTTSCSPGLPRHRLARTAPIQPRVWEVPLEEVOL 240
Db 180 PETGLFTLRSSELIVPTQGG-THPTTSCSPSLGLPRRRPLNTAPIQLRVREPDPPEGIQL 238

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OM protein - protein search, using sw model

Run on: March 15, 2005, 11:25:56 ; Search time: 82 Seconds
(without alignments)
2117.010 Million cell updates/sec

Title: US-10-091-019-3

Perfect score: 1805

Sequence: 1 MAAGTAVGANVLVLSMGAV.....IIEPGEGETAGSVGGSLV 339

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1802	99.8	404	1	RAGE_HUMAN	Q15109 homo sapien
2	1768	97.9	347	2	O86SN1	Q868n1 homo sapien
3	1480	81.9	416	1	RAGE_BOVIN	Q28173 bos taurus
4	1409	78.0	402	2	O6MG86	Q6mg86 rattus norv
5	1404.5	77.8	403	1	RAGE_MOUSE	Q62151 mus musculu
6	1402	77.6	402	2	O35444	Q35444 mus musculu
7	1401	77.6	402	1	RAGE_RAT	Q63495 rattus norv
8	1057	58.5	330	2	O6QP58	Q6qp58 canis famil
9	754.5	41.8	161	2	O6UFY5	Q6ufy5 sus scrofa
10	709	39.3	147	2	O71BG7	Q71bg7 homo sapien
11	553.5	30.6	119	2	O6TYZ6	Q6tyz6 canis famil
12	227.5	12.6	583	1	C166_MOUSE	Q61490 mus musculu
13	227.5	12.6	1366	1	ROB3_MOUSE	Q92214 mus musculu
14	225	12.5	573	2	O6GN50	Q6gn50 xenopus lae
15	224.5	12.4	1386	1	ROB3_HUMAN	Q96ms0 homo sapien
16	223.5	12.4	564	2	O6IOX4	Q6icx4 brachydanio
17	222.5	12.3	564	1	C166_BRARE	Q90460 brachydanio
18	222.5	12.3	583	1	C166_HUMAN	Q13740 homo sapien
19	221.5	12.3	564	2	O7ZU00	Q7zu00 brachydanio
20	220	12.2	521	1	C166_RABIT	O46651 oryctolagus
21	219.5	12.2	646	2	O95812	Q95812 homo sapien
22	219	12.1	555	1	C166_CARAU	Q90304 carassius a
23	218.5	12.1	646	2	O6PHR3	Q6phr3 homo sapien
24	217.5	12.0	646	1	MU18_HUMAN	P43121 homo sapien
25	217	12.0	570	2	O6GLY1	Q6gly1 xenopus lae
26	216	12.0	583	1	C166_RAT	Q35112 rattus norv
27	215	11.9	1134	2	O71B05	Q71b05 brachydanio
28	214	11.8	544	2	O7Z285	Q7z285 brachydanio
29	214	11.8	1340	2	O8NDA2	Q8nda2 homo sapien
30	214	11.8	1496	2	O92626	Q92626 homo sapien
31	210.5	11.7	330	2	O90242	Q90242 gallus gall

32	210.5	11.7	588	1	C166_CHICK	P42292 gallus gall
33	209	11.6	1612	1	ROB1_MOUSE	O89026 mus musculu
34	209	11.6	1651	1	ROB1_HUMAN	Q9y6n7 homo sapien
35	208	11.5	583	1	C166_BOVIN	Q9b613 bos taurus
36	205.5	11.4	606	2	O6IRH8	Q6irh8 rattus norv
37	204	11.3	521	1	C166_CANFA	O46634 canis famil
38	204	11.3	814	2	O8IVU1	Q8ivu1 homo sapien
39	204	11.3	5636	2	Q96RW7	Q96rw7 homo sapien
40	203	11.2	1651	1	ROB1_RAT	O55005 rattus norv
41	201	11.1	793	2	O70246	O70246 mus musculu
42	201	11.1	813	2	O8BQC3	Q8bqc3 mus musculu
43	201	11.1	1389	2	Q90Z69	Q90z69 brachydanio
44	201	11.1	1419	2	Q98SW3	Q98sw3 brachydanio
45	200.5	11.1	485	2	Q801W5	Q801w5 brachydanio

ALIGNMENTS

RESULT 1
RAGE_HUMAN STANDARD; PRT; 404 AA.
ID AC Q15109; Q15279; Q9H2X7; Q9V3R3;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Advanced glycosylation end product-specific receptor precursor
DE (Receptor for advanced glycosylation end products).
GN Name=AGER; Synonyms=RAGE;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lung;
RX MEDLINE=92340547; PubMed=1378843;
RA Nepper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,
RA Elliston K., Stern D., Shaw A.;
RT "Cloning and expression of a cell surface receptor for advanced
RT glycosylation end products of proteins.";
RL J. Biol. Chem. 267:14998-15004(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95137587; PubMed=7835890;
RA Sugaya K., Fukagawa T., Matsuoto K., Mita K., Takahashi E., Ando A.,
RA Inoko H., Ikemura T.;
RT "Three genes in the human MHC class III region near the junction with
RT the class II: gene for receptor of advanced glycosylation end
RT products, PBX2 homeobox gene and a notch homolog, human counterpart of
RT mouse mammary tumor gene int-3.";
RL Genomics 23:408-419(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E.,
RA Banta A., Spies T., Hood L.;
RT "Sequence determination of 300 kilobases of the human class III MHC
RT locus.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100.
RA Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y.,
RA Yamamoto H.;
RT "Molecular heterogeneity of the receptor for advanced glycation
RT endproducts.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Malherbe P., Richards J., Gaillard H., Thompson A., Diener C.,
RA Schuler A., Huber G.;
RT "cDNA cloning of a novel secreted isoform of the human receptor for
RT advanced glycation end products (RAGE) and characterization of cells
RT co-expressing cell-surface scavenger receptors and Swedish mutant

amyloid precursor protein.";
 RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Colling S.F., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haigh F.,
 RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP SEQUENCE OF 1-12 FROM N.A.
 RA Hudson B.I., Futers T.S.;
 RT "Novel polymorphisms in the receptor for advanced glycation end-
 RT products (RAGE) gene";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Mediates interactions of advanced glycosylation end
 CC products (AGE). These are nonenzymatically glycosylated proteins
 CC which accumulate in vascular tissue in aging and at an accelerated
 CC rate in diabetes. Receptor for amyloid beta peptide.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
 CC Secreted. (isoform 2).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q15109-1; Sequence=Displayed;
 CC Name=2; Synonyms=RAGSEC;
 CC IsoId=Q15109-2; Sequence=VSP_002551, VSP_002552;
 CC -1- TISSUE SPECIFICITY: Endothelial cells.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; M61211; AAA03574.1; -;
 DR EMBL; D28769; BAA05958.1; -;
 DR EMBL; U93336; AAB47491.1; -;
 DR EMBL; AB036432; BAA89369.1; -;
 DR EMBL; AJ133822; CAB43108.1; -;
 DR EMBL; BC020669; AAB20669.1; -;
 DR EMBL; AF208289; AAG35728.1; -;
 DR PIR; I61596; I61596.
 DR Genew; HGNC:320; AGER.
 DR H-InvDB; HIX0005749; -;
 DR MIM; 600214; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.

Pfam; PF00047; ig; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Alternative splicing; Glycoprotein; Immunoglobulin domain;
 KW Polymorphism; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 404 Advanced glycosylation end product-
 FT specific receptor.
 FT DOMAIN 23 342 Extracellular (Potential).
 FT TRANSMEM 343 363 Potential.
 FT DOMAIN 364 404 Cytoplasmic (Potential).
 FT DOMAIN 23 116 Ig-like V-type.
 FT DOMAIN 124 221 Ig-like C2-type 1.
 FT DOMAIN 227 317 Ig-like C2-type 2.
 FT DISULFID 38 99 Potential.
 FT DISULFID 144 208 Potential.
 FT DISULFID 259 301 Potential.
 FT CARBOHYD 81 81 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 380 384 Poly-Glu.
 FT VARSPLIC 54 67 Missing (in isoform 2).
 FT VARSPLIC 275 404 /FTId=VSP_002551.
 FT VARSPLIC 275 404 GVPLPLPPSEVLILPEIGPDQGTVCVATHSSHQPSRA
 FT VARSPLIC 275 404 VSIISIERGEGPTAGSGGLGTLALALGILGLTAAL
 FT VARSPLIC 275 404 LIGVILMORRORRGEKAPENQEEEEERAEELNSEEPAE
 FT VARSPLIC 275 404 ESSTGGP -> VSDLERGAGTRRGAGNCRLCGRAGNS
 FT VARSPLIC 275 404 FPGDGPGRGDSRPAHGHVAKAATPRRGEGPRKPGGRG
 FT VARSPLIC 275 404 GACRTESVGT (in isoform 2).
 FT VARSPLIC 275 404 /FTId=VSP_002552.
 FT VARSPLIC 275 404 Q -> R.
 FT VARSPLIC 275 404 /FTId=VAR_011338.
 FT CONFLICT 1 1 M -> G (in Ref. 1).
 FT SEQUENCE 404 AA; 42802 MW; 0D584C436C30CCE7 CRC64;
 Query Match 99.8%; Score 1802; DB 1; Length 404;
 Best Local Similarity 100.0%; Pred. No. 3.7e-106;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAGTAVGAWVLVLSLWAGVAVGAQNIITARIGEPLVLCCKGAPKPPORLEWKLMTGRTEA 60
 DB 1 MAAGTAVGAWVLVLSLWAGVAVGAQNIITARIGEPLVLCCKGAPKPPORLEWKLMTGRTEA 60
 QY 61 WKVLSPOGGPQWDSVARVLPNGSLFLPAVGIQDGIIFRCQAMNNGKETSNRVRYQI 120
 DB 61 WKVLSPOGGPQWDSVARVLPNGSLFLPAVGIQDGIIFRCQAMNNGKETSNRVRYQI 120
 QY 121 PGKPEIVDSASELTAGVNVKVTGTCVSEGSYPAGTSLWHLDGKPLVPNEKGVSKVKEQTRRH 180
 DB 121 PGKPEIVDSASELTAGVNVKVTGTCVSEGSYPAGTSLWHLDGKPLVPNEKGVSKVKEQTRRH 180
 QY 181 PETGLFTLQSELMTVPARGDPRFTSCSPGLPRHRLTAPIQPRVWEPVLEEVQL 240
 DB 181 PETGLFTLQSELMTVPARGDPRFTSCSPGLPRHRLTAPIQPRVWEPVLEEVQL 240
 QY 241 VVEPEGGAVPGGTVTTLTCEVPAQSPQIHWMDKGVPLPLPPSPVLILPEIGPDQGTYS 300
 DB 241 VVEPEGGAVPGGTVTTLTCEVPAQSPQIHWMDKGVPLPLPPSPVLILPEIGPDQGTYS 300
 QY 301 CVATHSSHGQESRAVSIISIERGEGPTAGSGGL 338
 DB 301 CVATHSSHGQESRAVSIISIERGEGPTAGSGGL 338
 RESULT 2
 Q86SN1 PRELIMINARY; PRT; 347 AA.
 ID Q86SN1
 AC Q86SN1; 24, Created
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Soluble form of receptor for advanced glycation endproducts
 DE precursor.
 GN Name=RAGE;

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22510265; PubMed=12495433; DOI=10.1042/BJ20021371;
RA Yonekura H., Yamamoto Y., Sakurai S., Petrova R.G., Abedin Md.J.,
RA Li H., Yasui K., Takeuchi M., Makita Z., Takasawa S., Okamoto H.,
RA Watanabe T., Yamamoto H.;
RT "Novel splice variants of the receptor for advanced glycation end-
RT products expressed in human vascular endothelial cells and pericytes,
RT and their putative roles in diabetes-induced vascular injury.";
RL Biochem. J. 370:11097-11093(2003).
DR EMBL; AB061668; BAC65465.1; -;
DR GO; GO:004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Receptor; Signal.
FT SIGNAL 1 22
SQ SEQUENCE 347 AA; 37050 MW; 519E377C4D6AC62C CRC64;
Query Match 97.9%; Score 1768; DB 2; Length 347;
Best Local Similarity 100.0%; Pred. No. 4,4e-104; Indels 0; Gaps 0;
Matches 331; Conservative 0; Mismatches 0;
QY 1 MAAGTAVGAWLVLSLWGAVGVAQNITARIIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60
Db 1 MAAGTAVGAWLVLSLWGAVGVAQNITARIIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60
QY 61 WKVLSPPQGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTSNRYRVYQI 120
Db 61 WKVLSPPQGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTSNRYRVYQI 120
QY 121 PKGPEIVDSASELTAGVPKNKGVCTVSEGSYPAGTILSHWLDGKPLVNEKGVSKQTRRH 180
Db 121 PKGPEIVDSASELTAGVPKNKGVCTVSEGSYPAGTILSHWLDGKPLVNEKGVSKQTRRH 180
QY 181 PETGLFTLQSELMTVPARGDPRPTSCFSFGLPRHRLRTAPIQRYWEPVPLEEVOL 240
Db 181 PETGLFTLQSELMTVPARGDPRPTSCFSFGLPRHRLRTAPIQRYWEPVPLEEVOL 240
QY 241 VVEPEGAVAPGTTVLTCEVPAQPSQIHMMKDGVLPLPSPVLILPEIGPDQGTYS 300
Db 241 VVEPEGAVAPGTTVLTCEVPAQPSQIHMMKDGVLPLPSPVLILPEIGPDQGTYS 300
QY 301 CVATHSHGPGQSRVAVSISITIEPGEAGTAG 331
Db 301 CVATHSHGPGQSRVAVSISITIEPGEAGTAG 331
RESULT 3
RAGE_BOVIN STANDARD; PRT; 416 AA.
ID _RAGE_BOVIN
AC Q28173;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Advanced glycosylation end product-specific receptor precursor
DE (Receptor for advanced glycosylation end products).
GN Name=AGER; Synonyms=RAGE;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE=Lung;
RX MEDLINE=92340547; PubMed=1378943;
RA Neepser M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,
RA Elliston K., Stern D., Shaw A.;
RT "Cloning and expression of a cell surface receptor for advanced
RT glycosylation end products of proteins.";
RL J. Biol. Chem. 267:14998-15004(1992).
CC -!- FUNCTION: Mediates interactions of advanced glycosylation end
CC products (AGE). These are nonenzymatically glycosylated proteins
CC which accumulate in vascular tissue in aging and at an accelerated
CC rate in diabetes.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Endothelial cells.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC -----
DR EMBL; M91212; AAA03575.1; -;
DR PIR; A42879; A42879.
DR HSSP; PI3590; I1B5.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 22
FT CHAIN 23 416
FT DOMAIN 23 352 Advanced glycosylation end product-
FT TRANSMEM 353 373 specific receptor.
FT DOMAIN 374 416 Extracellular (Potential).
FT DOMAIN 23 115 Potential.
FT DOMAIN 123 220 Cytoplasmic (Potential).
FT DOMAIN 238 327 Ig-like V-type.
FT DISULFID 38 98 Ig-like C2-type 1.
FT DISULFID 143 207 Ig-like C2-type 2.
FT DISULFID 269 311 Potential.
FT CARBOHYD 25 25 Potential.
FT CARBOHYD 80 80 N-linked (GlcNAc...) (Potential).
FT DOMAIN 391 396 Poly-Glu.
SQ SEQUENCE 416 AA; 44182 MW; B703815573E767AE CRC64;
Query Match 81.9%; Score 1480; DB 1; Length 416;
Best Local Similarity 80.5%; Pred. No. 8,8e-86;
Matches 281; Conservative 22; Mismatches 34; Indels 12; Gaps 2;

QY 1 MAAGTAVGAWLVLSLWGAVGVAQNITARIIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60
Db 1 MAAGTAVGAWLVLSLWGAVGVAQNITARIIGEPVLVKCKGAPKPPQRLWKLTGRTGA 60
QY 61 WKVLSPPQGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTSNRYRVYQI 120
Db 61 WKVLSPPQGGPWSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKTSNRYRVYQI 119
QY 121 PKGPEIVDSASELTAGVPKNKGVCTVSEGSYPAGTILSHWLDGKPLVNEKGVSKQTRRH 180
Db 120 PKGPEIVDSASELTAGVPKNKGVCTVSEGSYPAGTILSHWLDGKPLVNEKGVSKQTRRH 179
QY 181 PETGLFTLQSELMTVPARGDPRPTSCFSFGLPRHRLRTAPIQRYWEPVPLEEVOL 230
Db 180 PETGLFTLQSELMTVPARGDPRPTSCFSFGLPRHRLRTAPIQRYWEPVPLEEVOL 239

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QY 231 -EPVLEEVQVWVEPEGAVAPGCTVTLTCEVPAQSPQIHKMKDGVPLPLPSPVLILP 289
Db 240 VDAVPLKEVQVWVEPEGAVAPGCTVTLTCEVPAQSPQIHKMKDGVPLPLPSPVLILP 299
QY 290 EIGPDQGTYSVATHSHGQPSRAVSIIEFGEGPTAGSVGGSL 338
Db 300 EVGPDQGTYSVATHSHGQPSRAVSIIEFGEGPTAGSVGGSL 348

RESULT 4
Q6MG86
ID Q6MG86 PRELIMINARY; PRT; 402 AA.
AC Q6MG86;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Advanced glycosylation end product-specific receptor.
GN Name=Ager;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Brown Norway;
RX PubMed=15060004; DOI=10.1101/gr.1987704;
RA Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shiina T.,
RA Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.;
RT "The genomic sequence and comparative analysis of the rat major
RT histocompatibility complex.";
RL Genome Res. 14:631-639(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Brown Norway;
RA Boehm S., Borzym K., Gelling S., Gimmel V., Heitmann K., Kosiura A.,
RA Lang N., Lehrach S., Thiel J., Sontag M., Hurt P., Himmelbauer H.,
RA Sudbrak R., Reinhardt R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX883044; CAE83960.1;
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IgC2; 2.
DR SMART; SM00408; IgC2; 2.
DR PROSITE; PS08335; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 402 AA; 42644 MW; CEA49453C05E1CA1 CRC64;

Query Match 78.0%; Score 1409; DB 2; Length 402;
Best Local Similarity 78.1%; Pred. No. 2.6e-81;
Matches 264; Conservative 25; Mismatches 47; Indels 2; Gaps 2;

QY 1 MAAGTAVGAWVLVLSWGAVGQAQNTARIGPELVLCCKGAPKPPQRLWKLTGRTEA 60
Db 1 MPTGTVARAWVLVLAWGAVAGQNTARIGPELVLCCKGAPKPPQRLWKLTGRTEA 60
QY 61 WKVLSQGGPQWDSVARVLVPLNGSLFPAVCIODEGIFRCQANVNGKETKSNYRVVQI 120
Db 61 WKVLSQ-GDPWDSVARILVPLNGSLFPAVCIODEGIFRCQANVNGKETKSNYRVVQI 119
QY 121 PGKPEIVDSASBLTAGVPNKVTCVSEGSYPAGTILSWHLDGKPLVPNEKGVSKBOTRRH 180
Db 120 PGKPEIVNFASELTAQVFNKVTCSVSEGSYPAGTILSWHLDGKPLVPGKGVKKEETRRH 179
QY 181 PETGLFTLOSELMTVPARGDPRPFSCSFSGLPFRHRLFTAPIQPRVWEPVLEEVQ 240
Db 180 PETGLFTLSELVTVAQGG-TTPTYSFSLGLPRHRLPLNTAPIQPRVWEPVLEEVQ 238

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QY 241 VVEPEGAVAPGCTVTLTCEVPAQSPQIHKMKDGVPLPLPSPVLILPEIGPDQGTYS 300
Db 239 LVEPEGCTVAPGCTVTLTCEVPAQSPQIHKMKDGVPLPLPSPVLILPEVGHDEGIYS 298
QY 301 CVATHSHGQPSRAVSIIEFGEGPTAGSVGGSL 338
Db 299 CVATHSHGQPSPPVIRVTETGEGQAAGSVGGSL 336

RESULT 5
RAGE_MOUSE
ID RAGE_MOUSE STANDARD; PRT; 403 AA.
AC Q62151;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Advanced glycosylation end product-specific receptor precursor
DE (Receptor for advanced glycosylation end products).
GN Name=Ager; Synonyms=Rage;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c; TISSUE=Lung;
RX MEDLINE=97368045; PubMed=9224812;
RA Renard C., Chappuy O., Wautier M.P., Nagashima M., Lundh E.,
RA Morser J., Zhao L., Schmidt A.M., Scherrmann J.M., Wautier J.L.;
RT "Recombinant advanced glycation end product receptor pharmacokinetics
RT in normal and diabetic rats.";
RL Mol. Pharmacol. 52:54-62(1997).
CC -!- FUNCTION: Mediates interactions of advanced glycosylation end
CC products (AGE). These are nonenzymatically glycosylated proteins
CC which accumulate in vascular tissue in aging and at an accelerated
CC rate in diabetes.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Endothelial cells.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC
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CC
CC EMBL; L33412; AAA40040.1; -.
CC MGD; MGI:893592; Ager.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0006810; P:transport; IDA.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_C2.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00408; IgC2; 1.
CC PROSITE; PS08335; IG_LIKE; 3.
CC PROSITE; PS00290; IG_MHC; 1.
CC Glycoprotein; Immunoglobulin domain; Repeat; Signal; Transmembrane.
FT SIGNAL 1 22
FT CHAIN 23 403
FT DOMAIN 23 341
FT TRANSMEM 342 362
FT DOMAIN 363 403
FT DOMAIN 23 109
FT DOMAIN 123 220
FT DOMAIN 234 316
FT DISULFID 38 98
FT DISULFID 143 207
FT DISULFID 258 300

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FT CARBOHYD 25 25 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 80 80 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 403 AA; 42668 MW; 1279796FD1579357 CRC64;

Query Match 77.8%; Score 1404.5; DB 1; Length 403;
 Best Local Similarity 78.4%; Pred. No. 5.1e-81;
 Matches 265; Conservative 20; Mismatches 52; Indels 1; Gaps 1;

QY 1 MAAGTAVGAWLVLSLWGA VVGAGQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTEA 60
 DB 1 MPAGTAARAWLVLLWGA VAGGQNTARIGEPVLVLSCKGAPKPPQQLWKLTGRTEA 60

QY 61 WKVLSPOGGPWPDSVARVLPNGSLFPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYQI 120
 DB 61 WKVLSPO-GGPWDSVARVLPNGSLFPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYQI 119

QY 121 PKGPEIVDSASELTAGVPNKVGTCSGSPAGTILSHWLDGKPLVNEKGVSKVKEOTRRH 180
 DB 120 PKGPEIVDPASELTASVPNKVGTCSGSPAGTILSHWLDGKLLIPDGKETLVKEETRRH 179

QY 181 PETGLFTLQSELMTVPARGGDRPTFSCSPGLPRHRLARTAPIQRYVWEPVPLEEVOL 240
 DB 180 PETGLFTLASELTVIPTQGGTHPTFSCSPGLPRRPLNTAPIQLRVREPCPPPGIQL 239

QY 241 VVEPEGGAVAPGCTVTLTCEVPAQSPQIHMKDGVPLPLPSPVLILPEIGPDQGTYS 300
 DB 240 LVEPEGGIVAPGCTVTLTCAISAQPPQVHWIKDGLPLFLAPSVLLEPEVGHADGTYG 299

QY 301 CVATHSSHGQPQSRVAVSISIIIEPGESEGTAGSVGGSL 338
 DB 300 CVATHPSHGQPSPVPSIRVTETGDEGPAEGSVGGSL 337

RESULT 6
 ID O35444 PRELIMINARY; PRT; 402 AA.

AC O35444;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE RAGE (Advanced glycosylation end product-specific receptor).
 GN Name=RAGE; Synonyms=Ager;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14656967; DOI=10.1101/gr.1736803;
 RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,
 RA Campbell R.D., Hood L.;
 RT "Analysis of the gene-dense major histocompatibility complex class III
 region and its comparison to mouse";
 RL Genome Res. 13:2621-2636(2003).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Lung and heart;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Fawcett A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung and heart;
 RA Strausberg R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF030001; AAB82007.1; --
 DR EMBL; BC061182; AAB61182.1; --
 DR EMBL; BC061182; AAB61182.1; --
 DR EIR; T09062; T09062.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 402 AA; 42653 MW; DBFDC50A6C8CB902 CRC64;

Query Match 77.6%; Score 1402; DB 2; Length 402;
 Best Local Similarity 78.7%; Pred. No. 7.3e-81;
 Matches 266; Conservative 20; Mismatches 50; Indels 2; Gaps 2;

QY 1 MAAGTAVGAWLVLSLWGA VVGAGQNTARIGEPVLVKCKGAPKPPQRLWKLTGRTEA 60
 DB 1 MPAGTAARAWLVLLWGA VAGGQNTARIGEPVLVLSCKGAPKPPQQLWKLTGRTEA 60

QY 61 WKVLSPOGGPWPDSVARVLPNGSLFPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYQI 120
 DB 61 WKVLSPO-GGPWDSVARVLPNGSLFPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYQI 119

QY 121 PKGPEIVDSASELTAGVPNKVGTCSGSPAGTILSHWLDGKPLVNEKGVSKVKEOTRRH 180
 DB 120 PKGPEIVDPASELTASVPNKVGTCSGSPAGTILSHWLDGKLLIPDGKETLVKEETRRH 179

QY 181 PETGLFTLQSELMTVPARGGDRPTFSCSPGLPRHRLARTAPIQRYVWEPVPLEEVOL 240
 DB 180 PETGLFTLASELTVIPTQGGTHPTFSCSPGLPRRPLNTAPIQLRVREPCPPPGIQL 238

QY 241 VVEPEGGAVAPGCTVTLTCEVPAQSPQIHMKDGVPLPLPSPVLILPEIGPDQGTYS 300
 DB 239 LVEPEGGIVAPGCTVTLTCAISAQPPQVHWIKDGLPLFLAPSVLLEPEVGHADGTYG 298

QY 301 CVATHSSHGQPQSRVAVSISIIIEPGESEGTAGSVGGSL 338
 DB 299 CVATHPSHGQPSPVPSIRVTETGDEGPAEGSVGGSL 336

RESULT 7
 ID RAGE RAT STANDARD; PRT; 402 AA.

AC O63495;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Advanced glycosylation end product-specific receptor precursor
 DE (Receptor for advanced glycosylation end products).
 GN Name=Ager; Synonyms=Rage;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Lung;
 RX MEDLINE=97368045; PubMed=9224812;
 RA Renard C., Chappey O., Wautier M.P., Nagashima M., Lundh E.,
 RA Morser J., Zhao L., Schmidt A.M., Scherrmann J.M., Wautier J.L.;

RT "Recombinant advanced glycation end product receptor pharmacokinetics
 RL in normal and diabetic rats.";
 CC Mol. Pharmacol. 52:54-62(1997).
 CC -1- FUNCTION: Mediates interactions of advanced glycosylation end
 CC products (AGE). These are nonenzymatically glycosylated proteins
 CC which accumulate in vascular tissue in aging and at an accelerated
 CC rate in diabetics.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Endothelial cells.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -----
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 CC -----
 CC EMBL; L33413; AAA42027.1; -;
 CC RGD; 69258; Ager.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003598; Ig_C2.
 CC InterPro; IPR003006; Ig_MHC.
 CC Pfam; PF00047; Ig; 3.
 CC SMART; SM00408; IGC2; 1.
 CC PROSITE; PS00835; IG_LIKE; 3.
 CC PROSITE; PS00290; IG_MHC; 1.
 CC Glycoprotein; Immunoglobulin domain; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 402 Advanced glycosylation end product-
 FT specific receptor.
 FT DOMAIN 23 341 Extracellular (Potential).
 FT TRANSMEM 342 362 Potential.
 FT DOMAIN 363 402 Cytoplasmic (Potential).
 FT DOMAIN 23 109 Ig-like V-type.
 FT DOMAIN 123 219 Ig-like C2-type 1.
 FT DOMAIN 233 315 Ig-like C2-type 2.
 FT DISULFID 38 98 Potential.
 FT DISULFID 143 206 Potential.
 FT DISULFID 257 299 Potential.
 FT CARBOHYD 25 25 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 80 80 N-linked (GlcNAc...) (Potential).
 FT SEQUENCE 402 AA; 42663 MW; 594481BC3A51E94E CRC64;
 Query Match 77.6%; Score 1401; DB 1; Length 402;
 Best Local Similarity 77.8%; Pred. No. 8.4e-81;
 Matches 263; Conservative 25; Mismatches 48; Indels 2; Gaps 2;
 QY 1 MAAGTAVGAWVLVLSLWGVAGVQNTARIGBPLVLCCKGAPKPPQRLKWLNGRTGA 60
 DB 1 MPTGTVARAWVLVLSLWGVAGVQNTARIGBPLVLCCKGAPKPPQRLKWLNGRTGA 60
 QY 61 WKVLSFGQGGPNDVSVARVLPNGSLFPAVGIQDEGIFRCQAMNRNGKTSNYRVVQI 120
 DB 61 WKVLSFGQGGPNDVSVARVLPNGSLFPAVGIQDEGIFRCQAMNRNGKTSNYRVVQI 119
 QY 121 PGKPEIVDSASELTAGVPNKVGTCSGSPAGTSLSHLDGKPLVPNEKGVSKQTRRH 180
 DB 120 PGKPEIVDSASELTAGVPNKVGTCSGSPAGTSLSHLDGKPLVPNEKGVSKQTRRH 179
 QY 181 PETGLTLOSELMTVPARGDPRPTSCFSFGLPRHRLARTAPIQPRVWEPVLEEVQL 240
 DB 180 PETGLTLOSELMTVPARGDPRPTSCFSFGLPRHRLARTAPIQPRVWEPVLEEVQL 238
 QY 241 VVEPEGAVAGGTVTLTCEVAPQSPQIHKMGKGVLPPLPSPVLLPEIGPOQGYTS 300
 DB 239 LVEPEGAVAGGTVTLTCAISAPQPPQIHKMGKGVLPPLPSPVLLPEIGPOQGYTS 298
 QY 301 CVATHSHGPOBSRAVSISIIIEPGEPTAGSVGGSL 338
 DB 299 CVATHSHGPOBSRAVSISIIIEPGEPTAGSVGGSL 336

RESULT 8

Q6QP58 Q6QP58 PRELIMINARY; PRT; 330 AA.
 AC Q6QP58;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE RAGE (Fragment).
 OS Canis familiaris (Dog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 CC NCBI_TaxID=9615;
 RN [1]_TaxID=9615;
 RP SEQUENCE FROM N.A.
 RA Murua Escobar H., Soller J.T., Sterenczak K.A., Richter A., Meyer B.,
 RA Winkler S., Nolte I., Bullerdiek J.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY530943; AAS21266.1; -;
 DR InterPro; IPR003599; Ig-like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00409; IG; 2.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 FT NON_TER 1 330
 FT NON_TER 330 330
 SQ SEQUENCE 330 AA; 35418 MW; 16B15C31E78D99A2 CRC64;

Query Match 58.5%; Score 1057; DB 2; Length 330;
 Best Local Similarity 73.0%; Pred. No. 3.9e-59;
 Matches 208; Conservative 20; Mismatches 35; Indels 22; Gaps 5;
 QY 54 NTGRTEAMKVLSPQGGPNDVSVARVLPNGSLFPAVGIQDEGIFRCQAMNRNGKTSNY 113
 DB 1 NTGRTEAMKVLSPQGGPNDVSVARVLPNGSLFPAVGIQDEGIFRCQAMNRNGKTSNY 59
 QY 114 RVVYQIPKPEIVDSASELTAGVPNKVGTCSGSPAGTSLSHLDGKPLVPNEKGVSV 173
 DB 60 QRVVYQIPKPEIVDSASELTAGVPNKVGTCSGSPAGTSLSHLDGKPLVPNEKGVSV 119
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 QY 234 PLEEVQLVVEPEGAVAGGTVTLTCEVAPQSPQIHKMGKGVLPPLPSPVLLPEIGP 293
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 QY 294 ODQGYTSCVATHSHGPOBSRAVSISIIIEPGEPTAGSVGGSL 338
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 AC Q6UFY5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Receptor for advanced glycosylation end products (Fragment).
 GN Name=RAGE;
 OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 CC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schupp N., Stopper H., Heidland A.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 18:50:14 ; Search time 1561.84 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
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1	336	100.0	1218 6	CQ730900 Sequence
2	336	100.0	1223 6	BD176670 Soluble R
3	336	100.0	1223 9	AB061668 Homo sapi
4	336	100.0	1268 9	AB036432 Homo sapi
5	336	100.0	1436 9	BC020669 Homo sapi
6	336	100.0	1451 9	AB061669 Homo sapi
7	332.8	99.0	1391 6	AR321600 Sequence
8	332.8	99.0	1391 9	HUMRAGE
9	270.6	80.5	1426 4	BOVRAGE
10	270.6	80.5	1426 6	AR321599 Sequence
11	248.4	73.9	358 4	AY382178 Canis fam
12	242.2	72.1	1399 10	BC061182 Mus muscu
13	242.2	72.1	1420 10	RAYRECEP
14	242	72.0	1250 9	HSAL133822 Homo sapi
15	239	71.1	1348 6	AR321601 Sequence
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ALIGNMENTS

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LOCUS	Sequence 16834 from Patent WO2068579.				
DEFINITION	CQ730900				
ACCESSION	CQ730900.1	GI:42306010			
VERSION					
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.				
TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof				
JOURNAL	Patent: WO 02068579-A 16834 06-SEP-2002;				
PE Corporation (NY) (US)					
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Db	127	AGAAACACACCCCGGCTGGAATGGAACACTGAACACAGCCCGGACAGAGCTTGGAG	186		
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Db	187	GTCTCTGTCTCTCCCGAGGAGGCCCTCGGACAGTGGCTCGTCTCTTCCCAACGGC	246		
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Db      247  |||||TCCCTCTTCCTCCGCTGTCGGATCCAGGATGAGGGAATTTTCGGTGCACGCAATG 306
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Qy      301  AAGCCAGAAATTTAGATTCTGCCTCTGAACCTCAGC 336
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LOCUS   BD176670
DEFINITION Soluble RAGE protein. 1223 bp DNA linear PAT 18-MAR-2003
ACCESSION BD176670
VERSION   BD176670.1 GI:29122380
KEYWORDS  WO 02074805-A/1.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 1223)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          Yonekura, H., Yonekura, H., Yamamoto, Y., Sakurai, S. and Watanabe, T.
          Soluble RAGE protein
          Patent: WO 02074805-A 1 26-SEP-2002;
          JAPAN AS REPRESENTED BY PRESIDENT OF KANAZAWA UNIVERSITY, HIROSHI
          YAMAMOTO, HIDETO YONEKURA, YASUHIKO YAMAMOTO, SHIGERU SAKURAI, TAKUO
          WATANABE
          OS Homo sapiens (human)
          PN WO 02074805-A/1
          PD 26-SEP-2002
          PF 19-MAR-2002 WO 2002JP002623
          PR 19-MAR-2001 JP 01P 078409, 10-AUG-2001 JP 01P 243114 PR
          25-FEB-2002 JP 02P 048182
          PI HIROSHI YAMAMOTO, HIDETO YONEKURA, YASUHIKO YAMAMOTO, SHIGERU PI
          SAKURAI,
          PT TAKUO WATANABE
          PC C07K14/47, C12N15/12, C12N1/21, C12N5/10, C12N1/19, A61K39/395, PC
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          A61P37/08,
          PC G01N33/15, G01N33/50, G01N33/53, G01N33/577
          CC Soluble RAGE protein
          FH Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 7.4e-86;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GCTCAAAATCATCAGCCCGGATTGGCGCCACTGGTCTGAAGTGTAAAGGGGCCCCC 60
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Qy      121  GTCTGTCTCTCCAGGAGAGAGCCCTCGGACAGTGTGCTGTCTCTCTCCCAACGCG 180
Db      211  GTCTGTCTCTCCAGGAGAGAGCCCTCGGACAGTGTGCTGTCTCTCTCCCAACGCG 270
Qy      181  TCCCTCTCTCTCCGCTGTCCGGATCCAGGATGAGGGATTTCCGGTGCAGGCAATG 240
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Qy      301  AAGCCAGAAATTTAGATTCTGCCTCTGAACCTCAGC 336
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LOCUS   AB061668
DEFINITION Homo sapiens RAGE mRNA for soluble form of receptor for advanced
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ACCESSION AB061668
VERSION   AB061668.1 GI:28971759
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          Yonekura, H., Yamamoto, Y., Sakurai, S., Petrova, R.G., Abedin, Md.J.,
          Li, H., Yasui, K., Takeuchi, M., Makita, Z., Takasawa, S., Okamoto, H.,
          Watanabe, T. and Yamamoto, H.
          Novel splice variants of the receptor for advanced glycation
          end-products expressed in human vascular endothelial cells and
          pericytes, and their putative roles in diabetes-induced vascular
          injury
          Biochem. J. 370 (Pt 3), 1097-1109 (2003)
          12495433
REFERENCE 2 (bases 1 to 1223)
AUTHORS   Yonekura, H., Yamamoto, Y., Sakurai, S. and Yamamoto, H.
          Direct Submission
          Submitted (11-MAY-2001) Hideto Yonekura, Kanazawa University,
          Graduate School of Medical Science; 13-1 Takara-machi, Kanazawa,
          Ishikawa 920-8640, Japan (E-mail:hyone@med.kanazawa-u.ac.jp,
          Tel:81-76-265-2182, Fax:81-76-234-4226)
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DEFINITION transcript variant 1, mRNA (cdna clone MGC:22357 IMAGE:4718076),
complete cds.
ACCESSION BC020669.1 GI:18088362
VERSION BC020669
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1436)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
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Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
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McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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Best Local Similarity 100.0%; Pred. No. 7.4e-86; Indels 0; Gaps 0;
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DB 391 AGCCAGAAATGTAGATTCTGCTCTGAATCAAG 426

RESULT 4
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LOCUS Homo sapiens RAGE mRNA for advanced glycation endproducts receptor,
DEFINITION complete cds.
ACCESSION AB036432
VERSION AB036432.1 GI:6691625
KEYWORDS advanced glycation endproducts receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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AUTHORS Abidin,M.J., Yonekura,H., Migita,H., Karsawa,J., Yamamoto,Y. and
Yamamoto,H.
TITLE Molecular heterogeneity of the receptor for advanced glycation
endproducts
JOURNAL Unpublished
AUTHORS Abidin,M.J., Yonekura,H. and Yamamoto,H.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-2000) Hideto Yonekura, Kanazawa University School
of Medicine, Department of Biochemistry; 13-1 Takara-machi,
Kanazawa, Ishikawa 920-8640, Japan
(E-mail:hyone@med.kanazawa-u.ac.jp, Tel:++81-76-265-2181,
Fax:++81-76-234-4226)
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E., Schnercher, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932
2 (bases 1 to 1436)
Direct Submission
Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILML at: <http://image.llnl.gov>
Series: IRAL Plate: 37 Row: e Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 26787960.

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.4e-86;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCTCAAAACATCACACCCGGATTGGCGAGCCACTGGTGCTGAAGTGTAAAGGGGCCCCC 60

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QY 121 GTCTCTCTCTCCCGAGGAGGAGCCCTCGGACAGTGTGGCTCTCTCTCCCAACGCGC 180
Db 206 GTCTCTCTCTCCCGAGGAGGAGCCCTCGGACAGTGTGGCTCTCTCTCCCAACGCGC 265
QY 181 TCCTCTCTCTCTCCCGCTGTCGGGATCCAGGATGAGGGATTTCCGGTGCAGGCAATG 240
Db 266 TCCTCTCTCTCTCCCGCTGTCGGGATCCAGGATGAGGGATTTCCGGTGCAGGCAATG 325
QY 241 AACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGTTCCTGGG 300
Db 326 AACAGGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGTTCCTGGG 385
QY 301 AAGCCGAAATGTAGATTCTGCTCTGAACTCAGC 336
Db 386 AAGCCGAAATGTAGATTCTGCTCTGAACTCAGC 421

RESULT 6
LOCUS AB061669
DEFINITION Homo sapiens RAGE mRNA for N-terminal truncated form of receptor for advanced glycation endproducts, complete cds.
ACCESSION AB061669
VERSION AB061669.1 GI:28971761
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Yonekura, H., Yamamoto, Y., Sakurai, S., Petrova, R.G., Abedin, Md.J., Li, H., Yasui, K., Takeuchi, M., Makita, Z., Takasawa, S., Okamoto, H., Watanabe, T., and Yamamoto, H.
TITLE Novel splice variants of the receptor for advanced glycation end-products expressed in human vascular endothelial cells and pericytes, and their putative roles in diabetes-induced vascular injury
JOURNAL Biochem. J. 370 (Pt 3), 1097-1109 (2003)
MEDLINE 22510265
PUBMED 12495433
REFERENCE 2 (bases 1 to 1451)
AUTHORS Yonekura, H., Yamamoto, Y., Sakurai, S. and Yamamoto, H.
TITLE Direct Submission
JOURNAL Submitted (11-MAY-2001) Hideto Yonekura, Kanazawa University, Graduate School of Medical Science; 13-1 Takara-machi, Kanazawa, Ishikawa 920-8640, Japan (E-mail: hyone@med.kanazawa-u.ac.jp, Tel:81-76-265-2182, Fax:81-76-234-4226)
FEATURES
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1. .1451
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/mol_type="mRNA"
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511. .1422
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Qy <th>301</th> <th>AGCCAGAAATCTAGATTTCTGCCTCTGAACCTCACG</th> <th>336</th>	301	AGCCAGAAATCTAGATTTCTGCCTCTGAACCTCACG	336
Db <th>367</th> <th>AGCCAGAAATCTAGATTTCTGCCTCTGAACCTCACG</th> <th>402</th>	367	AGCCAGAAATCTAGATTTCTGCCTCTGAACCTCACG	402
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LOCUS			linear
DEFINITION			PRI 09-DEC-1993
ACCESSION			Human receptor for advanced glycosylation end products (RAGE) mRNA, partial cds.
VERSION			M91211.1 GI:190845
KEYWORDS			RAGE; cell surface receptor.
SOURCE			Homo sapiens (human)
ORGANISM			Homo sapiens
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS			1 (bases 1 to 1391) Keeper, M., Schmidt, A.M., Brett, J., Yan, S.D., Wang, F., Pan, Y.C., Elliston, K., Stern, D. and Shaw, A.
TITLE			Cloning and expression of a cell surface receptor for advanced glycosylation end products of proteins
JOURNAL			J. Biol. Chem. 267 (21), 14998-15004 (1992)
MEDLINE			92340547
PUBMED			1378843
REFERENCE			2 (bases 1 to 1391) Shaw, A.
AUTHORS			Direct Submission
TITLE			Submitted (15-APR-1992) A. Shaw, Department of Cellular and Molecular Biology, Merck Sharp and Dohme Research Laboratories, West Point, PA 19486 USA
JOURNAL			Original source text: Homo sapiens cDNA to mRNA.
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Matches 334; Conservative			0; Mismatches 2; Indels 0; Gaps 0;
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Qy      181 TCCCTCTCTCTCCAGGAGGAGGCGCTTGGGACAGTGTGGTGTGCTTCCCAAGCGG 240
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Qy      301 AAGCCAGAAATGTAGATTCTGCTCTGAAGTCAAG 336
Db      367 AAGCCAGAAATGTAGATTCTGCTCTGAAGTCAAG 402

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RESULT 9
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LOCUS
DEFINITION
  Cow receptor for advanced glycosylation end products (RAGE) mRNA,
  complete cds.
ACCESSION
  M91212.1 GI:163650
VERSION
  RAGE; cell surface receptor.
KEYWORDS
  Bos taurus (cow)
ORGANISM
  Bos taurus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
  Bovinae; Bos.
REFERENCE
  1 (bases 1 to 1426)
  Nepper, M., Schmidt, A.M., Brett, J., Yan, S.D., Wang, F., Pan, Y.C.,
  Elliston, K., Stern, D. and Shaw, A.
  Cloning and expression of a cell surface receptor for advanced
  glycosylation end products of proteins
  J. Biol. Chem. 267 (21), 14998-15004 (1992)
MEDLINE
  92340547
  1378843
PUBMED
  1378843
REFERENCE
  2 (bases 1 to 1426)
  Shaw, A.
  Direct Submission
  Submitted (15-APR-1992) A. Shaw, Department of Cellular and
  Molecular Biology, Merck Sharp and Dohme Research Laboratories,
  West Point, PA 19486 USA
  Original source text: Bos taurus cDNA to mRNA.
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COMMENT

FEATURES

source

source

CDS

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Best Local Similarity 90.4%; Pred. No. 5.3e-67;
Matches 301; Conservative 0; Mismatches 29; Indels 3; Gaps 1;
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Qy 124 CTGTCTCCAGGGAGAGGCGCTTGGGACAGTGTGGTGTGCTTCCCAAGCGGTCC 183
Db 199 CTGTCTCCAGGGAGAGGCGCTTGGGACAGTGTGGTGTGCTTCCCAAGCGGTCC 255
Qy 184 CTGTCTCTCCGGTGTGGGATCCAGATGAGGGGATTTTCCGGTCCAGGCAATGAAC 243
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RESULT 10
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LOCUS
DEFINITION
  Sequence 2 from patent US 6563015.
ACCESSION
  AR321599
VERSION
  AR321599.1 GI:33706828
KEYWORDS
  Unknown.
ORGANISM
  Unknown.
REFERENCE
  1 (bases 1 to 1426)
  Stern, D.M., Schmidt, A.M. and Yan, S.D.
  Transgenic mice over-expressing receptor for advanced glycation
  endproduct (RAGE) and mutant APP in brain and uses thereof
  Patent: US 6563015-A 2 13-MAY-2003;
  Location/Qualifiers
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: March 14, 2005, 17:18:58 ; Search time 211.972 Seconds
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Perfect score: 336
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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: Geneseqn2001as.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	336	100.0	336	6 ABQ79957	Abq79957 Human RAG
2	336	100.0	957	2 AAV06518	AAV06518 Human RAG
3	336	100.0	1020	6 ABQ79956	Abq79956 Human sol
4	336	100.0	1023	2 AAV12394	AAV12394 Human sol
5	336	100.0	1023	2 AAV06517	AAV06517 Human RAG
6	336	100.0	1090	12 ADM80824	Adm80824 Human CAD
7	336	100.0	1194	12 ADP19657	Adp19657 Human LP2
8	336	100.0	1223	6 ABV73151	Abv73151 Human sol
9	336	100.0	1223	10 ADG37043	Adg37043 Receptor
10	336	100.0	1239	12 ADP19663	Adp19663 Human LP2
11	336	100.0	1268	10 ADG33024	Adg33024 Human DNA
12	336	100.0	1291	12 ADP19655	Adp19655 Human LP2
13	336	100.0	1329	12 ADP19665	Adp19665 Human LP2
14	336	100.0	1339	12 ADP19661	Adp19661 Human LP2
15	336	100.0	1384	12 ADP19659	Adp19659 Human LP2
16	336	100.0	1391	6 ABQ79955	Abq79955 Human RAG
17	336	100.0	1415	6 ABQ99597	Abq99597 Human cod
18	336	100.0	1436	12 ADK00130	Adk00130 Human RAG
19	336	100.0	1463	6 ABQ99598	Abq99598 Human cod
20	336	100.0	1627	9 ACC59921	Acc59921 Human REM

21	334.4	99.5	1146	13 ADS10302	Adsl10302 Human the
22	334.4	99.5	1217	10 ADE95563	Ade95563 Human NOV
23	334.4	99.5	1582	4 AAH57444	Aah57444 Human lun
24	334.4	99.5	1761	12 ADK00128	Adk00128 Human RAG
25	332.8	99.0	957	2 AAV12395	AAV12395 Human mat
26	332.8	99.0	1391	6 ABK10856	Abk10856 DNA encod
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37	242	72.0	1173	10 ADE95567	Ade95567 Human NOV
38	242	72.0	1226	10 ADE95565	Ade95565 Human NOV
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40	242	72.0	1678	9 ACC59907	Acc59907 Human REM
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42	239	71.1	1348	6 ABK10857	Abk10857 DNA encod
43	239	71.1	1348	6 AAD36953	Aad36953 Mouse rec
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ALIGNMENTS

RESULT 1
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ID ABQ79957 standard; DNA; 336 BP.
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AC ABQ79957;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human RAGE V-domain nucleotide sequence.

XX Receptor for Advanced Glycated end product; RAGE; recombinant; nootropic;
XX antiarteriosclerotic; antidiabetic; cytostatic; nephrotropic; vasotropic;
XX neuroprotective; antiinflammatory; gene therapy; human; ds.

OS Homo sapiens.
XX
PN WO200270667-A2.
XX
PD 12-SEP-2002.

PF 05-MAR-2002; 2002WO-US006881.
XX
PR 05-MAR-2001; 2001US-0273418P.
XX
PA (TRAN-) TRANSTECH PHARMA INC.
XX
PI Harris R, Shen J, Shahbaz M;
XX
DR WPI; 2002-713443/77.

XX High level expression of recombinant Receptors for Advanced Glycated end
PT products (RAGE) proteins for treating increased levels of advanced
PT glycosylation end products, comprises infecting cells with a high titer
PT recombinant virus.
XX
PS Claim 14; Fig 2C; Sipp; English.

XX The invention relates to a method for high level expression of
CC recombinant forms of the Receptor for Advanced Glycated end products
CC (RAGE) or its fragments: The method involves (i) subcloning a nucleotide
CC sequence encoding RAGE or its fragment into a virus; (ii) preparing a
CC high titer stock of recombinant virus; and (iii) infecting host cells
CC with the high titer recombinant virus under conditions such that

CC predetermined levels of RAGE or its fragment is produced, where the
 CC predetermined levels of RAGE comprises at least 25 mg recombinant protein
 CC per liter of culture. The method is useful for high level expression of
 CC recombinant RAGE polypeptide or its fragment which may be useful in
 CC preventing, treating or ameliorating diseases associated with increased
 CC levels of advanced glycosylation end products, such as atherosclerosis,
 CC diabetes and its symptoms, amyloidosis, kidney failure, Alzheimer's
 CC disease, inflammation, systemic lupus nephritis, inflammatory lupus
 CC nephritis, cancer or erectile dysfunction. The present sequence
 CC represents the nucleotide sequence of the V-domain of human RAGE
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 XX Sequence 336 BP; 81 A; 95 C; 99 G; 61 T; 0 U; 0 Other;
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 Best Local Similarity 100.0%; Pred. No. 9.5e-93;
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 DB |||||
 QY 241 AACAGGAATGGAAGAGAGCCCTCTGGGACAGTGTGGCTCGTCTCTCCCAACGGC 300
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 QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAATCTCAGC 336
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 DB |||||
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 ID AAV06518 standard; DNA; 957 BP.
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 AC AAV06518;
 XX
 DT 08-MAY-1998 (first entry)
 XX
 DE Human RAGE polypeptide (318 amino acid residues) encoding DNA.
 XX
 KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;
 KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;
 KW Alzheimer's disease; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1. .1023
 FT /tag= a
 FT /product= "RAGE polypeptide"
 XX
 PN WO9739121-A1.
 XX
 XX 23-OCT-1997.
 PD
 PF 11-APR-1997; 97WO-EP001832.
 XX
 PR 16-APR-1996; 96US-00633147.
 XX
 PA (SCHD) SCHERING AG.
 XX

PI Morser MJ, Nagashima M;
 XX
 DR WPI; 1997-526458/48.
 DR P-PSDB; AAW33754.
 XX
 PT New soluble advanced glycosylation end-product receptor polypeptide -
 PT used for reducing vascular permeability, complications of diabetes etc.,
 PT also for purification and to screen for modulators.
 XX
 XX Claim 12; Fig 1B; 91pp; English.
 XX
 CC This genomic DNA encodes a human advanced glycosylation end-product
 CC receptor (RAGE) polypeptide (318 amino acid residues). The RAGE
 CC polypeptides and its active fragments or their mimetics, inhibit
 CC interaction between advanced glycosylation end-products (AGE) and a
 CC receptor (specifically RAGE). They are used to treat diseases associated
 CC with AGE/RAGE interaction, such as increased vascular permeability,
 CC diabetes mellitus (particularly complications such as micro- or macro-
 CC vasculopathy or occlusive vascular disorders such as neuropathy,
 CC nephropathy, retinopathy or atherosclerosis) or haemodialysis-associated
 CC amyloidosis, also activation of microglial cells by beta-amyloid peptides
 CC in Alzheimer's disease or age-related disorders such as oxidative stress.
 CC These RAGE polypeptides are also used, when immobilised, to purify AGE
 CC from a protein mixture and to screen for compounds that are agonists and
 CC antagonists of AGE/RAGE interaction. They can also be used diagnostically
 CC to detect abnormal levels of AGE. Antibodies against RAGE polypeptides
 CC are useful as immunoassay reagents for measurement of RAGE levels, and as
 CC inhibitors of interaction between AGE and RAGE or other receptors, and for
 CC purification and quantification of RAGE polypeptides. The encoding
 CC nucleic acids are used to express recombinant RAGE and as probes for
 CC isolating related genes
 XX
 SQ Sequence 957 BP; 207 A; 286 C; 289 G; 175 T; 0 U; 0 Other;
 Query Match 100.0%; Score 336; DB 2; Length 957;
 Best Local Similarity 100.0%; Pred. No. 1.4e-92;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB |||||
 QY 1 GCTCAAAACATCATCAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 60
 DB |||||
 QY 61 AAGAAACACCCAGCGGCTGGAATGGAATGAACTGAACACAGCGCGGACAGAACTGGAG 120
 DB |||||
 QY 61 AAGAAACACCCAGCGGCTGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 120
 DB |||||
 QY 121 GTCTCTCTCTCCAGGAGAGGCCCTCTGGGACAGTGTGGCTCGTCTCTCCCAACGGC 180
 DB |||||
 QY 121 GTCTCTCTCTCCAGGAGAGGCCCTCTGGGACAGTGTGGCTCGTCTCTCCCAACGGC 180
 DB |||||
 QY 181 TCCCTCTCTCTCCAGGAGAGGCCCTCTGGGACAGTGTGGCTCGTCTCTCCCAACGGC 240
 DB |||||
 QY 181 TCCCTCTCTCTCCAGGAGAGGCCCTCTGGGACAGTGTGGCTCGTCTCTCCCAACGGC 240
 DB |||||
 QY 241 AACAGGAATGGAAGAGAGCCCTCTGGGACAGTGTGGCTCGTCTCTCCCAACGGC 300
 DB |||||
 QY 241 AACAGGAATGGAAGAGAGCCCTCTGGGACAGTGTGGCTCGTCTCTCCCAACGGC 300
 DB |||||
 QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAATCTCAGC 336
 DB |||||
 QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAATCTCAGC 336
 DB |||||
 RESULT 3
 ABQ79956
 ID ABQ79956 standard; DNA; 1020 BP.
 XX
 AC ABQ79956;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Human soluble RAGE (sRAGE) encoding DNA.
 XX

KW Receptor for Advanced Glycated end product; RAGE; recombinant; nootropic;
 KW antidiabetic; antidiabetic; cytosolic; nephrotropic; vasotropic;
 KW neuroprotective; antiinflammatory; gene therapy; human; gene; ds.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH 1. .1020
 FT /*tag= a
 FT /product= "sRAGE"
 FT /note= "soluble, extracellular portion of RAGE"

XX WO200270667-A2.

PN 12-SEP-2002.

XX 05-MAR-2002; 2002WO-US006881.

XX 05-MAR-2001; 2001US-0273418P.

XX (TRAN-) TRANSTECH PHARMA INC.

XX Harris R, Shen J, Shahbaz M;

XX WPI; 2002-713443/77.

DR P-PSDB; ABB82164.

XX High level expression of recombinant Receptors for Advanced Glycated end products (RAGE) proteins for treating increased levels of advanced glycosylation end products, comprises infecting cells with a high titer recombinant virus.

XX Claim 13; Fig 2B; 51pp; English.

XX The invention relates to a method for high level expression of recombinant forms of the Receptor for Advanced Glycated end products (RAGE) or its fragments. The method involves (i) subcloning a nucleotide sequence encoding RAGE or its fragment into a virus; (ii) preparing a high titer stock of recombinant virus; and (iii) infecting host cells with the high titer recombinant virus under conditions such that predetermined levels of RAGE or its fragment is produced, where the predetermined levels of RAGE comprises at least 25 mg recombinant protein per liter of culture. The method is useful for high level expression of recombinant RAGE polypeptide or its fragment which may be useful in preventing, treating or ameliorating diseases associated with increased levels of advanced glycosylation end products, such as atherosclerosis, diabetes and its symptoms, amyloidosis, kidney failure, Alzheimer's disease, inflammation, systemic lupus nephritis, inflammatory lupus nephritis, cancer or erectile dysfunction. The present sequence represents the nucleotide sequence of human sRAGE (soluble, extracellular portion of RAGE)

XX Sequence 1020 BP; 216 A; 299 C; 316 G; 189 T; 0 U; 0 Other;

Query Match 100.0%; Score 336; DB 6; Length 1020;
 Best Local Similarity 100.0%; Pred. No. 1.4e-92;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAGTGTAAAGGGGCCCC 60

DB 67 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAGTGTAAAGGGGCCCC 126

QY 61 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAG 120

DB 127 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAG 186

QY 121 GTCTGTCTCCAGGAGAGAGCCCTGGGACAGTGTGGTCTGTCTTCTCCACGGC 180

DB 187 GTCTGTCTCCAGGAGAGAGCCCTGGGACAGTGTGGTCTGTCTTCTCCACGGC 246

QY 181 TCCCTCTTCTCCAGGAGAGAGCCCTGGGACAGTGTGGTCTGTCTTCTCCACGGC 240

DB 247 TCCCTCTTCTCCAGGAGAGAGCCCTGGGACAGTGTGGTCTGTCTTCTCCACGGC 306

QY 241 AACAGGAATGGAAGAGAGACCAAGTCCAACCTACCGAGTCCGTCTTACCAAGATTCCTGGG 300
 DB 307 AACAGGAATGGAAGAGAGACCAAGTCCAACCTACCGAGTCCGTCTTACCAAGATTCCTGGG 366
 QY 301 AAGCCAGAAATTTAGATTCTGCCTCTGAACCTCAG 336
 DB 367 AAGCCAGAAATTTAGATTCTGCCTCTGAACCTCAG 402

RESULT 4

AAV12394

ID AAV12394 standard; DNA; 1023 BP.

XX AAV12394;

DT 14-MAY-1998 (first entry)

DE Human soluble receptor to an advanced glycosylation end product DNA.

XX Human; soluble receptor; advanced glycosylation end product; RAGE; AGE;
 KW antibody; vascular permeability; diabetes mellitus; ds.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FH 1. .1023
 FT /*tag= a
 FT /product= "soluble RAGE"

XX WO9739125-A1.

XX 23-OCT-1997.

PP 11-APR-1997; 97WO-EP001834.

PR 16-APR-1996; 96US-00633148.

XX (SCHD) SCHERING PATENTE AG.

XX Morser MJ, Nagaehima M, Hollander DA;

XX WPI; 1997-558580/51.

DR P-PSDB; AAW44199.

XX Anti-advanced glycosylation end product polypeptide antibody - prevents receptor binding and therefore reduces vascular permeability, useful to treat diabetes mellitus.

XX Disclosure; Page 39; 90pp; English.

XX The present sequence encodes a soluble human receptor to an advanced glycosylation end product (RAGE) polypeptide. The present invention describes an isolated antibody (Ab), specifically immunoreactive with RAGE. Advanced glycosylation end products (AGE) of proteins are non-enzymatically glycosylated proteins, which accumulate in vascular tissue in ageing, and at an accelerated rate in individuals with diabetes. The Ab, which prevents the interaction between an AGE and it's receptor (RAGE), reduces vascular permeability. The Ab can be used to treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis associated amyloidosis or atherosclerosis. The Ab can also be used for the isolation and purification of human RAGE polypeptide

XX Sequence 1023 BP; 218 A; 299 C; 317 G; 189 T; 0 U; 0 Other;

Query Match 100.0%; Score 336; DB 2; Length 1023;
 Best Local Similarity 100.0%; Pred. No. 1.4e-92;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAGTGTAAAGGGGCCCC 60

DB 67 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAGTGTAAAGGGGCCCC 126

QY 61 AAGAAACACCCAGCGCTGGAAATGAACTGAACACAGCCGCGACAGAGCTTGAAG 120
DB 127 AAGAAACACCCAGCGCTGGAAATGAACTGAACACAGCCGCGACAGAGCTTGAAG 186
QY 121 GTCTGTCTCCAGGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 180
DB 187 GTCTGTCTCCAGGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 246
QY 181 TCCCTCTCTCCAGGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 240
DB 247 TCCCTCTCTCCAGGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 306
QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGCTCTACAGATTCTCTGG 300
DB 307 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGCTCTACAGATTCTCTGG 366
QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 336
DB 367 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 402

RESULT 5
AAV06517 standard; DNA; 1023 BP.
XX AAV06517;
AC AC
XX 08-MAY-1998 (first entry)
XX Human RAGE polypeptide (340 amino acid residues) encoding DNA.
XX Advanced glycosylation end-product receptor; RAGE; screening; AGE;
KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;
KW Alzheimer's disease; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 1. .1023
FT /*tag= a
FT /product= "RAGE polypeptide"
XX WO9739121-A1.
XX 23-OCT-1997.
XX 11-APR-1997; 97WO-EP001832.
XX 16-APR-1996; 96US-00633147.
XX (SCHD) SCHERING AG.
XX Morser MJ, Nagashima M;
XX WPI; 1997-526458/48.
XX P-PSDB; AAW33753.
XX New soluble advanced glycosylation end-product receptor polypeptide -
PT used for reducing vascular permeability, complications of diabetes etc.,
PT also for purification and to screen for modulators.
XX Claim 12; Fig 1A; 91pp; English.
XX This genomic DNA encodes a human advanced glycosylation end-product
CC receptor (RAGE) polypeptide (340 amino acid residues). The RAGE
CC polypeptides and its active fragments or their mimetics, inhibit
CC interaction between advanced glycosylation end-products (AGE) and a
CC receptor (specifically RAGE). They are used to treat diseases associated
CC with AGE/RAGE interaction, such as increased vascular permeability,
CC diabetes mellitus (particularly complications such as micro- or macro-
CC vasculopathy or occlusive vascular disorders such as neuropathy, or
CC nephropathy, retinopathy or atherosclerosis) or haemodialysis-associated

CC amyloidosis, also activation of microglial cells by beta-amyloid peptides
CC in Alzheimer's disease or age-related disorders such as oxidative stress.
CC These RAGE polypeptides are also used, when immobilised, to purify AGE
CC from a protein mixture and to screen for compounds that are agonists and
CC antagonists of AGE/RAGE interaction. They can also be used diagnostically
CC to detect abnormal levels of AGE. Antibodies against RAGE polypeptides
CC are useful as immunoassay reagents for measurement of RAGE levels, and as
CC inhibitors of interaction between AGE and RAGE or other receptors, and for
CC purification and quantification of RAGE polypeptides. The encoding
CC nucleic acids are used to express recombinant RAGE and as probes for
CC isolating related genes
XX

QY Sequence 1023 BP; 218 A; 299 C; 317 G; 189 T; 0 U; 0 Other;
Query Match 100.0%; Score 336; DB 2; Length 1023;
Best Local Similarity 100.0%; Pred. No. 1.4e-92;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCAAAACATCACAGCCGCGATTGGCGAGCCACTGTGTGAAGTGAAGGGGCCCCC 60
DB 67 GCTCAAAACATCACAGCCGCGATTGGCGAGCCACTGTGTGAAGTGAAGGGGCCCCC 126
QY 61 AAGAAACACCCAGCGCTGGAAATGAACTGAACACAGCCGCGACAGAGCTTGAAG 120
DB 127 AAGAAACACCCAGCGCTGGAAATGAACTGAACACAGCCGCGACAGAGCTTGAAG 186
QY 121 GTCTGTCTCCAGGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 180
DB 187 GTCTGTCTCCAGGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 246
QY 181 TCCCTCTCTCCAGGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 240
DB 247 TCCCTCTCTCCAGGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 306
QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGCTCTACAGATTCTCTGG 300
DB 307 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGCTCTACAGATTCTCTGG 366
QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 336
DB 367 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 402

RESULT 6
ADM80824
ID ADM80824 standard; cDNA; 1090 BP.
XX ADM80824;
AC ADM80824;
XX 03-JUN-2004 (first entry)
XX Human CADECM-11 encoding cDNA SEQ ID NO:53.
XX human; cell adhesion and extracellular matrix protein; CADECM;
KW neuroprotective; cytostatic; anorectic; immune disorder;
KW neurological disorder; developmental disorder;
KW connective tissue disorder; cell proliferative disorder; cancer; obesity;
KW Tangier disease; gene; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 31. .1008
FT /*tag= a
FT /product= "CADECM-11"
XX WO2004015396-A2.
XX 19-FEB-2004.
XX 12-AUG-2003; 2003WO-US025418.
XX 13-AUG-2002; 2002US-0403781P.
PR


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PR 30-AUG-2002; 2002US-0407034P.
PR 13-SEP-2002; 2002US-0410566P.
PR 24-SEP-2002; 2002US-0413482P.
PR 25-SEP-2002; 2002US-0413890P.
PR 08-NOV-2002; 2002US-0424904P.
PR 13-NOV-2002; 2002US-0426222P.
XX
PA (INCV-) INCVTE CORP.
XX
XX Elliott VS, Khare R, Emerling BM, Kable AF, Tran UK, Jin P;
PI Becha SD, Marquis JP, Swarnakar A, Chawla NK, Ramkumar J;
PI Hafalia AJA, Lee SY, Jiang X, Jackson AA, Richardson TW, Blake JJ;
PI Wang JT, Chien D, Yang YG;
XX
XX WPI; 2004-191795/18.
DR P-PSDB; ADM80782.
XX
XX New cell adhesion and extracellular matrix proteins, useful in
PT diagnosing, treating and preventing immune, neurological, developmental,
PT connective tissue and cell proliferative disorders including cancer.
XX
PS Claim 5; SEQ ID NO 53; 272pp; English.
XX
XX The present sequence encodes a human cell adhesion and extracellular
CC matrix protein designated CADECM. CADECM sequences has neuroprotective,
CC cytostatic and anorectic activities. The CADECM polypeptides and
CC polynucleotides are useful in diagnosing, treating and preventing immune,
CC neurological, developmental, connective tissue and cell proliferative
CC disorders including cancer, e.g. breast, prostate, ovarian, lung or colon
CC cancer, obesity and Tangier disease.
XX
XX Sequence 1090 BP; 265 A; 289 C; 351 G; 185 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 336; DB 12; Length 1090;
Best Local Similarity 100.0%; Pred No. 1.4e-92;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTCAAAACATCACAGCCCGGATTGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 60
DB 97 GGTCAAAACATCACAGCCCGGATTGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 156
QY 61 AAGAACACACCCGCGCTGGAATGGAACACTGACACAGCCGCGACAGCTTGGAG 120
DB 157 AAGAACACACCCGCGCTGGAATGGAACACTGACACAGCCGCGACAGCTTGGAG 216
QY 121 GTCCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGCTCTTCCCAACGGC 180
DB 217 GTCCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGCTCTTCCCAACGGC 276
QY 181 TCCCTCTTCTCCCGCTTCGGGATCCAGGATGAGGGGATTTTCGGTGCAGGCAATG 240
DB 277 TCCCTCTTCTCCCGCTTCGGGATCCAGGATGAGGGGATTTTCGGTGCAGGCAATG 336
QY 241 ACAGAAATGGAAGAGACCAAGTCCACTACCGATGAGGGGATTTTCAGATTTCTGGG 300
DB 337 ACAGAAATGGAAGAGACCAAGTCCACTACCGATGAGGGGATTTTCAGATTTCTGGG 396
QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAAG 336
DB 397 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAAG 432
RESULT 7
ADP19657
ID ADP19657 standard; cDNA; 1194 BP.
XX
XX ADP19657;
XX
XX 12-AUG-2004 (first entry)
XX
XX Human LP2001 encoding cDNA SEQ ID NO:3.
XX
XX human; LP2001; antidiabetic; neuroprotective; nootropic;
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KW antinflammatory; antirheumatic; antiarthritic; vulnery; cytostatic;
KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;
KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;
KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;
KW systemic lupus erythematosus; gene; ss.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
CDS 46..927
FT /*tag= b
FT /product= "LP2001"
FT /note= "the present sequence only seems to encodes amino
FT acids 1 to 294 of the LP2001 protein"
FT sig_peptide 46..114
FT /*tag= a
FT mat_peptide 115..924
FT /*tag= c
XX
XX WO2004044126-A2.
XX
XX 27-MAY-2004.
XX
XX 05-NOV-2003; 2003WO-US032734.
XX
XX 14-NOV-2002; 2002US-0426253P.
XX (ELIL ) LILLY & CO ELI.
XX
XX Na S, Perkins DR;
XX
XX WPI; 2004-411705/38.
DR P-PSDB; ADP19658.
XX
XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or
PT LP2003) for diagnosing and treating disorders associated with aberrant
PT levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome
PT identification.
XX
XX Claim 1; SEQ ID NO 3; 111pp; English.
XX
XX The present sequence encodes human LP2001, which is used in the
CC exemplification of the present invention. The present invention
CC describes: (1) an isolated nucleic acid (1) comprising DNA having at
CC least 95% sequence identity to a polynucleotide selected from the group
CC consisting of: (a) a polynucleotide having a nucleotide sequence as shown
CC in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a
CC polypeptide or mature form of a polypeptide having the amino acid
CC sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide
CC fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide
CC having a nucleotide sequence which is complementary to the nucleotide
CC sequence of a polynucleotide as in (a), (b) or (c); (2) a vector
CC comprising (1); (3) a host cell comprising the vector; (4) producing an
CC LP polypeptide; (5) an isolated polypeptide produced by the above method
CC and comprising an amino acid sequence comprising about 95% sequence
CC identity to a sequence of amino acid residues comprising LP2001, LP2003,
CC LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric
CC molecule comprising an LP polypeptide fused to a heterologous amino acid
CC sequence; (7) an antibody which specifically binds to an LP polypeptide
CC described above; (8) a composition (C) comprising a therapeutic amount of
CC an active agent selected from an LP polypeptide, an agonist to an LP
CC polypeptide, an antagonist to an LP polypeptide, an LP polypeptide
CC antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a
CC polynucleotide in combination with a pharmaceutical carrier; and (9)
CC diagnosing or treating a mammal suffering from a disease, condition or
CC disorder associated with aberrant levels of an LP-polypeptide. (C) has
CC antidiabetic, neuroprotective, nootropic, cytostatic, immunosuppressive,
CC antirheumatic, antiarthritic, vulnery, cytostatic, antiinflammatory,
CC nephrotropic and dermatological activities, and can be used in gene
CC therapy. The compositions (C) and methods are useful for diagnosing or
CC treating disorders associated with aberrant levels of an LP polypeptide,
CC such as diabetes and its complications, Alzheimer's disease,
CC inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple
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CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They
 CC may also be used for chromosome identification. The LP polypeptide can
 CC also be used in manufacturing a medication for the treatment of the above
 CC -mentioned diseases, conditions or disorders associated with aberrant
 CC levels of the LP polypeptide.

XX Sequence 1194 BP; 268 A; 326 C; 389 G; 209 T; 0 U; 2 Other;

Query Match 100.0%; Score 336; DB 12; Length 1194;
 Best Local Similarity 100.0%; Pred. No. 1.5e-92;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCAAAACATCAGACCCCGATTGGCGACCACTGCTGCTGAAGTGAAGGGGCCCC 60
 Db 112 GCTCAAAACATCAGACCCCGATTGGCGACCACTGCTGCTGAAGTGAAGGGGCCCC 171
 QY 61 AAGAAACACCCCGCGCTGGATGGAATGAACACAGCCCGGACAGAGCTTGGAG 120
 Db 172 AAGAAACACCCCGCGCTGGATGGAATGAACACAGCCCGGACAGAGCTTGGAG 231
 QY 121 GTCTCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGCTGCTTCCCAACGCG 180
 Db 232 GTCTCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGCTGCTTCCCAACGCG 291
 QY 181 TCCCTCTTCTCCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCCAGGCAATG 240
 Db 292 TCCCTCTTCTCCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCCAGGCAATG 351
 QY 241 AACAGGAATCGAAGGACCAAGTCCACTACCGAGTCCGCTCTACAGATTCTCGG 300
 Db 352 AACAGGAATCGAAGGACCAAGTCCACTACCGAGTCCGCTCTACAGATTCTCGG 411
 QY 301 AAGCCAGAAATTTAGATTCTGCTCTGAACTCAG 336
 Db 412 AAGCCAGAAATTTAGATTCTGCTCTGAACTCAG 447

RESULT 8
 ABV73151

ID ABV73151 standard; DNA; 1223 BP.

XX ABV73151;

DT 08-JAN-2003 (first entry)

XX Human soluble RAGE protein encoding DNA.

XX RAGE; soluble receptor; advanced glycation endproduct; antidiabetic;
 KW nontropic; neuroprotective; antiarteriosclerotic; antiulcer; human; gene;
 XX db.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 25..1068

XX /*tag= a

XX /product= "soluble RAGE protein"

XX WO200274805-A1.

XX 26-SEP-2002.

XX 19-MAR-2002; 2002WO-JP002623.

XX 19-MAR-2001; 2001JP-00078409.

XX 10-AUG-2001; 2001JP-00243114.

XX 25-FEB-2002; 2002JP-00048182.

XX (UYKA-) UNIV JAPAN KANAZAWA.

XX Yamamoto H, Yonekura H, Yamamoto Y, Sakurai S, Watanabe T;

XX WPI; 2002-740851/80.

DR

DR P-PSDB; ABB82298.

XX Soluble advanced glycation endproduct receptor polypeptides and
 PT substances modifying their activity for treatment and prevention of
 PT disorders associated with diabetes and aging.

XX Claim 4; Page 118-120; 127pp; Japanese.

XX The invention relates to soluble receptor polypeptides for advanced
 CC glycation endproducts (soluble RAGE) and encoding polynucleotides. The
 CC soluble RAGE protein can be prepared by standard recombinant methodology.
 CC The protein, polynucleotide and modulators can be used for the
 CC prevention, treatment and diagnosis of diabetic complications, diseases
 CC of aging, disorders of glycation of metabolic proteins, Alzheimer's
 CC disease, arteriosclerosis and ulceration, and study of the mechanism and
 CC pathology of these diseases. The present sequence represents the human
 CC soluble RAGE protein encoding DNA

XX Sequence 1223 BP; 286 A; 341 C; 387 G; 209 T; 0 U; 0 Other;

Query Match 100.0%; Score 336; DB 6; Length 1223;

Best Local Similarity 100.0%; Pred. No. 1.5e-92;

Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCAGACCCCGATTGGCGAGCCACTGTGTGCTGAAGTGAAGGGGCCCC 60
 Db 91 GCTCAAAACATCAGACCCCGATTGGCGAGCCACTGTGTGCTGAAGTGAAGGGGCCCC 150
 QY 61 AAGAAACACCCCGCGCTGGATGGAATGGAACACAGCCCGGACAGAGCTTGGAG 120
 Db 151 AAGAAACACCCCGCGCTGGATGGAATGGAACACAGCCCGGACAGAGCTTGGAG 210
 QY 121 GTCTCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGCTGCTTCCCAACGCG 180
 Db 211 GTCTCTCTCCCGAGGAGGAGCCCTGGGACAGTGTGCTGCTTCCCAACGCG 270
 QY 181 TCCCTCTTCTCCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCCAGGCAATG 240
 Db 271 TCCCTCTTCTCCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCCAGGCAATG 330
 QY 241 AACAGGAATGGAAGGACCAAGTCCACTACCGAGTCCGCTGTCTACAGATTCTCGG 300
 Db 331 AACAGGAATGGAAGGACCAAGTCCACTACCGAGTCCGCTGTCTACAGATTCTCGG 390
 QY 301 AAGCCAGAAATTTAGATTCTGCTCTGAACTCAG 336
 Db 391 AAGCCAGAAATTTAGATTCTGCTCTGAACTCAG 426

RESULT 9
 ADG37043

ID ADG37043 standard; cDNA; 1223 BP.

XX ADG37043;

DT 26-FEB-2004 (first entry)

XX Receptor for advanced glycation endproducts (RAGE) cDNA.

XX ss; gene; receptor for advanced glycation endproducts; RAGE;
 KW diabetic complication; glycosuria nephropathy; glycosuria retinopathy;
 KW Alzheimer's disease; arteriosclerosis; Down's syndrome;
 KW multiple sclerosis; amyloidosis; autoimmune disease; inflammation;
 KW cancer; wound healing; human.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 25..1068

XX /*tag= a

XX /product= "RAGE"

XX JP2003230382-A.

```
XX 19-AUG-2003.
XX
XX
XX 08-FEB-2002; 2002JP-00032155.
XX
XX 08-FEB-2002; 2002JP-00032155.
XX
XX (KANA-) KANAZAWA DAIGAKUCHO.
XX
XX WPI; 2003-820207/77.
XX P-PSDB; ADG37044.
XX
XX New advanced glycation endproducts-receptor for advanced glycation
PT endproducts antagonist useful for treating or preventing diabetic
PT complication, glycosuria nephropathy, and glycosuria retinopathy.
XX
XX Example 1; SEQ ID NO 1; 23pp; Japanese.
XX
XX The invention relates to a receptor for advanced glycation endproducts
CC (RAGE). An AGE-RAGE antagonist composition is useful for treating or
CC preventing diabetic complication (e.g., glycosuria nephropathy,
CC glycosuria retinopathy), Alzheimer's disease, atherosclerosis, Down's
CC syndrome, multiple sclerosis, amyloidosis, autoimmune disease,
CC inflammation, cancer, wound healing, etc. The present sequence represents
CC cDNA encoding the receptor for advanced glycation endproducts (RAGE).
XX
XX Sequence 1223 BP; 286 A; 341 C; 387 G; 209 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 336; DB 10; Length 1223;
Best Local Similarity 100.0%; Pred. No. 1.5e-92;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCAAAACATCATCAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCCC 60
DB 91 GCTCAAAACATCATCAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCCC 150
QY 61 AGAAACACACCCAGCGGTGGTAATGGAATCTGAACACAGCCGCGACAGAGCTTGGAG 120
DB 151 AGAAACACACCCAGCGGTGGTAATGGAATCTGAACACAGCCGCGACAGAGCTTGGAG 210
QY 121 GTCTCTCTCCCGAGGAGGAGCCCTCGGACAGTGTCTGTCTCTTCCCAACGCG 180
DB 211 GTCTCTCTCCCGAGGAGGAGCCCTCGGACAGTGTCTGTCTCTTCCCAACGCG 270
QY 181 TCCTCTCTCTCCCGGTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 240
DB 271 TCCTCTCTCTCCCGGTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 330
QY 241 ACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCCTGGG 300
DB 331 ACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCCTGGG 390
QY 301 AGCCAGAAATGTAGATTCTGCTCTGAATCAAG 336
DB 391 AGCCAGAAATGTAGATTCTGCTCTGAATCAAG 426
RESULT 10
ADP19663
ID ADP19663 standard; cDNA; 1239 BP.
XX
XX ADP19663;
XX
XX 12-AUG-2004 (first entry)
XX
XX Human LP2004 encoding cDNA SEQ ID NO:9.
XX
XX human; LP2004; antidiabetic; neuroprotective; nootropic;
KW antiinflammatory; antirheumatic; antiarthritic; vulnery; cytostatic;
KW immunosuppressive; nephrotropic; dermatologic; gene therapy; diabetes;
KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;
KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;
KW systemic lupus erythematosus; gene; ss.
```

```
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 46..1113
FT /tag= b
FT /product= "LP2004"
FT /note= "the present sequence only seems to encodes amino
FT acids 1 to 356 of the LP2004 protein"
FT
FT sig_peptide 46..114
FT /tag= a
FT mat_peptide 115..1110
FT /tag= c
XX
XX WO2004044126-A2.
XX
XX 27-MAY-2004.
XX
XX 05-NOV-2003; 2003WO-US032734.
XX
XX 14-NOV-2002; 2002US-0426253P.
XX (ELIL ) LILLY & CO ELI.
XX
XX Na S, Perkins DR;
XX
XX WPI; 2004-411705/38.
XX P-PSDB; ADP19664.
XX
XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or
PT LP2003) for diagnosing or treating disorders associated with aberrant
PT levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome
PT identification.
XX
XX Claim 1; SEQ ID NO 9; 111pp; English.
XX
XX The present sequence encodes human LP2004, which is used in the
XX exemplification of the present invention. The present invention
XX describes: (1) an isolated nucleic acid (1) comprising DNA having at
XX least 95% sequence identity to a polynucleotide selected from the group
XX consisting of: (a) a polynucleotide having a nucleotide sequence as shown
XX in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a
XX polypeptide or mature form of a polypeptide having the amino acid
XX sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide
XX fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide
XX having a nucleotide sequence which is complementary to the nucleotide
XX sequence of a polynucleotide as in (a), (b) or (c); (2) a vector
XX comprising (1); (3) a host cell comprising the vector; (4) producing an
XX LP polypeptide; (5) an isolated polypeptide produced by the above method
XX and comprising an amino acid sequence comprising about 95% sequence
XX identity to a sequence of amino acid residues comprising LP2001, LP2003,
XX LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric
XX molecule comprising an LP polypeptide fused to a heterologous amino acid
XX sequence; (7) an antibody which specifically binds to an LP polypeptide
XX described above; (8) a composition (C) comprising a therapeutic amount of
XX an active agent selected from an LP polypeptide, an agonist to an LP
XX polypeptide, an antagonist to an LP polypeptide, an LP polypeptide
XX antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a
XX polynucleotide in combination with a pharmaceutical carrier; and (9)
XX diagnosing or treating a mammal suffering from a disease, condition or
XX disorder associated with aberrant levels of an LP-polypeptide. (C) has
XX antidiabetic, neuroprotective, nootropic, antiinflammatory,
XX antirheumatic, antirarthritic, vulnery, cytostatic, immunosuppressive,
XX nephrotropic and dermatological activities, and can be used in gene
XX therapy. The compositions (C) and methods are useful for diagnosing or
XX treating disorders associated with aberrant levels of an LP polypeptide,
XX such as diabetes and its complications, Alzheimer's disease,
XX inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple
XX sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They
XX also can be used for chromosome identification. The LP polypeptide can
XX also be used in manufacturing a medicament for the treatment of the above
XX -mentioned diseases, conditions or disorders associated with aberrant
XX levels of the LP polypeptide.
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FT mat_peptide 115..1086
 XX /*tag= c
 PN WO2004044126-A2.
 XX 27-MAY-2004.
 XX 05-NOV-2003; 2003WO-US032734.
 XX 14-NOV-2002; 2002US-0426253P.
 XX (ELIL) LILLY & CO ELI.
 XX Na S, Perkins DR;
 PI WPI; 2004-411705/38.
 DR P-PSDB; ADP19656.
 XX
 PT New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or
 PT LP2003) for diagnosing or treating disorders associated with aberrant
 PT levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome
 PT identification.
 XX
 PS Example 2; SEQ ID NO 1; 111pp; English.
 XX
 CC The present sequence encodes human LP2000, which is used in the
 CC exemplification of the present invention. The present invention
 CC describes: (1) an isolated nucleic acid (1) comprising DNA having at
 CC least 95% sequence identity to a polynucleotide selected from the group
 CC consisting of: (a) a polynucleotide having a nucleotide sequence as shown
 CC in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a
 CC polypeptide or mature form of a polypeptide having the amino acid
 CC sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide
 CC fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide
 CC having a nucleotide sequence which is complementary to the nucleotide
 CC sequence of a polynucleotide as in (a), (b) or (c); (2) a vector
 CC comprising (1); (3) a host cell comprising the vector; (4) producing an
 CC LP polypeptide; (5) an isolated polypeptide produced by the above method
 CC and comprising an amino acid sequence comprising about 95% sequence
 CC identity to a sequence of amino acid residues comprising LP2001, LP2003,
 CC LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric
 CC molecule comprising an LP polypeptide fused to a heterologous amino acid
 CC sequence; (7) an antibody which specifically binds to an LP polypeptide
 CC described above; (8) a composition (C) comprising a therapeutic amount of
 CC an active agent selected from an LP polypeptide, an agonist to an LP
 CC polypeptide, an antagonist to an LP polypeptide, an LP polypeptide
 CC antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a
 CC polynucleotide in combination with a pharmaceutical carrier; and (9)
 CC diagnosing or treating a mammal suffering from a disease, condition or
 CC disorder associated with aberrant levels of an LP-polypeptide. (C) has
 CC antidiabetic, neuroprotective, nootropic, antiinflammatory,
 CC antirheumatic, antiarthritic, vulnerary, cytostatic, immunosuppressive,
 CC nephrotropic and dermatological activities, and can be used in gene
 CC therapy. The compositions (C) and methods are useful for diagnosing or
 CC treating disorders associated with aberrant levels of an LP polypeptide,
 CC such as diabetes and its complications, Alzheimer's disease,
 CC inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple
 CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They
 CC may also be used for chromosome identification. The LP polypeptide can
 CC also be used in manufacturing a medicament for the treatment of the above
 CC mentioned diseases, conditions or disorders associated with aberrant
 CC levels of the LP polypeptide.
 XX
 SQ Sequence 1291 BP; 299 A; 360 C; 403 G; 227 T; 0 U; 2 Other;
 XX
 Query Match 100.0%; Score 336; DB 12; Length 1291;
 Best Local Similarity 100.0%; Pred. No. 1.5e-92;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 60
 DB |||||
 112 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 171

QY 61 AAGAAACCAACCCAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAACTTGGAG 120
 DB |||||
 172 AAGAAACCAACCCAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAACTTGGAG 231
 QY 121 GTCTGTCTCTCCAGGAGAGGCGCCCTGGGACAGTGTGGCTGTCTTCCCAACGGC 180
 DB |||||
 232 GTCTGTCTCTCCAGGAGAGGCGCCCTGGGACAGTGTGGCTGTCTTCCCAACGGC 291
 QY 181 TCCCTCTTCTCCGCTGTCTGGGATCCAGGATGAGGGGATTTTCCGTGCCAGGCAATG 240
 DB |||||
 292 TCCCTCTTCTCCGCTGTCTGGGATCCAGGATGAGGGGATTTTCCGTGCCAGGCAATG 351
 QY 241 AACAGGAATGGAAGAGAGACCAAGTCCCACTACCGAGTCCGTCTACAGATTCTCTGG 300
 DB |||||
 352 AACAGGAATGGAAGAGAGACCAAGTCCCACTACCGAGTCCGTCTACAGATTCTCTGG 411
 QY 301 AAGCCAGAAATGTAGATTCTGCCTCTGAACCTCACG 336
 DB |||||
 412 AAGCCAGAAATGTAGATTCTGCCTCTGAACCTCACG 447
 XX
 RESULT 13
 ADP19665
 ID ADP19665 standard; cDNA; 1329 BP.
 XX
 AC ADP19665;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human LP2005 encoding cDNA SEQ ID NO:11.
 XX
 KW human; LP2005; antidiabetic; neuroprotective; nootropic;
 KW antiinflammatory; antirheumatic; antiarthritic; vulnerary; cytostatic;
 KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;
 KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;
 KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;
 KW systemic lupus erythematosus; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 46..1206
 FT /*tag= b
 FT /product= "LP2005"
 FT /note= "the present sequence only seems to encodes amino
 FT acids 1 to 386 of the LP2005 protein"
 FT sig_peptide 46..114
 FT /*tag= a
 FT mat_peptide 115..1203
 FT /*tag= c
 PN WO2004044126-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 05-NOV-2003; 2003WO-US032734.
 XX
 PR 14-NOV-2002; 2002US-0426253P.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Na S, Perkins DR;
 XX
 DR WPI; 2004-411705/38.
 DR P-PSDB; ADP19666.
 XX
 XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or
 PT LP2003) for diagnosing or treating disorders associated with aberrant
 PT levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome
 PT identification.
 XX
 XX Claim 1; SEQ ID NO 11; 111pp; English.
 XX

CC The present sequence encodes human LP2005, which is used in the
 CC exemplification of the present invention. The present invention
 CC describes: (1) an isolated nucleic acid (1) comprising DNA having at
 CC least 95% sequence identity to a polynucleotide selected from the group
 CC consisting of: (a) a polynucleotide having a nucleotide sequence as shown
 CC in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a
 CC polypeptide or mature form of a polypeptide having the amino acid
 CC sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide
 CC fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide
 CC having a nucleotide sequence which is complementary to the nucleotide
 CC comprising (1); (3) a host cell comprising the vector; (4) producing an
 CC LP polypeptide; (5) an isolated polypeptide produced by the above method
 CC and comprising an amino acid sequence comprising about 95% sequence
 CC identity to a sequence of amino acid residues comprising LP2001, LP2003,
 CC LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric
 CC molecule comprising an LP polypeptide fused to a heterologous amino acid
 CC sequence; (7) an antibody which specifically binds to an LP polypeptide
 CC described above; (8) a composition (C) comprising a therapeutic amount of
 CC an active agent selected from an LP polypeptide, an agonist to an LP
 CC polypeptide, an antagonist to an LP polypeptide, an LP polypeptide
 CC antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a
 CC polynucleotide in combination with a pharmaceutical carrier; and (9)
 CC diagnosing or treating a mammal suffering from a disease, condition or
 CC disorder associated with aberrant levels of an LP-polypeptide. (C) has
 CC anti-diabetic, neuroprotective, nootropic, anti-inflammatory,
 CC anti-rheumatic, antiarthritic, vulnary, cytotatic, immunosuppressive,
 CC nephrotropic and dermatological activities, and can be used in gene
 CC therapy. The compositions (C) and methods are useful for diagnosing or
 CC treating disorders associated with aberrant levels of an LP polypeptide,
 CC such as diabetes and its complications, Alzheimer's disease,
 CC inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple
 CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They
 CC may also be used for chromosome identification. The LP polypeptide can
 CC also be used in manufacturing a medicament for the treatment of the above
 CC mentioned diseases, conditions or disorders associated with aberrant
 CC levels of the LP polypeptide.

XX
 SQ Sequence 1329 BP; 289 A; 379 C; 424 G; 235 T; 0 U; 2 Other;

Query Match 100.0%; Score 336; DB 12; Length 1329;
 Best Local Similarity 100.0%; Pred. No. 1.6e-92;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCAAAACATCATCAGCCCGGATTGGCGAGCCACTGGTCTCAAGTGTAAAGGGGCCCC 60
 DB 112 GCTCAAAACATCATCAGCCCGGATTGGCGAGCCACTGGTCTCAAGTGTAAAGGGGCCCC 171
 QY 61 AGAAACACACCCAGCGGTGGAAATGGAATGGAACACAGCGCGGACAGAACTTGGGAAG 120
 DB 172 AGAAACACACCCAGCGGTGGAAATGGAATGGAACACAGCGCGGACAGAACTTGGGAAG 231
 QY 121 GTCTCTCTCTCCAGGAGAGGCGCCCTGGGACAGTGGCTCGTGTCTTCCCAACGCG 180
 DB 232 GTCTCTCTCTCCAGGAGAGGCGCCCTGGGACAGTGGCTCGTGTCTTCCCAACGCG 291
 QY 181 TCCCTTCTCTCTCCGCTCTCGGATTCACAGGATGAGGGGATTTCCGCTGCGAGCAATG 240
 DB 292 TCCCTTCTCTCTCCGCTCTCGGATTCACAGGATGAGGGGATTTCCGCTGCGAGCAATG 351
 QY 241 ACAGGAATGGAAGAGACCAAGTCCAACTACCACTCCGTTCTACAGATTCCTGGG 300
 DB 352 ACAGGAATGGAAGAGACCAAGTCCAACTACCACTCCGTTCTACAGATTCCTGGG 411
 QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAATCAAG 336
 DB 412 AAGCCAGAAATGTAGATTCTGCTCTGAATCAAG 447

RESULT 14

ADP19661

ID ADP19661 standard; cDNA; 1339 BP.

XX

AC ADP19661;
 XX 12-AUG-2004 (first entry)
 DT Human LP2003 encoding cDNA SEQ ID NO:7.
 DE human; LP2003; anti-diabetic; neuroprotective; nootropic;
 KW anti-inflammatory; antirheumatic; antiarthritic; vulnary; cytotatic;
 KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;
 KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;
 KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;
 KW systemic lupus erythematosus; gene; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 46..1137
 CDS /tag= b
 FT /product= "LP2003"
 FT /note= "the present sequence only seems to encodes amino
 FT acids 1 to 363 of the LP2003 protein"
 FT 46..114
 FT /tag= a
 FT sig_peptide
 FT mat_peptide 115..1134
 FT /tag= c
 XX WO2004044126-A2.
 XX 27-MAY-2004.
 XX 05-NOV-2003; 2003WO-US032734.
 XX 14-NOV-2002; 2002US-0426253P.
 XX (ELIL) LILLY & CO ELI.
 XX Na S, Perkins DR;
 XX WPI: 2004-411705/38.
 DR P-PSDB; ADP19662.
 XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or
 PT LP2003) for diagnosing or treating disorders associated with aberrant
 PT levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome
 PT identification.
 XX Claim 1; SEQ ID NO 7; 11pp; English.

CC The present sequence encodes human LP2003, which is used in the
 CC exemplification of the present invention. The present invention
 CC describes: (1) an isolated nucleic acid (1) comprising DNA having at
 CC least 95% sequence identity to a polynucleotide selected from the group
 CC consisting of: (a) a polynucleotide having a nucleotide sequence as shown
 CC in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a
 CC polypeptide or mature form of a polypeptide having the amino acid
 CC sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide
 CC fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide
 CC having a nucleotide sequence which is complementary to the nucleotide
 CC sequence of a polynucleotide as in (a), (b) or (c); (2) a vector
 CC comprising (1); (3) a host cell comprising the vector; (4) producing an
 CC LP polypeptide; (5) an isolated polypeptide produced by the above method
 CC and comprising an amino acid sequence comprising about 95% sequence
 CC identity to a sequence of amino acid residues comprising LP2001, LP2003,
 CC LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric
 CC molecule comprising an LP polypeptide fused to a heterologous amino acid
 CC sequence; (7) an antibody which specifically binds to an LP polypeptide
 CC described above; (8) a composition (C) comprising a therapeutic amount of
 CC an active agent selected from an LP polypeptide, an agonist to an LP
 CC polypeptide, an antagonist to an LP polypeptide, an LP polypeptide
 CC antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a
 CC polynucleotide in combination with a pharmaceutical carrier; and (9)
 CC diagnosing or treating a mammal suffering from a disease, condition or
 CC disorder associated with aberrant levels of an LP-polypeptide. (C) has

CC antidiabetic, neuroprotective, nootropic, antiinflammatory,
CC antirheumatic, antiarthritic, vulnary, cytosatic, immunosuppressive,
CC nephrotropic and dermatological activities, and can be used in gene
therapy. The compositions (C) and methods are useful for diagnosing or
treating disorders associated with aberrant levels of an LP polypeptide,
CC such as diabetes and its complications, Alzheimer's disease,
CC inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple
CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They
CC may also be used for chromosome identification. The LP polypeptide can
CC also be used in manufacturing a medicament for the treatment of the above
CC -mentioned diseases, conditions or disorders associated with aberrant
CC levels of the LP polypeptide.

XX
SQ Sequence 1339 BP; 318 A; 366 C; 421 G; 232 T; 0 U; 2 Other;
Query Match 100.0%; Score 336; DB 12; Length 1339;
Best Local Similarity 100.0%; Pred. No. 1.6e-92;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCC 60
Db 112 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCC 171

QY 61 AAGAACACACCCAGCGGCTGAATGGAACCTGAACACAGCCGCGACAGAGCTTGGAG 120
Db 172 AAGAACACACCCAGCGGCTGAATGGAACCTGAACACAGCCGCGACAGAGCTTGGAG 231

QY 121 GTCCTGTCTCCCGAGGAGGCCCTCGGACAGTGTGCTGTCTCTCCCAACGCG 180
Db 232 GTCCTGTCTCCCGAGGAGGCCCTCGGACAGTGTGCTGTCTCTCCCAACGCG 291

QY 181 TCCTCTTCTCCCGCTGTGGGATCCAGATAGAGGGATTTTCGGTGCAGGCAATG 240
Db 292 TCCTCTTCTCCCGCTGTGGGATCCAGATAGAGGGATTTTCGGTGCAGGCAATG 351

QY 241 ACAGAGAAAGGAGGACCAAGTCCACTACCGATCGGTCTACAGATTTCTGGG 300
Db 352 AACAGAAATGGAAGAGACCAAGTCCACTACCGATCGGTCTACAGATTTCTGGG 411

QY 301 AAGCCAGAAATTTAGATTCTGCTCTGAATCTACG 336
Db 412 AAGCCAGAAATTTAGATTCTGCTCTGAATCTACG 447

RESULT 15
ADP19659
ID ADP19659 standard; cDNA; 1384 BP.
AC ADP19659;
XX
XX 12-AUG-2004 (first entry)
DE Human LP2002 encoding cDNA SEQ ID NO:5.
XX
KW human; LP2002; antidiabetic; neuroprotective; nootropic;
KW antiinflammatory; antirheumatic; antiarthritic; vulnary; cytosatic;
KW immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;
KW Alzheimer's disease; inflammation; rheumatoid arthritis; wound;
KW autoimmune disease; multiple sclerosis; cancer; lupus nephritis;
KW systemic lupus erythematosus; gene; ss.

XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 46..1308
FT /*tag= b
FT /product= "LP2002"
FT /note= "the present sequence only seems to encodes amino
FT acids 1 to 420 of the LP2002 protein"
FT 46..114
FT sig_peptide /*tag= a
FT 115..1305
FT mat_peptide /*tag= c

XX WO2004044126-A2.
XX 27-MAY-2004.
XX 05-NOV-2003; 2003WO-US032734.
XX 14-NOV-2002; 2002US-0426253P.
XX (ELIL) LILLY & CO ELI.
XX Na S, Perkins DR;
XX WPI; 2004-411705/38.
XX P-PSDB; ADP19660.
XX New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or
XX LP2003) for diagnosing or treating disorders associated with aberrant
XX levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome
XX identification.
XX Example 2; SEQ ID NO 5; 111pp; English.
XX
XX The present sequence encodes human LP2002, which is used in the
XX exemplification of the present invention. The present invention
XX describes: (1) an isolated nucleic acid (1) comprising DNA having at
XX least 95% sequence identity to a polynucleotide selected from the group
XX consisting of: (a) a polynucleotide having a nucleotide sequence as shown
XX in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a
XX polypeptide or mature form of a polypeptide having the amino acid
XX sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide
XX fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide
XX having a nucleotide sequence which is complementary to the nucleotide
XX sequence of a polynucleotide as in (a), (b) or (c); (2) a vector
XX comprising (1); (3) a host cell comprising the vector; (4) producing an
XX LP polypeptide; (5) an isolated polypeptide produced by the above method
XX and comprising an amino acid sequence comprising about 95% sequence
XX identity to a sequence of amino acid residues comprising LP2001, LP2003,
XX LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric
XX molecule comprising an LP polypeptide fused to a heterologous amino acid
XX sequence; (7) an antibody which specifically binds to an LP polypeptide
XX described above; (8) a composition (C) comprising a therapeutic amount of
XX an active agent selected from an LP polypeptide, an agonist to an LP
XX polypeptide, an antagonist to an LP polypeptide, an LP polypeptide
XX antibody, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a
XX polynucleotide in combination with a pharmaceutical carrier; and (9)
XX diagnosing or treating a mammal suffering from a disease, condition or
XX disorder associated with aberrant levels of an LP-polypeptide. (C) has
XX antidiabetic, neuroprotective, nootropic, antiinflammatory,
XX antirheumatic, antiarthritic, vulnary, cytosatic, immunosuppressive,
XX nephrotropic and dermatological activities, and can be used in gene
XX therapy. The compositions (C) and methods are useful for diagnosing or
XX treating disorders associated with aberrant levels of an LP polypeptide,
XX such as diabetes and its complications, Alzheimer's disease,
XX inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple
XX sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They
XX may also be used for chromosome identification. The LP polypeptide can
XX also be used in manufacturing a medicament for the treatment of the above
XX -mentioned diseases, conditions or disorders associated with aberrant
XX levels of the LP polypeptide.

XX
SQ Sequence 1384 BP; 312 A; 386 C; 444 G; 240 T; 0 U; 2 Other;
Query Match 100.0%; Score 336; DB 12; Length 1384;
Best Local Similarity 100.0%; Pred. No. 1.6e-92;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCC 60
Db 112 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCC 171

QY 61 AAGAACACACCCAGCGGCTGAATGGAACCTGAACACAGCCGCGACAGAGCTTGGAG 120

Db 172 AAGAAACCCAGCCGCTGGAATGGAATGGAACACAGCCCGGACAGAAGCTTGGAG 231
Qy 121 GTCTGTCTCCAGGAGGAGGCCCTGGGACAGTGTGGCTCGTCTTCCCAACGGC 180
Db 232 GTCTGTCTCCAGGAGGAGGCCCTGGGACAGTGTGGCTCGTCTTCCCAACGGC 291
Qy 181 TCCCTCTTCCCTCCGCTGTGGGATCCAGGATGAGGGGATTTCCGGTGCCAGGCAATG 240
Db 292 TCCCTCTTCCCTCCGCTGTGGGATCCAGGATGAGGGGATTTCCGGTGCCAGGCAATG 351
Qy 241 AACAGGATCGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCCCTGG 300
Db 352 AACAGGATCGAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCCCTGG 411
Qy 301 AAGCCAGAAATTGTAGATTCTGCCTCTGAACACG 336
Db 412 AAGCCAGAAATTGTAGATTCTGCCTCTGAACACG 447

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	336	100.0	1020	19 US-10-091-019-2	Sequence 2, Appli
3	336	100.0	1223	19 US-10-472-507A-1	Sequence 1, Appli
4	336	100.0	1391	16 US-10-091-019-1	Sequence 1, Appli
5	336	100.0	1415	18 US-10-115-635-351	Sequence 351, App
6	336	100.0	1463	18 US-10-115-635-352	Sequence 352, App
7	334.4	99.5	1217	17 US-10-309-290-95	Sequence 95, Appli
8	332.8	99.0	1405	8 US-08-905-709-3	Sequence 3, Appli
9	332.8	99.0	1405	8 US-08-755-235-3	Sequence 3, Appli
10	332.8	99.0	1405	18 US-10-850-861-3	Sequence 3, Appli
11	270.6	80.5	1438	8 US-08-905-709-1	Sequence 1, Appli

12	270.6	80.5	1438	8	US-08-755-235-1	Sequence 1, Appli
13	270.6	80.5	1438	18	US-10-850-861-1	Sequence 1, Appli
14	242	72.0	1173	17	US-10-309-290-99	Sequence 99, Appli
15	242	72.0	1226	17	US-10-309-290-97	Sequence 97, Appli
16	197	58.6	203	16	US-10-029-386-16362	Sequence 16362, A
17	197	58.6	485	13	US-10-027-632-257559	Sequence 257559,
18	197	58.6	485	17	US-10-027-632-257559	Sequence 257559,
19	197	58.6	553	16	US-10-029-386-2662	Sequence 2662, Ap
20	197	58.6	62944	9	US-09-954-456-2257	Sequence 2257, Ap
21	197	58.6	62944	11	US-09-968-007A-129	Sequence 129, App
22	120.2	35.8	3673778	16	US-10-312-841-2	Sequence 2, Appli
23	112.8	33.6	3673778	16	US-10-312-841-1	Sequence 1, Appli
24	93	27.7	1842	13	US-10-027-632-98444	Sequence 98444, A
25	93	27.7	1842	13	US-10-027-632-98445	Sequence 98445, A
26	93	27.7	1842	17	US-10-027-632-98444	Sequence 98445, A
27	93	27.7	1842	17	US-10-027-632-98445	Sequence 98445, A
28	38.4	11.4	26591	9	US-09-764-877-2678	Sequence 2678, Ap
29	38.4	11.4	26591	17	US-10-242-515-2678	Sequence 2678, Ap
30	37.8	11.2	581	13	US-10-027-632-134093	Sequence 134093,
31	37.8	11.2	581	13	US-10-027-632-134094	Sequence 134094,
32	37.8	11.2	581	17	US-10-027-632-134093	Sequence 134093,
33	37.8	11.2	581	17	US-10-027-632-134094	Sequence 134094,
34	36	10.6	1596	17	US-10-369-493-43122	Sequence 43122, A
35	35.6	10.6	396	18	US-10-437-963-53857	Sequence 53857, A
36	35.4	10.5	755	18	US-10-653-047-4384	Sequence 4384, Ap
37	34.4	10.2	1440	9	US-09-917-800A-1738	Sequence 1738, Ap
38	34	10.1	274	16	US-10-029-386-13779	Sequence 13779, A
39	34	10.1	328	9	US-09-815-343-540	Sequence 540, App
40	34	10.1	328	17	US-10-097-105-540	Sequence 540, App
41	34	10.1	533	16	US-10-029-386-72	Sequence 72, Appli
42	34	10.1	5874	18	US-10-719-993-370	Sequence 370, App
43	34	10.1	60787	13	US-10-087-192-1774	Sequence 1774, Ap
44	34	10.1	74648	18	US-10-719-993-6875	Sequence 6875, Ap
45	33.8	10.1	50000	17	US-10-364-505-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-10-091-019-4
; Sequence 4, Application US/10091019
; Publication No. US20030166063A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Shen, Jane M.
; APPLICANT: Shabbaz, Manouchehr M.
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins
; FILE REFERENCE: 41305-270555
; CURRENT APPLICATION NUMBER: US/10/091,019
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/273,418
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-091-019-4

Query Match 100.0%; Score 336; DB 16; Length 336;
Best Local Similarity 100.0%; Pred. No. 2.9e-99;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GCTCAAAACATCACAGCCCGGATTGCGAGCCACCTGGTCTCAAGTGTAAAGGGGCCCCC	60
Db	1	GCTCAAAACATCACAGCCCGGATTGCGAGCCACCTGGTCTCAAGTGTAAAGGGGCCCCC	60
Qy	61	AAGAAACACCCACCGCGCTGGAATGGAACCTGAACACAGCGCGGACAGAACTTGGAG	120
Db	61	AAGAAACACCCACCGCGCTGGAATGGAACCTGAACACAGCGCGGACAGAACTTGGAG	120

QY 121 GTCCTGTCTCCAGGAGGAGGCGCTCGGACAGTGTGCTGCTTCCCAACGGC 180
Db 121 GTCCTGTCTCCAGGAGGAGGCGCTCGGACAGTGTGCTGCTTCCCAACGGC 180
QY 181 TCCCTCTTCTCCGCTGTGGGATCCAGGATGAGGGGATTTCCGGTCCAGGCAATG 240
Db 181 TCCCTCTTCTCCGCTGTGGGATCCAGGATGAGGGGATTTCCGGTCCAGGCAATG 240
QY 241 AACAGGATGGAAGGAGACCAAGTCCAACTACGAGTCCGCTGTACGAGTTCCTGGG 300
Db 241 AACAGGATGGAAGGAGACCAAGTCCAACTACGAGTCCGCTGTACGAGTTCCTGGG 300
QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 336
Db 301 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 336

RESULT 2

US-10-091-019-2
; Sequence 2, Application US/10091019
; Publication No. US20030166063A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Shen, Jane M.
; APPLICANT: Shahbaz, Manouchehr M.
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins
; FILE REFERENCE: 41305-270555
; CURRENT APPLICATION NUMBER: US/10/091,019
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/273,418
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1020)
; OTHER INFORMATION:

US-10-091-019-2

Query Match 100.0%; Score 336; DB 16; Length 1020;
Best Local Similarity 100.0%; Pred. No. 3.7e-99;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGCTGCTGAAGTGAAGGGGCCCCC 60
Db 67 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGCTGCTGAAGTGAAGGGGCCCCC 126
QY 61 AAGAAACACCCAGCGGCTGGAATGGAATGAACTGAACACAGGCGGACAGAGCTTGGAG 120
Db 127 AAGAAACACCCAGCGGCTGGAATGGAATGGAATGGAACCTGAACACAGGCGGACAGAGCTTGGAG 186
QY 121 GTCCTGTCTCCAGGAGGAGGCGCTCGGACAGTGTGGCTGCTGCTTCCCAACGGC 180
Db 187 GTCCTGTCTCCAGGAGGAGGCGCTCGGACAGTGTGGCTGCTGCTTCCCAACGGC 246
QY 181 TCCCTCTTCTCCGCTGTCCGGATCCAGGATGAGGGGATTTCCGGTCCAGGCAATG 240
Db 247 TCCCTCTTCTCCGCTGTCCGGATCCAGGATGAGGGGATTTCCGGTCCAGGCAATG 306
QY 241 AACAGGAATGGAAGGAGACCAAGTCCAACTACGAGTCCGCTGTACAGATTCTCTGG 300
Db 307 AACAGGAATGGAAGGAGACCAAGTCCAACTACGAGTCCGCTGTACAGATTCTCTGG 366
QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 336
Db 367 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 402

RESULT 3

US-10-472-507A-1
; Sequence 1, Application US/10472507A
; Publication No. US20050033017A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, Hiroshi
; APPLICANT: Yonekura, Hideto
; APPLICANT: Yamamoto, Yasuhiko
; APPLICANT: Sakurai, Shigeru
; APPLICANT: Watanabe, Takuo
; TITLE OF INVENTION: Soluble RAGE Protein
; FILE REFERENCE: 026350-089
; CURRENT APPLICATION NUMBER: US/10/472,507A
; CURRENT FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: PCT/JP02,02623
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: JP 2001-78409
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: JP 2001-243114
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: JP 2002-48182
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1223
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)....(1068)
; OTHER INFORMATION:

US-10-472-507A-1

Query Match 100.0%; Score 336; DB 19; Length 1223;
Best Local Similarity 100.0%; Pred. No. 3.8e-99;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGCTGCTGAAGTGAAGGGGCCCCC 60
Db 91 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGCTGCTGAAGTGAAGGGGCCCCC 150
QY 61 AAGAAACACCCAGCGGCTGGAATGGAATGAACTGAACACAGGCGGACAGAGCTTGGAG 120
Db 151 AAGAAACACCCAGCGGCTGGAATGGAATGGAATGGAACCTGAACACAGGCGGACAGAGCTTGGAG 210
QY 121 GTCCTGTCTCCAGGAGGAGGCGCTCGGACAGTGTGGCTGCTGCTTCCCAACGGC 180
Db 211 GTCCTGTCTCCAGGAGGAGGCGCTCGGACAGTGTGGCTGCTGCTTCCCAACGGC 270
QY 181 TCCCTCTTCTCCGCTGTCCGGATCCAGGATGAGGGGATTTCCGGTCCAGGCAATG 240
Db 271 TCCCTCTTCTCCGCTGTCCGGATCCAGGATGAGGGGATTTCCGGTCCAGGCAATG 330
QY 241 AACAGGAATGGAAGGAGACCAAGTCCAACTACGAGTCCGCTGTCTACAGATTCTCTGG 300
Db 331 AACAGGAATGGAAGGAGACCAAGTCCAACTACGAGTCCGCTGTCTACAGATTCTCTGG 390
QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 336
Db 391 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 426

RESULT 4

US-10-091-019-1
; Sequence 1, Application US/10091019
; Publication No. US20030166063A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Shen, Jane M.
; APPLICANT: Shahbaz, Manouchehr M.
; TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins
; FILE REFERENCE: 41305-270555
; CURRENT APPLICATION NUMBER: US/10/091,019
; CURRENT FILING DATE: 2002-03-05

```

; PRIOR APPLICATION NUMBER: US 60/273,418
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1391
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-091-019-1

Query Match      100.0%; Score 336; DB 16; Length 1391;
Best Local Similarity 100.0%; Pred. No. 3.9e-99;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 60
DB 67 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 126

QY 61 AAGAAACACCCAGCGCTGGAATGGAATGGAACACAGGCCGGACAGAACTTGGAAAG 120
DB 127 AAGAAACACCCAGCGCTGGAATGGAATGGAACACAGGCCGGACAGAACTTGGAAAG 186

QY 121 GTCTGTCTCCCGAGGAGGCCCTCGGACAGTGTGGTCTGCTTCCCAACGGC 180
DB 187 GTCTGTCTCCCGAGGAGGCCCTCGGACAGTGTGGTCTGCTTCCCAACGGC 246

QY 181 TCCCTCTTCTCCCGCTGTCCGGATCCAGGATGAGGGGATTTCCGGTGCAGCAATG 240
DB 247 TCCCTCTTCTCCCGCTGTCCGGATCCAGGATGAGGGGATTTCCGGTGCAGCAATG 306

QY 241 AACAGGAATGGAAGAGAGCCAAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCTCTGGG 300
DB 307 AACAGGAATGGAAGAGAGCCAAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCTCTGGG 366

QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAATCAAG 336
DB 367 AAGCCAGAAATGTAGATTCTGCTCTGAATCAAG 402

RESULT 5
US-10-115-635-351
; Sequence 351, Application US/10115635
; Publication No. US20040137434A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 797CON
; CURRENT APPLICATION NUMBER: US/10/115,635
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/714,936
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 362
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 351
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(1239)
US-10-115-635-351

Query Match      100.0%; Score 336; DB 18; Length 1463;
Best Local Similarity 100.0%; Pred. No. 3.9e-99;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 60
DB 91 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 150

RESULT 6
US-10-115-635-352
; Sequence 352, Application US/10115635
; Publication No. US20040137434A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 797CON
; CURRENT APPLICATION NUMBER: US/10/115,635
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/714,936
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 362
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 352
; LENGTH: 1463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(1287)
US-10-115-635-352

Query Match      100.0%; Score 336; DB 18; Length 1463;
Best Local Similarity 100.0%; Pred. No. 3.9e-99;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 60
DB 91 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 150
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QY 61 AAGAAACACCCCGGCTGGAATGGAACCTGAACACAGGCGGACAGAGCTTGAAG 120
Db 151 AAGAAACACCCCGGCTGGAATGGAACCTGAACACAGGCGGACAGAGCTTGAAG 210
QY 121 GTCCTGTCTCCCGAGGAGGAGGCGCTGGACAGTGTGGCTGTGCTTCCCAACGGC 180
Db 211 GTCCTGTCTCCCGAGGAGGAGGCGCTGGACAGTGTGGCTGTGCTTCCCAACGGC 270
QY 181 TCCCTCTTCTCCCGGCTGTGGGATCCAGATGAGGGGATTTCCGGTCCAGGCAATG 240
Db 271 TCCCTCTTCTCCCGGCTGTGGGATCCAGATGAGGGGATTTCCGGTCCAGGCAATG 330
QY 241 AACAGGAATGAAAGGAGACCAAGTCCCACTACCGAGTCCGCTGTCTACCAAGATTCTCTGG 300
Db 331 AACAGGAATGAAAGGAGACCAAGTCCCACTACCGAGTCCGCTGTCTACCAAGATTCTCTGG 390
QY 301 AAGCAGAAATGTAGATTCTGCTCTGAATCAAG 336
Db 391 AAGCAGAAATGTAGATTCTGCTCTGAATCAAG 426

RESULT 7
US-10-309-290-95
; Sequence 95, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chhillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; FILE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31

; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 95
; LENGTH: 1217
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(1214)
US-10-309-290-95

Query Match 99.5%; Score 334.4; DB 17; Length 1217;
Best Local Similarity 99.7%; Pred. No. 1.3e-98;
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCAGAGCCGGATTTGGCGAGCCACTGTGTCTGAAGTGTAAAGGGGGCCCC 60
Db 69 GCTCAAAACATCAGAGCTCGGATTTGGCGAGCCACTGTGTCTGAAGTGTAAAGGGGGCCCC 128
QY 61 AAGAAACACCCCGGCTGGAATGGAACCTGAACACAGGCGGACAGAGCTTGAAG 120
Db 129 AAGAAACACCCCGGCTGGAATGGAACCTGAACACAGGCGGACAGAGCTTGAAG 188
QY 121 GTCCTGTCTCCCGAGGAGGAGGCGCTGGACAGTGTGGCTGTGCTTCCCAACGGC 180
Db 189 GTCCTGTCTCCCGAGGAGGAGGCGCTGGACAGTGTGGCTGTGCTTCCCAACGGC 248
QY 181 TCCCTCTTCTCCCGGCTGTGGGATCCAGATGAGGGGATTTCCGGTCCAGGCAATG 240
Db 249 TCCCTCTTCTCCCGGCTGTGGGATCCAGATGAGGGGATTTCCGGTCCAGGCAATG 308
QY 241 AACAGGAATGAAAGGAGACCAAGTCCCACTACCGAGTCCGCTGTCTACCAAGATTCTCTGG 300
Db 309 AACAGGAATGAAAGGAGACCAAGTCCCACTACCGAGTCCGCTGTCTACCAAGATTCTCTGG 368
QY 301 AAGCAGAAATGTAGATTCTGCTCTGAATCAAG 336
Db 369 AAGCAGAAATGTAGATTCTGCTCTGAATCAAG 404

RESULT 8
US-08-905-709-3
; Sequence 3, Application US/08905709
; Publication No. US20010039256A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David
; APPLICANT: Schmidt, Ann M.
; TITLE OF INVENTION: A METHOD TO PREVENT ACCELERATED
; TITLE OF INVENTION: ATHEROSCLEROSIS USING (SRAGE) SOLUBLE RECEPTOR FOR
; NUMBER OF INVENTION: ADVANCED GLYCATION ENDPRODUCTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,709
; FILING DATE: 05-AUG-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:

```
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/52876
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-905-709-3

Query Match          99.0%; Score 332.8; DB 8; Length 1405;
Best Local Similarity 99.4%; Pred. No. 4.3e-98;
Matches 334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCAACAGCCCGGATGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCCC 60
DB 67 GCTCAAAACATCAACAGCCCGGATGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCCC 126
QY 61 AGAARACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAG 120
DB 127 AGAARACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAG 186
QY 121 GTCTCTCTCTCCCGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 180
DB 187 GTCTCTCTCTCCCGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 246
QY 181 TCCTCTCTCTCCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 240
DB 247 TCCTCTCTCTCCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 306
QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 300
DB 307 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 366
QY 301 AAGCCAGAAATTTGTAGATTCTGCCTCTGAACCTCAGC 336
DB 367 AAGCCAGAAATTTGTAGATTCTGCCTCTGAACCTCAGC 402

RESULT 9
US-08-755-235-3
; Sequence 3, Application US/08755235
; Publication No. US20030059423A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1405
; TYPE: DNA
; ORGANISM: Human
US-08-755-235-3

Query Match          99.0%; Score 332.8; DB 8; Length 1405;
Best Local Similarity 99.4%; Pred. No. 4.3e-98;
Matches 334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCAACAGCCCGGATGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCCC 60
DB 67 GCTCAAAACATCAACAGCCCGGATGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCCC 126
QY 61 AGAARACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAG 120
DB 127 AGAARACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAG 186
QY 121 GTCTCTCTCTCCCGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 180
DB 187 GTCTCTCTCTCCCGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 246
QY 181 TCCTCTCTCTCCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 240
DB 247 TCCTCTCTCTCCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 306
QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 300
DB 307 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 366
QY 301 AAGCCAGAAATTTGTAGATTCTGCCTCTGAACCTCAGC 336
DB 367 AAGCCAGAAATTTGTAGATTCTGCCTCTGAACCTCAGC 402
```

```
DB 127 AAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAG 186
QY 121 GTCTCTCTCTCCCGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 180
DB 187 GTCTCTCTCTCCCGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 246
QY 181 TCCTCTCTCTCCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 240
DB 247 TCCTCTCTCTCCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 306
QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 300
DB 307 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 366
QY 301 AAGCCAGAAATTTGTAGATTCTGCCTCTGAACCTCAGC 336
DB 367 AAGCCAGAAATTTGTAGATTCTGCCTCTGAACCTCAGC 402

RESULT 10
US-10-850-861-3
; Sequence 3, Application US/10850861
; Publication No. US20040228855A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/10/850,861
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/08/755,235
; PRIOR FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1405
; TYPE: DNA
; ORGANISM: Human
US-10-850-861-3

Query Match          99.0%; Score 332.8; DB 18; Length 1405;
Best Local Similarity 99.4%; Pred. No. 4.3e-98;
Matches 334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCAACAGCCCGGATGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCCC 60
DB 67 GCTCAAAACATCAACAGCCCGGATGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCCC 126
QY 61 AAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAG 120
DB 127 AAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCGGACAGAGCTTGGAG 186
QY 121 GTCTCTCTCTCCCGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 180
DB 187 GTCTCTCTCTCCCGAGGAGGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 246
QY 181 TCCTCTCTCTCCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 240
DB 247 TCCTCTCTCTCCCGCTGTGCGGATCCAGGATGAGGGGATTTCCGGTGCAGGCAATG 306
QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 300
DB 307 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 366
QY 301 AAGCCAGAAATTTGTAGATTCTGCCTCTGAACCTCAGC 336
DB 367 AAGCCAGAAATTTGTAGATTCTGCCTCTGAACCTCAGC 402

RESULT 11
US-08-905-709-1
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Sequence 1, Application US/08905709
 Publication No. US20010039256A1
 GENERAL INFORMATION:
 APPLICANT: Stern, David M.
 APPLICANT: Schmidt, Ann Marie
 APPLICANT: Wu, Jun
 TITLE OF INVENTION: A METHOD TO PREVENT ACCELERATED
 TITLE OF INVENTION: ATHEROSCLEROSIS USING (sRAGE) SOLUBLE RECEPTOR FOR
 TITLE OF INVENTION: ADVANCED GLYCATION ENDPRODUCTS
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/905,709
 FILING DATE: 05-AUG-1997
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 0575/52876
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0526
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1438 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-905-709-1

Query Match 80.5%; Score 270.6; DB 8; Length 1438;
 Best Local Similarity 90.4%; Pred. No. 8.2e-78;
 Matches 301; Conservative 0; Mismatches 29; Indels 3; Gaps 1;
 QY 4 CAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCCCAAG 63
 DB 79 CAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCCCAAG 138
 QY 64 AAACACCCCGAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAGCTTGGAGGTC 123
 DB 139 AAACACCCCGAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAGCTTGGAGGTC 198
 QY 124 CTGTCTCCCGAGGAGGAGCCCTGGGACAGTGGCTGGTCTTCCCAACGGCTCC 183
 DB 199 CTGTCTCCCGAG--GGAGACCCCTGGGATAGCGTGGTCTCCCAACGGCTCC 255
 QY 184 CTCTTCTTCCGCTCTCGGATCCAGATGAGGGATTTCCGTTGCGAGCAATGAAC 243
 DB 256 CTCTTCTTCCGCTCTCGGATCCAGATGAGGGACTTCCGTTGCGGCAACGAGC 315
 QY 244 AGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTTCTACAGATTCCTGGGAAG 303
 DB 316 CGGAGCGGAAGAGAGACCAAGTCTAACTACCGAGTCCGATCTATCAGATTCCTGGGAAG 375
 QY 304 CAGAAATTTGATTTCTGCTCTGAACCTCAGC 336
 DB 376 CCAGAAATTTGATTTCTGCTCTGAACCTCAGC 408

RESULT 12
 US-08-755-235-1
 Sequence 1, Application US/08755235

Publication No. US20030059423A1
 GENERAL INFORMATION:
 APPLICANT: Stern, David M.
 APPLICANT: Schmidt, Ann Marie
 APPLICANT: Wu, Jun
 TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
 FILE REFERENCE: 0575/50159
 CURRENT APPLICATION NUMBER: US/08/755,235
 CURRENT FILING DATE: 1996-11-22
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1
 LENGTH: 1438
 TYPE: DNA
 ORGANISM: Bovine
 US-08-755-235-1

Query Match 80.5%; Score 270.6; DB 8; Length 1438;
 Best Local Similarity 90.4%; Pred. No. 8.2e-78;
 Matches 301; Conservative 0; Mismatches 29; Indels 3; Gaps 1;
 QY 4 CAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCCCAAG 63
 DB 79 CAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCCCAAG 138
 QY 64 AAACACCCCGAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAGCTTGGAGGTC 123
 DB 139 AAACACCCCGAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAGCTTGGAGGTC 198
 QY 124 CTGTCTCCCGAGGAGGAGCCCTGGGACAGTGGCTGGTCTTCCCAACGGCTCC 183
 DB 199 CTGTCTCCCGAG--GGAGACCCCTGGGATAGCGTGGTCTCCCAACGGCTCC 255
 QY 184 CTCTTCTTCCGCTCTCGGATCCAGATGAGGGATTTCCGTTGCGAGCAATGAAC 243
 DB 256 CTCTTCTTCCGCTCTCGGATCCAGATGAGGGACTTCCGTTGCGGCAACGAGC 315
 QY 244 AGAATGGAAGAGAGACCAAGTCCAACTACCGAGTCCGTTCTACAGATTCCTGGGAAG 303
 DB 316 CGGAGCGGAAGAGAGACCAAGTCTAACTACCGAGTCCGATCTATCAGATTCCTGGGAAG 375
 QY 304 CAGAAATTTGATTTCTGCTCTGAACCTCAGC 336
 DB 376 CCAGAAATTTGATTTCTGCTCTGAACCTCAGC 408

RESULT 13
 US-10-850-861-1
 Sequence 1, Application US/10850861
 Publication No. US2004022885A1
 GENERAL INFORMATION:
 APPLICANT: Stern, David M.
 APPLICANT: Schmidt, Ann Marie
 APPLICANT: Wu, Jun
 TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
 FILE REFERENCE: 0575/50159
 CURRENT APPLICATION NUMBER: US/10/850,861
 CURRENT FILING DATE: 2004-05-20
 PRIOR APPLICATION NUMBER: US/08/755,235
 PRIOR FILING DATE: 1996-11-22
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1
 LENGTH: 1438
 TYPE: DNA
 ORGANISM: Bovine
 US-10-850-861-1

Query Match 80.5%; Score 270.6; DB 18; Length 1438;
 Best Local Similarity 90.4%; Pred. No. 8.2e-78;
 Matches 301; Conservative 0; Mismatches 29; Indels 3; Gaps 1;
 QY 4 CAAACATCACAGCCCGGATTGGCGAGCCACTGGTGTGAAGTGTAAAGGGGGCCCCCAAG 63

79	CAAACAATCACAGCCCGGATCGGGAAGCCA	CTGCTGCTGAAC	TGCAAGGGAGCCCCCAAG	138
Qy				
64	AAACACCCACCGCGCTGGAATGGAATGAAACTGAACACAGGCGGACAGAAAGCTTGGAAAGTC	123		
Db				
139	AAACACCCACGAGCTGGAATGGAATGGAATGGAACACAGCGCGGACAGAAAGCTTGGAAAGTC	198		
Qy				
124	CTGTCTCTCCACGGGAGAGAGGCCCTCTGGGACAGTGTGTGCTGTGTCCTTCCAAACGGCTCC	183		
Db				
199	CTGTCTCTCCACG--GAGAGCCCTGGGATAGCGTGTGCTCGGGTCTCTCCCAACGGCTCC	255		
Qy				
184	CTCTCTCTTCCGGCTGTCCGGATCCAGATCAGAGGGAATTTTCGGTGCACAGCAAGTAAC	243		
Db				
256	CTCTCTCTCCCGCTGTGGGATCCAGATCAGGGGACTTTCCGGTGCCGGGCAACGAGC	315		
Qy				
244	AGGAATGGAAAGGAGACCAAGTCCAATCAACGAGTCCGCTGTCTACCAAGATTCTCTGGGAAG	303		
Db				
316	CGGAGCGGAAAGAGNCCAAAGTCTAACTACCGAGTCCGAGTCTATCAGATTCTCTGGGAAG	375		
Qy				
304	CAGAAATTGTATGATCTGCTCTGAACTCAACG	336		
Db				
376	CAGAAATTGTGATCTGCTCTGAACTCATG	408		
Qy				

RESULT 14

US-10-309-290-99

Sequence 99, Application US/10309290

Publication No. US20040023241A1

GENERAL INFORMATION:

APPLICANT: Alsobrook II, John P.

APPLICANT: Anderson, David W.

APPLICANT: Boldog, Ferenc L.

APPLICANT: Burgess, Catherine E.

APPLICANT: Chillakuru, Rajeev A.

APPLICANT: Edinger, Shlomit R.

APPLICANT: Gerlach, Valerie L.

APPLICANT: Gorman, Linda

APPLICANT: Gould-Rothberg, Bonnie E.

APPLICANT: Guo, Xiaojia

APPLICANT: Jeffers, Michael E.

APPLICANT: Ji, Weizhen

APPLICANT: Li, Li

APPLICANT: Malyankar, Uriel M.

APPLICANT: Miller, Charles E.

APPLICANT: Murphey, Ryan

APPLICANT: Patturajan, Meera

APPLICANT: Payman, John A.

APPLICANT: Rastelli, Luca

APPLICANT: Rieger, Daniel K.

APPLICANT: Shenoy, Suresh G.

APPLICANT: Smithson, Glennnda

APPLICANT: Starling, Gary

APPLICANT: Taupier, Raymond J.

APPLICANT: Voess, Edward Z.

APPLICANT: Zhong, Haihong

APPLICANT: Zhong, Mei

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS OF USE

FILE REFERENCE: 21402-502A

CURRENT APPLICATION NUMBER: US/10/309,290

CURRENT FILING DATE: 2002-12-02

PRIOR APPLICATION NUMBER: 60/336,600

PRIOR FILING DATE: 2001-12-05

PRIOR APPLICATION NUMBER: 60/338,285

PRIOR FILING DATE: 2001-12-07

PRIOR APPLICATION NUMBER: 60/341,346

PRIOR FILING DATE: 2001-12-12

PRIOR APPLICATION NUMBER: 60/341,477

PRIOR FILING DATE: 2001-12-17

PRIOR APPLICATION NUMBER: 60/341,540

PRIOR FILING DATE: 2001-12-17

PRIOR APPLICATION NUMBER: 60/342,592

PRIOR FILING DATE: 2001-12-20

PRIOR APPLICATION NUMBER: 60/344,297

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; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 99
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1170)
US-10-309-290-99

Query Match      72.0%; Score 242; DB 17; Length 1173;
Best Local Similarity 87.5%; Pred. No. 1.7e-68;
Matches 294; Conservative 0; Mismatches 0; Indels 42; Gaps 1

Qy      1  GCTCAAAACATCACGCCCGGATGGCGAGCCACTGGTGCTGTAAGTGTGAAGGGGCGCCCC 60
Db      67  GCTCAAAACATCACGCCCGGATGGCGAGCCACTGGTGCTGTAAGTGTGAAGGGGCGCCCC 126

Qy      61  AAGAAACCAACCCACAGCGGCTGGGAATGAAACTGAAACACAGCGCCGACAGAAAGCTTTGGAAG 120
Db      127  AAGAAACCAACCCACAGCGGCTGGGAATGAAACT

Qy      121  GTCCCTGTCTCCCAAGGAGAGAGGCCCTCTGGGACAGTGTGGCTGTGTCTTCCCAACCGCG 180
Db      159  -----GGAGGAGGCCCTCTGGGACAGTGTGGCTGTGTCTTCCCAACCGCG 204

Qy      181  TCCTCTCTCTTCGGGCTGTCCGGATCCAGGATGAGGGGATTTCCGGTGCACAGCAATG 240
Db      205  TCCTCTCTCTTCGGGCTGTCCGGATCCAGATGAGGGGATTTTCGGTGCACAGCAATG 264

Qy      241  AACAGGAATGGAAAGGAGAGCAAGTCCAACTACCGAGTCCCGTGTCTACCAAGATTCCTGGG 300
Db      265  AACAGGNAATGGAAAGGAGAGCAAGTCCAACTACCGAGTCCCGTGTCTACCAAGATTCCTGGG 324

Qy      301  AAGCCAGAAATGTAGATTCTGCCTCTGAACTCAGC 336
Db      325  AAGCCAGAAATGTAGATTCTGCCTCTGAACTCAGC 360

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RESULT 15
US-10-309-290-97
; Sequence 97, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillaikuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malynkar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 18:01:28 ; Search time 1333.11 Seconds

(without alignments)
9593.774 Million cell updates/sec

Title: US-10-091-019-4

Perfect score: 336

Sequence: 1 gctcaaacatcacagcccg.....attctgcctctgaactcacg 336

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	336	100.0	553	4	BI772105 603059188
2	336	100.0	715	4	BG529831 602558918
3	336	100.0	724	4	BG536369 602564760
4	336	100.0	729	4	BG545652 602572917
5	336	100.0	730	4	BG539104 602568478
6	336	100.0	750	4	BG548202 602575359
7	336	100.0	755	4	BG529866 602558957
8	336	100.0	841	4	BI771266 603054610
9	336	100.0	1163	9	AY421474 Pan trogl
10	336	100.0	1194	5	BQ067161 AGENCOURT
11	336	100.0	1215	9	AY421473 Homo sapi
12	334.4	99.5	774	4	BG506672 601861271
13	332.8	99.0	549	4	BG546024 602573327
14	331.2	98.6	538	4	BG484869 602505568
15	325	96.7	692	4	BG483796 602503447
16	325	96.7	822	4	BG540530 602569259
17	325	96.7	832	4	BG548148 602575303
18	324	96.4	613	4	BG570489 602591356
19	324	96.4	724	4	BI772019 603058871
20	324	96.4	894	4	BG538911 602568563
21	323.4	96.2	810	4	BG569848 602590474
22	322.4	96.0	736	4	BG540452 602568768
23	321.8	95.8	605	4	BG570394 602590833
24	314	93.5	599	4	BG538906 602568558

25	314	93.5	835	4	BG548514
26	310.4	92.4	698	4	BG537129
27	307.2	91.4	770	4	BG547990
28	286.8	85.4	876	4	BG535844
29	270.6	80.5	585	1	AV612348
30	270.6	80.5	644	1	AV610398
31	270.6	80.5	650	1	AV611162
32	269.2	80.1	633	1	AV611204
33	269	80.1	659	1	AV609932
34	265	78.9	723	4	BG534930
35	264.4	78.7	549	4	BG538294
36	261	77.7	742	4	BG533975
37	250	74.4	399	4	BM721731
38	247.8	73.8	656	4	BG537945
39	244	72.6	777	4	BG545464
40	242.2	72.1	537	6	CB598482
41	242.2	72.1	718	7	CK366081
42	242.2	72.1	719	7	CK366019
43	242.2	72.1	720	7	CK366743
44	242.2	72.1	742	7	CK364097
45	242.2	72.1	743	7	CK364561

ALIGNMENTS

RESULT 1
LOCUS BI772105 553 bp mRNA linear EST 25-SBP-2001
DEFINITION 603059188F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5208812 5', mRNA sequence.
ACCESSION BI772105
VERSION BI772105.1 GI:15763683
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 553)
AUTHORS NIH-MGC <http://mgc.mci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM11523 row: 0 column: 21
High quality sequence stop: 553.
Location/Qualifiers
1..553
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5208812"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."

FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5208812"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."

ORIGIN

sequence: 5'-CACGCCCATTTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-CT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

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ORIGIN
Query Match      100.0%; Score 336; DB 4; Length 724;
Best Local Similarity 100.0%; Pred. No. 5.1e-83;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTTGGCGAGCCACTGCTGCTGAAGTGTAAAGGGGGCCCC 60
DB 79 GCTCAAAACATCACAGCCCGGATTTGGCGAGCCACTGCTGCTGAAGTGTAAAGGGGGCCCC 138

QY 61 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCCGACAGAACTTGGAG 120
DB 139 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCCGACAGAACTTGGAG 198

QY 121 GTCCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCGTGTCTTCCCAACGGC 180
DB 199 GTCCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCGTGTCTTCCCAACGGC 258

QY 181 TCCCTTCTTCCCTTCCCGAGTCCAGGATGAGGAGGATTTCCGTTCCAGGCAATG 240
DB 259 TCCCTTCTTCCCTTCCCGAGTCCAGGATGAGGAGGATTTCCGTTCCAGGCAATG 318

QY 241 PACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTTCTACAGATTCTCTGG 300
DB 319 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTTCTACAGATTCTCTGG 378

QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 336
DB 379 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 414

RESULT 4
BG545652      729 bp mRNA linear EST 04-APR-2001
LOCUS 602572917F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4700836 5',
DEFINITION mRNA sequence.
ACCESSION BG545652
VERSION BG545652.1 GI:13544317
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1535 row: b column: 05
High quality sequence stop: 701.
Location/Qualifiers
1. .729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4700836"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"

FEATURES
source
1. .729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4700836"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"

ORIGIN
Query Match      100.0%; Score 336; DB 4; Length 729;
Best Local Similarity 100.0%; Pred. No. 5.1e-83;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTTGGCGAGCCACTGCTGCTGAAGTGTAAAGGGGGCCCC 60
DB 99 GCTCAAAACATCACAGCCCGGATTTGGCGAGCCACTGCTGCTGAAGTGTAAAGGGGGCCCC 158

QY 61 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCCGACAGAACTTGGAG 120
DB 159 AAGAAACACCCAGCGGCTGGAATGGAACCTGAACACAGCGCCGACAGAACTTGGAG 218

QY 121 GTCCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCGTGTCTTCCCAACGGC 180
DB 219 GTCCTGTCTCCCGAGGAGGAGCCCTGGGACAGTGTGGCTCGTGTCTTCCCAACGGC 278

QY 181 TCCCTTCTTCCCTTCCCGGATCCAGGATGAGGAGGATTTCCGTTCCAGGCAATG 240
DB 279 TCCCTTCTTCCCTTCCCGGATCCAGGATGAGGAGGATTTCCGTTCCAGGCAATG 338

QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTTCTACAGATTCTCTGG 300
DB 339 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTTCTACAGATTCTCTGG 398

QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 336
DB 399 AAGCCAGAAATGTAGATTCTGCTCTGAACCTCAGC 434

RESULT 5
BG539104      730 bp mRNA linear EST 03-APR-2001
LOCUS 602568478F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4693027 5',
DEFINITION mRNA sequence.
ACCESSION BG539104
VERSION BG539104.1 GI:13531337
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1514 row: 1 column: 20
High quality sequence stop: 653.
Location/Qualifiers
1. .730
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

FEATURES
source
1. .730
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

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/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccctcgccc); Site 2: SfiI (ggccattagccc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCCATTTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-CT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

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/clon="IMAGE:4693027"
/lab host="DH10B (T1 phage-resistant)"
/clon lib="NIH_MGC_77"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

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ORIGIN
Query Match 100.0%; Score 336; DB 4; Length 730;
Best Local Similarity 100.0%; Pred. No. 5.1e-83;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGTGTGAAGTGAAGGGGCCCC 60
DB 104 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGTGTGAAGTGAAGGGGCCCC 163
QY 61 AAGAAACACCCAGCGGCTGGAATGGAATCTGAACACAGCCCGGACAGAGCTTGAAG 120
DB 164 AAGAAACACCCAGCGGCTGGAATGGAATCTGAACACAGCCCGGACAGAGCTTGAAG 223
QY 121 GTCTGTCTCCAGGAGAGAGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 180
DB 224 GTCTGTCTCCAGGAGAGAGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 283
QY 181 TCCTCTTCTCTCCGCTGTCGAGATCCAGGATGAGGGGATTTCCGGTCCAGGCAATG 240
DB 284 TCCTCTTCTCTCCGCTGTCGAGATCCAGGATGAGGGGATTTCCGGTCCAGGCAATG 343
QY 241 ACAGGAATGGAAGAGAGCAAGTCCAACTACCGAGTCCGTGTCTTACAGATTCTCTGG 300
DB 344 ACAGGAATGGAAGAGAGCAAGTCCAACTACCGAGTCCGTGTCTTACAGATTCTCTGG 403
QY 301 AAGCCAGAAATTTAGATTCTGCTCTGAACTCAAG 336
DB 404 AAGCCAGAAATTTAGATTCTGCTCTGAACTCAAG 439

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RESULT 6
BG548202 750 bp mRNA linear EST 04-APR-2001
LOCUS 60257359F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4703246 5',
DEFINITION mRNA sequence.
ACCESSION BG548202
VERSION BG548202.1 GI:13546867
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 750)
NIH-MGC http://imgc.ncbi.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1541 row: f column: 15
High quality sequence stop: 633.
Location/Qualifiers
1. .750

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clon="IMAGE:4703246"
/lab host="DH10B (T1 phage-resistant)"
/clon lib="NIH_MGC_77"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

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ORIGIN
Query Match 100.0%; Score 336; DB 4; Length 750;
Best Local Similarity 100.0%; Pred. No. 5.1e-83;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGTGTGAAGTGAAGGGGCCCC 60
DB 80 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGTGTGAAGTGAAGGGGCCCC 139
QY 61 AAGAAACACCCAGCGGCTGGAATGGAATCTGAACACAGCCCGGACAGAGCTTGAAG 120
DB 140 AAGAAACACCCAGCGGCTGGAATGGAATCTGAACACAGCCCGGACAGAGCTTGAAG 199
QY 121 GTCTGTCTCCAGGAGAGAGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 180
DB 200 GTCTGTCTCCAGGAGAGAGCCCTGGGACAGTGTGCTGTCTTCCCAACGGC 259
QY 181 TCCTCTTCTCTCCGCTGTCGAGATCCAGGATGAGGGGATTTCCGGTCCAGGCAATG 240
DB 260 TCCTCTTCTCTCCGCTGTCGAGATCCAGGATGAGGGGATTTCCGGTCCAGGCAATG 319
QY 241 AACAGGAATGGAAGAGAGCAAGTCCAACTACCGAGTCCGTGTCTTACAGATTCTCTGG 300
DB 320 AACAGGAATGGAAGAGAGCAAGTCCAACTACCGAGTCCGTGTCTTACAGATTCTCTGG 379
QY 301 AAGCCAGAAATTTAGATTCTGCTCTGAACTCAAG 336
DB 380 AAGCCAGAAATTTAGATTCTGCTCTGAACTCAAG 415

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RESULT 7
BG529866 755 bp mRNA linear EST 03-APR-2001
LOCUS 602558957F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4696622 5',
DEFINITION mRNA sequence.
ACCESSION BG529866
VERSION BG529866.1 GI:13521403
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 755)
NIH-MGC http://imgc.ncbi.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1524 row: b column: 15

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High quality sequence stop: 727.
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 1. .755
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:469622"
 /tissue_type="embryonal carcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC 61"
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1: SfII (ggccgctggc); Site_2: SfII (ggccattatggc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCGGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

Query Match 100.0%; Score 336; DB 4; Length 755;
 Best Local Similarity 100.0%; Pred. No. 5.1e-83;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGTGCTGAAGTGAAGGGGGCCCC 60
 DB 111 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGTGCTGAAGTGAAGGGGGCCCC 170

QY 61 AAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGGCGCGGACAGAACTTGAAG 120
 DB 171 AAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGGCGCGGACAGAACTTGAAG 230

QY 121 GTCCTCTCTCCAGAGAGAGCGCCCTGGGACAGTGTGGTCTGCTTCCCAACGGC 180
 DB 231 GTCCTCTCTCCAGAGAGAGCGCCCTGGGACAGTGTGGTCTGCTTCCCAACGGC 290

QY 181 TCCTCTCTCCAGAGAGAGCGCCCTGGGACAGTGTGGTCTGCTTCCCAACGGC 240
 DB 291 TCCTCTCTCCAGAGAGAGCGCCCTGGGACAGTGTGGTCTGCTTCCCAACGGC 350

QY 241 AACAGGAATGGAAGAGAGACCAAGTCCAACTACCAAGTCCGCTGTCTACCAAGTCTCTGGG 300
 DB 351 AACAGGAATGGAAGAGAGACCAAGTCCAACTACCAAGTCCGCTGTCTACCAAGTCTCTGGG 410

QY 301 AAGCCAGAAATGTAGATTCTGCCTCTGAACCTCAG 336
 DB 411 AAGCCAGAAATGTAGATTCTGCCTCTGAACCTCAG 446

RESULT 8
 LOCUS BI771266 841 bp mRNA linear EST 25-SEP-2001
 DEFINITION G03054610F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5203922 5', mRNA sequence.

BI771266 GI:15762844
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 841)
 NIH-MGC <http://img.ncbi.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Inyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLAM11511 row: d column: 03
 High quality sequence stop: 840.
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5203922"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_122"
 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT; Site 1: NotI; Site 2: EcoRV (deleted); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."

Query Match 100.0%; Score 336; DB 4; Length 841;
 Best Local Similarity 100.0%; Pred. No. 5.3e-83;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGTGCTGAAGTGAAGGGGGCCCC 60
 DB 150 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGTGCTGAAGTGAAGGGGGCCCC 209

QY 61 AAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGGCGCGGACAGAACTTGAAG 120
 DB 210 AAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGGCGCGGACAGAACTTGAAG 269

QY 121 GTCCTGTCTCCAGAGAGAGCGCCCTGGGACAGTGTGGTCTGCTTCCCAACGGC 180
 DB 270 GTCCTGTCTCCAGAGAGAGCGCCCTGGGACAGTGTGGTCTGCTTCCCAACGGC 329

QY 181 TCCTCTCTTCCGCTGTCCGGATCCAGGATCAGGAGGATTTCCCGTGCCAGGCAATG 240
 DB 330 TCCTCTCTTCCGCTGTCCGGATCCAGGATCAGGAGGATTTCCCGTGCCAGGCAATG 389

QY 241 AACAGGAATGGAAGAGAGACCAAGTCCAACTACCAAGTCCGCTGTCTACCAAGTCTCTGGG 300
 DB 390 AACAGGAATGGAAGAGAGACCAAGTCCAACTACCAAGTCCGCTGTCTACCAAGTCTCTGGG 449

QY 301 AAGCCAGAAATGTAGATTCTGCCTCTGAACCTCAG 336
 DB 450 AAGCCAGAAATGTAGATTCTGCCTCTGAACCTCAG 485

RESULT 9
 LOCUS AY421474 1163 bp DNA linear GSS 17-DEC-2003
 DEFINITION Pan troglodytes AGER gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

AY421474
 ACCESSION AY421474
 VERSION AY421474.1 GI:39748336
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 1 (bases 1 to 1163)
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE
JOURNAL
COMMENT
 This sequence was made by sequencing genomic exons and ordering them based on alignment.
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 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 <1. .>1163
 /gene="AGER"
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ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 5.6e-83;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCAAAACATCAGCCCGGATTGGCGAGCCACTGGTGAAGTGAAGGGGCCCC 60
 Db 15 GCTCAAAACATCAGCCCGGATTGGCGAGCCACTGGTGAAGTGAAGGGGCCCC 74
 QY 61 AAGAAACACCCAGCGGCTGGAAATGGAACCTGAACACAGCCGCGACAGAACTTGGAA 120
 Db 75 AAGAAACACCCAGCGGCTGGAAATGGAACCTGAACACAGCCGCGACAGAACTTGGAA 134
 QY 121 GTCTCTCTCCAGGAGAGAGCCCTGGACAGTGTGCTGTCTTCCCAACGCG 180
 Db 135 GTCTCTCTCCAGGAGAGAGCCCTGGACAGTGTGCTGTCTTCCCAACGCG 194
 QY 181 TCCTCTCTCTCCGCGTGTGGGATCCAGGATGAGGGATTTCCGCTGCGAGCAATG 240
 Db 195 TCCTCTCTCTCCGCGTGTGGGATCCAGGATGAGGGATTTCCGCTGCGAGCAATG 254
 QY 241 ACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 300
 Db 255 ACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 314
 QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAATCAGC 336
 Db 315 AAGCCAGAAATGTAGATTCTGCTCTGAATCAGC 350
RESULT 10
LOCUS
DEFINITION
 AGENCOURT_6767496 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5751524
 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 Homo sapiens (human)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM12784 row: d column: 21
 High quality sequence start: 22
 High quality sequence stop: 630.
FEATURES
 Location/Qualifiers
 1. .1194
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5751524"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_115"
 /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
ORIGIN
 Query Match 100.0%; Score 336; DB 5; Length 1194;
 Best Local Similarity 100.0%; Pred. No. 5.7e-83;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCAAAACATCAGCCCGGATTGGCGAGCCACTGGTGAAGTGAAGGGGCCCC 60
 Db 101 GCTCAAAACATCAGCCCGGATTGGCGAGCCACTGGTGAAGTGAAGGGGCCCC 160
 QY 61 AAGAAACACCCAGCGGCTGGAAATGGAACCTGAACACAGCCGCGACAGAACTTGGAA 120
 Db 161 AAGAAACACCCAGCGGCTGGAAATGGAACCTGAACACAGCCGCGACAGAACTTGGAA 220
 QY 121 GTCTGTCTCCAGGAGAGAGCCCTGGACAGTGTGCTGTCTTCCCAACGCG 180
 Db 221 GTCTGTCTCCAGGAGAGAGCCCTGGACAGTGTGCTGTCTTCCCAACGCG 280
 QY 181 TCCTCTCTCTCCGCGTGTGGGATCCAGGATGAGGGATTTCCGCTGCGAGCAATG 240
 Db 281 TCCTCTCTCTCCGCGTGTGGGATCCAGGATGAGGGATTTCCGCTGCGAGCAATG 340
 QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCTCTGG 300
 Db 341 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACCAAGATTCTCTGG 400
 QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAATCAGC 336
 Db 401 AAGCCAGAAATGTAGATTCTGCTCTGAATCAGC 436

RESULT 11
LOCUS
DEFINITION
 Homo sapiens AGER gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 Homo sapiens (human)
REFERENCE
AUTHORS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1215)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302
 2 (bases 1 to 1215)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 Location/Qualifiers
 1..1215
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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 /gene="AGER"
 /locus_tag="HOM7569"

ORIGIN

Query Match 100.0%; Score 336; DB 9; Length 1215;
 Best Local Similarity 100.0%; Pred. No. 5.7e-83;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACCTGGTCTCAAGTGAAGGGGCCCC 60
 DB 67 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACCTGGTCTCAAGTGAAGGGGCCCC 126

QY 61 AAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAACTTGGAG 120
 DB 127 AAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAACTTGGAG 186

QY 121 GTCTGTCTTCCCGAGGAGGCGCCCTGGGACAGTGTGGCTCGTCTTCCCAACGCG 180
 DB 187 GTCTGTCTTCCCGAGGAGGCGCCCTGGGACAGTGTGGCTCGTCTTCCCAACGCG 246

QY 181 TCCCTCTTCTTCCCGTCTCGGATCCAGGATGAGGGATTTCCGGTCCAGGCAATG 240
 DB 247 TCCCTCTTCTTCCCGTCTCGGATCCAGGATGAGGGATTTCCGGTCCAGGCAATG 306

QY 241 AACAGAAATGGAAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACAGATTCTGGG 300
 DB 307 AACAGAAATGGAAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACAGATTCTGGG 366

QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAATCAGC 336
 DB 367 AAGCCAGAAATGTAGATTCTGCTCTGAATCAGC 402

RESULT 12
 BG506672
 LOCUS 601861271F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4070993 5',
 DEFINITION mRNA sequence.
 ACCESSION BG506672
 VERSION BG506672.1 GI:13468189
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 774)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Cloned through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLC915 row: n column: 18
 High quality sequence stop: 723.
 Location/Qualifiers
 1..774
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4070993"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 77"
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
 SfiI (ggccgctcgcc); Site 2: SfiI (ggccattagcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGAGCGGCACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

FEATURES

source
 Location/Qualifiers
 1..774
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4070993"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 77"
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
 SfiI (ggccgctcgcc); Site 2: SfiI (ggccattagcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGAGCGGCACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 99.5%; Score 334.4; DB 4; Length 774;
 Best Local Similarity 99.7%; Pred. No. 1.5e-82;
 Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACCTGGTCTCAAGTGAAGGGGCCCC 60
 DB 98 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACCTGGTCTCAAGTGAAGGGGCCCC 157

QY 61 AAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAACTTGGAG 120
 DB 158 AAGAAACACACCCAGCGGCTGGAATGGAACCTGAACACAGGCGGACAGAACTTGGAG 217

QY 121 GTCTGTCTTCCCGAGGAGGCGCCCTGGGACAGTGTGGCTCGTCTTCCCAACGCG 180
 DB 218 GTCTGTCTTCCCGAGGAGGCGCCCTGGGACAGTGTGGCTCGTCTTCCCAACGCG 277

QY 181 TCCCTCTTCTTCCCGTCTCGGATCCAGGATGAGGGATTTCCGGTCCAGGCAATG 240
 DB 278 TCCCTCTTCTTCCCGTCTCGGATCCAGGATGAGGGATTTCCGGTCCAGGCAATG 337

QY 241 AACAGAAATGGAAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACAGATTCTGGG 300
 DB 338 AACAGAAATGGAAGAGACCAAGTCCAACTACCGAGTCCGCTGTCTACAGATTCTGGG 397

QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAATCAGC 336
 DB 398 AAGCCAGAAATGTAGATTCTGCTCTGAATCAGC 433

RESULT 13
 BG546024
 LOCUS 602573327F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4701318 5',
 DEFINITION mRNA sequence.
 ACCESSION BG546024
 VERSION BG546024.1 GI:13544689
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 549)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM1536 row: f column: 07
 High quality sequence stop: 544.
 Location/Qualifiers
 1. 549

FEATURES

source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4701318"
 /lab_hosts="DH10B (TI phage-resistant)"
 /clone_lib="NIH_MGC_77"
 /notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcgctcgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCGCATATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 99.0%; Score 332.8; DB 4; Length 549;
 Best Local Similarity 99.4%; Pred. No. 3.8e-82;
 Matches 334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATGGGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 60
 DB |||||
 QY 95 GCTCAAAACATCACAGCCCGGATGGGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 154
 DB |||||
 QY 61 AAGAAACACCCAGCGGCTGGAAATGGAATGAACTGAACACAGCCGGACAGAACTTGGGAAG 120
 DB |||||
 QY 155 AAGAAACACCCAGCGGCTGGAAATGGAATGGAATGGAACACAGCCGGACAGAACTTGGGAAG 214
 DB |||||
 QY 121 GTCTGTCTCCAGGAGAGAGCCCTGGGACAGTGTGGTCTGTCCTTCCCAACGCGC 180
 DB |||||
 QY 215 GTCTGTCTCCAGGAGAGAGCCCTGGGACAGTGTGGTCTGTCCTTCCCAACGCGC 274
 DB |||||
 QY 181 TCCTCTCTCTCCGCTGTGGGATCCAGGATGAGGGATTTCCGGTGCAGGCAATG 240
 DB |||||
 QY 275 TCCTCTCTCTCCGCTGTGGGATCCAGGATGAGGGATTTCCGGTGCAGGCAATG 334
 DB |||||
 QY 241 ACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGGG 300
 DB |||||
 QY 335 ACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGGG 394
 DB |||||
 QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAATCACTCAG 336
 DB |||||
 QY 395 AAGCCAGAAATGTAGATTCTGCTCTGAATCACTCAG 430
 DB |||||

RESULT 14

BG484869

LOCUS BG484869 538 bp mRNA linear EST 21-MAR-2001
 DEFINITION 602505568F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4618816 5', mRNA sequence.

ACCESSION BG484869

VERSION BG484869.1 GI:13417148

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 538)

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM1377 row: h column: 17
 High quality sequence stop: 534.
 Location/Qualifiers
 1. 538

FEATURES

source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4618816"
 /lab_hosts="DH10B (TI phage-resistant)"
 /clone_lib="NIH_MGC_77"
 /notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcgctcgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCGCATATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 98.6%; Score 331.2; DB 4; Length 538;
 Best Local Similarity 99.1%; Pred. No. 1.1e-81;
 Matches 333; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTCAAAACATCACAGCCCGGATGGGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 60
 DB |||||
 QY 99 GCTCAAAACATCACAGCCCGGATGGGAGCCACTGGTCTGAAGTGTAAAGGGGGCCCC 158
 DB |||||
 QY 61 AAGAAACACCCAGCGGCTGGAAATGGAATGGAACACAGCCGGACAGAACTTGGGAAG 120
 DB |||||
 QY 159 AAGAAACACCCAGCGGCTGGAAATGGAATGGAACACAGCCGGACAGAACTTGGGAAG 218
 DB |||||
 QY 121 GTCTGTCTCCAGGAGAGAGCCCTGGGACAGTGTGGTCTGTCCTTCCCAACGCGC 180
 DB |||||
 QY 219 GTCTGTCTCCAGGAGAGAGCCCTGGGACAGTGTGGTCTGTCCTTCCCAACGCGC 278
 DB |||||
 QY 181 TCCTCTCTCTCCGCTGTGGGATCCAGGATGAGGGATTTCCGGTGCAGGCAATG 240
 DB |||||
 QY 279 TCCTCTCTCTCCGCTGTGGGATCCAGGATGAGGGATTTCCGGTGCAGGCAATG 338
 DB |||||
 QY 241 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGGG 300
 DB |||||
 QY 339 AACAGGAATGGAAGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGGG 398
 DB |||||
 QY 301 AAGCCAGAAATGTAGATTCTGCTCTGAATCACTCAG 336
 DB |||||
 QY 399 AAGCCAGAAATGTAGATTCTGCTCTGAATCACTCAG 434
 DB |||||

RESULT 15

BG483796

LOCUS

DEFINITION

602503447F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4617035 5', mRNA sequence.

ACCESSION BG483796

VERSION BG483796.1 GI:13415985

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

BG483796 692 bp mRNA linear EST 21-MAR-2001
 602503447F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4617035 5', mRNA sequence.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 692)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1372 row: n column: 12
High quality sequence stop: 622.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

1. .692
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4617035"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and
3' adaptors used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 96.7%; Score 325; DB 4; Length 692;
Best Local Similarity 99.7%; Pred. No. 6.1e-80;
Matches 336; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 60
DB 79 GCTCAAAACATCACAGCCCGGATTGGCGAGCCACTGGTCTGAAGTGAAGGGGGCCCC 138
QY 61 AAGAAACACCCAGCGGCTGGAATGGAATGAACTGAACACAGCGCGGACAGAGCTTGGAG 120
DB 139 AAGAAACACCCAGCGGCTGGAATGGAATGAACTGAACACAGCGCGGACAGAGCTTGGAG 198
QY 121 GTCTCTGTCTCCCGAGGAGGCCCCCTGGGACAGTGTGGCTCGTGTCTTCCCAACGGC 180
DB 199 GTCTCTGTCTCCCGAGGAGGCCCCCTGGGACAGTGTGGCTCGTGTCTTCCCAACGGC 258
QY 181 TCCCTCTCTCTCCGGCTGTCCGGATCCAGGATGAGGGATTTCCGGTCCAGGCAATG 240
DB 259 TCCCTCTCTCTCCGGCTGTCCGGATCCAGGATGAGGGATTTCCGGTCCAGGCAATG 318
QY 241 AACAGGAATGG-AAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 299
DB 319 AACAGGAATGGAAAGGAGACCAAGTCCAACTACCGAGTCCGTGTCTACAGATTCTCTGG 378
QY 300 GAAGCCAGAAATTTAGATTCTGCCTCTGAACCTCAG 336
DB 379 GAAGCCAGAAATTTAGATTCTGCCTCTGAACCTCAG 415

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Job time : 1334.11 secs

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